

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:28:13 ; Search time 97.25 Seconds
(without alignments)
67.608 Million cell updates/sec

Title: US-10-612-162A-1

Sequence: 1 VVARSMGKEDLIWELL 17

Scoring table: BLOSUM62

Gapor 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 21056922

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%

Listing first 45 summaries

```
Database :
1: Genesegp1.edec04:*
2: genesegp1.980s:*
3: genesegp1.990s:*
4: genesegp2.000s:*
5: genesegp2.001s:*
6: genesegp2.002s:*
7: genesegp2.003s:*
8: genesegp2.004s:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	17	ADG46075	Adg46075 Human CDY
2	86	100.0	200	ADP30379	Adp30379 Human sec
3	86	100.0	320	ADH89432	Adh89432 Human tr
4	86	100.0	371	ADL70790	Adl70790 Transferr
5	86	100.0	539	AAU02980	Aau02980 Angiofem
6	86	100.0	575	ABR83321	AbR83321 Human me
7	86	100.0	643	ABM83778	Abm83778 Human di
8	86	100.0	645	ABM83783	Abm83783 Human di
9	86	100.0	646	AAU02938	Aau02938 Angiofem
10	86	100.0	665	AAU02937	Aau02937 Angiofem
11	86	100.0	679	ABP72820	Abp72820 Human tr
12	86	100.0	679	ADH89360	Adh89360 Human tr
13	86	100.0	679	ADK15869	Adk15869 Mature h
14	86	100.0	679	ADL70732	Adl70732 Human tr
15	86	100.0	679	ADL24413	Adl24413 Human tr
16	86	100.0	696	AAPT0384	AapT0384 Sequence
17	86	100.0	698	AAI12499	Aai12499 Human tr
18	86	100.0	698	AAE64492	Aae64492 Human tr
19	86	100.0	698	AAW54354	Aaw54354 SetoTrans
20	86	100.0	698	AAYS0717	AayS0717 Human ser
21	86	100.0	698	ABP72819	Abp72819 Human tr
22	86	100.0	698	ADd45282	AdD45282 Human P
23	86	100.0	698	ADf74796	AdF74796 Human NOV
24	86	100.0	698	ADf74800	Adf74800 Human NOV
25	86	100.0	698	ADh34559	Adh34559 Human tr

ALIGNMENTS

26	86	100.0	698	8	ADH89359	Adh89359	Human tra
27	86	100.0	698	8	ADH15868	Adh15868	Human tra
28	86	100.0	698	8	ADL70731	Adl70731	Human tra
29	86	100.0	698	8	ADL24412	Adl24412	Human tra
30	86	100.0	698	8	ADP21259	Adp21259	Human tra
31	86	100.0	1074	2	AAW07621	AAw07621	Human tra
32	86	100.0	1410	2	AAW07622	AAw07622	LDLR/TF c
33	86	100.0	1410	6	ABU04319	Abu04319	Human exp
34	86	100.0	1418	4	AAU2831	Aau2831	Human exp
35	86	100.0	1418	6	ABU04138	Abu04138	Human exp
36	76	88.4	685	8	ADL70768	Adl70768	Bovine tr
37	76	88.4	685	8	ADL24462	Adl24462	Bovine tr
38	76	88.4	704	8	ADP21260	Adp21260	Bovine tr
39	75	87.2	676	8	ADL70764	Adl70764	Rabbit tr
40	75	87.2	676	8	ADL24458	Adl24458	Rabbit tr
41	71	82.6	689	3	AAV49270	Aav49270	Lactoferr
42	71	82.6	708	2	AAAR1037	Aaar1037	Dyactulin
43	71	82.6	708	2	AAW09343	Aaw09343	Bovine la
44	71	82.6	708	2	AAW57318	Aaw57318	Bovine la
45	71	82.6	708	2	AAW86022	Aaw86022	Bovine la

26	86	100.0	698	8	ADH89359	Human tra
27	86	100.0	698	8	ADL15668	Human tra
28	86	100.0	698	8	ADL70731	Human tra
29	86	100.0	698	8	ADL24412	Human tra
30	86	100.0	698	8	ADP21259	Human tra
31	86	100.0	1074	2	AAW07621	LDLR/TF C
32	86	100.0	1074	2	AAW07622	LDLR/TF C
33	86	100.0	1410	6	ABU04139	Human exp
34	86	100.0	1418	4	AAU32831	Novel human
35	86	100.0	1418	6	ABU04138	Novel human
36	76	88.4	685	8	ADL70768	Bovine tr
37	76	88.4	685	8	ADL24462	Bovine tr
38	76	88.4	704	8	ADP21260	Bovine tr
39	75	87.2	676	8	ADL70764	Bovine tr
40	75	87.2	676	8	ADL24458	Rabbit tr
41	AA749270	689	3	AAV49270	Lacifer tr	
42	AA71037	689	3	AA71037	Dreacilin.	
43	AAW09343	708	2	AAW09343	Bovine la	
44	AAW57318	708	2	AAW57318	Bovine la	
45	71	82.6	708	2	AAW86022	Bovine la

CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcoholics. The antibodies allow direct detection of CDR in solution,
CC eliminating the need for immobilizing it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDR peptide
CC fragments used in the method of the invention.

CC Sequence 17 AA:

Query Match 100.0%; Score 86; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17
1 VVARSWGKEDLIWELL 17

ADP30379 standard; protein; 200 AA.

ADP30379;

12-AUG-2004 (first entry)

Human secreted protein SEQ ID #1146.

Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide;
cancer; inflammatory; immune; human secreted protein.

Homo sapiens.

WO2004035732-A2.

29-APR-2004.

28-AUG-2003; 2003WO-US026780.

29-AUG-2002; 2002US-0406576P.

29-AUG-2002; 2002US-0406579P.

29-AUG-2002; 2002US-0406585P.

29-AUG-2002; 2002US-0406588P.

29-AUG-2002; 2002US-0406608P.

29-AUG-2002; 2002US-0406611P.

29-AUG-2002; 2002US-0406612P.

29-AUG-2002; 2002US-0406640P.

29-AUG-2002; 2002US-0406642P.

29-AUG-2002; 2002US-0406653P.

29-AUG-2002; 2002US-0406655P.

29-AUG-2002; 2002US-0406666P.

17-SEP-2002; 2002US-0410946P.

17-SEP-2002; 2002US-0410947P.

17-SEP-2002; 2002US-0410948P.

17-SEP-2002; 2002US-0410949P.

17-SEP-2002; 2002US-0410953P.

17-SEP-2002; 2002US-0410957P.

17-SEP-2002; 2002US-0410958P.

17-SEP-2002; 2002US-0410959P.

17-SEP-2002; 2002US-0410960P.

17-SEP-2002; 2002US-0410961P.

17-SEP-2002; 2002US-0411019P.

17-SEP-2002; 2002US-0411022P.

17-SEP-2002; 2002US-0411023P.

17-SEP-2002; 2002US-0411024P.

17-SEP-2002; 2002US-0411032P.

17-SEP-2002; 2002US-0411035P.

17-SEP-2002; 2002US-0411037P.

17-SEP-2002; 2002US-0411041P.

17-SEP-2002; 2002US-0411045P.

17-SEP-2002; 2002US-0411046P.

17-SEP-2002; 2002US-0411048P.

17-SEP-2002; 2002US-0411052P.

17-SEP-2002; 2002US-0411055P.

17-SEP-2002; 2002US-0411073P.

17-SEP-2002; 2002US-0411082P.

17-SEP-2002; 2002US-0411101P.

17-SEP-2002; 2002US-0411111P.

18-APR-2003; 2003US-0463708P.

18-APR-2003; 2003US-0463732P.

18-APR-2003; 2003US-0463732P.

02-MAY-2003; 2003US-0467199P.

02-MAY-2003; 2003US-0467201P.

02-MAY-2003; 2003US-0467203P.

02-MAY-2003; 2003US-0467230P.

19-MAY-2003; 2003US-0471306P.

19-MAY-2003; 2003US-0471336P.

22-MAY-2003; 2003US-0472420P.

22-MAY-2003; 2003US-0472430P.

09-JUN-2003; 2003US-0476609P.

09-JUN-2003; 2003US-0476641P.

08-JUL-2003; 2003US-0485218P.

08-JUL-2003; 2003US-0485223P.

08-JUL-2003; 2003US-0485224P.

08-JUL-2003; 2003US-0485325P.

14-JUL-2003; 2003US-0486446P.

14-JUL-2003; 2003US-0486480P.

15-JUL-2003; 2003US-0486891P.

15-JUL-2003; 2003US-0486960P.

08-AUG-2003; 2003US-0493341P.

08-AUG-2003; 2003US-0493370P.

08-AUG-2003; 2003US-0493373P.

08-AUG-2003; 2003US-0493377P.

(FIVE-) FIVE PRIME THERAPEUTICS INC.

Williams LT, Chu K, Lee B, Hestir K, Beaurang PA, Behrens D,

Halenbeck RF, Huang MM, Kothakota S, Halsehan L, Himmelman T,

Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;

WPI; 2004-348438/32.

New nucleic acid molecule for diagnosing, preventing or treating diseases

such as proliferative (e.g. cancer), inflammatory, immune, metabolic,

genetic, bacterial and viral diseases.

Claim 1; SEQ ID NO 2377; 428bp; English.

The present invention relates to an isolated nucleic acid molecule

encoding a polypeptide which is believed to be cytostatic,

antiinflammatory, immunosuppressive, antibacterial and virucidal. The

composition and methods are useful for diagnosing, preventing and

treating diseases such as proliferative (e.g. cancer), inflammatory,

immune, metabolic, genetic, bacterial and viral diseases. The present

sequence represents a human secreted protein. The present sequence is

available on WIPWEB and is not in the specification.

Sequence 200 AA:

Query Match 100.0%; Score 86; DB 8; Length 200;
Best Local Similarity 100.0%; Pred. No. 4.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17
124 VVARSWGKEDLIWELL 140

ADH89432

ADH89432 standard; protein; 220 AA.

ADH89432;

XX 15-APR-2004 (first entry)
XX Human transferrin fusion protein-related mTF PREX0080 protein SegID76.
XX fusion protein; transferrin protein; glycosylation;
XX antibody variable region; cytosolic; antibacterial; virucide;
XX antiparasitic; immunosuppressive; antiarthritic; gene therapy;
XX septic shock; endotoxic shock; cachexia syndrome; bacterial infection;
XX viral infection; parasitic infection; neoplasm; autoimmune disease;
XX arthritis; graft rejection; PREX0080; mTF.
XX Unidentified.
XX US2003226155-A1.
XX 04-DEC-2003.
XX 10-MAR-2003, 2003US-00384060.
XX 30-AUG-2001; 2001US-015745P.
XX 30-NOV-2001; 2001US-0334059P.
XX 30-AUG-2002; 2002US-00231494.
XX 30-AUG-2002; 2002US-0406977P.
XX (BIOR-) BIOREXIS PHARM CORP.
XX Sadeghi H, Prior CP, Turner A;
XX WPI; 2004-022093/02.
XX N-PSDB; ADH99431.
XX New fusion protein comprising a transferrin protein exhibiting reduced
XX glycosylation fused to at least one antibody variable region, useful for
XX preparing a composition for treating e.g., septic shock, neoplasm or
XX autoimmune disease.
XX Example 2; SEQ ID NO 76; 82pp; English.
XX This invention relates to a novel fusion protein which comprises a
XX transferrin protein exhibiting reduced glycosylation fused to at least
XX one antibody variable region. The invention may be useful for the
XX development of compounds with cytostatic, antibacterial, virucide,
XX antiparasitic, immunosuppressive or antiarthritic activity. In addition,
XX the sequences disclosed may be useful for gene therapy. The fusion
XX protein is useful for preparing a composition for treating a disease or
XX disease symptom in a patient for example septic shock, endotoxic shock,
XX cachexia syndrome associated with bacterial, viral or parasitic
XX infections, neoplasm, autoimmune disease, arthritis or adverse effects
XX associated with treatment for preventing graft rejection. The present
XX sequence is that of a protein which was used in the exemplification of
XX the invention.
XX Sequence 220 AA;
XX
XX Query Match 100.0%; Score 86; DB 8; Length 220;
XX Best Local Similarity 100.0%; Pred. No. 4; 7e-06;
XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 VVARSWGKEDLIWELL 17
XX 183 VVARSWGKEDLIWELL 199
XX
XX RESULT 4
XX ADL70790
XX ID ADL70790 standard; protein; 371 AA.
XX
XX AC ADL70790;
XX
XX 03-JUN-2004 (first entry)
XX
XX Transferrin N-domain protein, SEQ ID 63.
XX
XX DE

XX Immunosuppressive; Haemostatic; Antiallergic; Antisthmatic;
XX Dermatological; Antiinflammatory; Antibacterial; Vasotropic;
XX Nephrotoxic; Neuroprotective; Cytostatic; Cerebroprotective; Vulnerary;
XX Antiparkinsonian; Nocotropic; Cardiant; Antianaemic; Antithrombotic;
XX Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;
XX Tf; transferrin fusion protein; Tf fusion protein.
XX Synthetic.
XX WO2004020588-A2.
XX 11-MAR-2004.
XX 28-AUG-2003; 2003WO-US026779.
XX 30-AUG-2002; 2002US-0406977P.
XX 10-MAR-2003; 2003US-00384060.
XX 09-JUL-2003; 2003US-0485404P.
XX (BIOR-) BIOREXIS PHARM CORP.
XX Prior CP, Turner AJ, Sadeghi H;
XX WPI; 2004-239175/22.
XX N-PSDB; ADL70789.
XX Novel library containing several fusion proteins each of which comprises
XX first transferrin polypeptide fused to at least one second peptide,
XX useful for screening for transferrin fusion protein having the particular
XX activity.
XX Example 13; SEQ ID NO 63; 243pp; English.
XX The present invention relates to a library (I) of modified fusion
XX proteins of transferrin (Tf) and therapeutic proteins with increased
XX serum half-life or serum stability. Preferred fusion proteins include
XX those modified so that the Tf moiety exhibits no or reduced
XX glycosylation, iron binding and/or Tf receptor binding. The transferrin
XX fusion proteins are useful for treating, preventing or ameliorating
XX disorders or diseases of endocrine system, nervous system, immune system,
XX respiratory system, cardiovascular system, diseases and/or disorders
XX relating to cell proliferation, and/or diseases or disorders relating to
XX blood. The modified fusion proteins are useful in diagnosis, prognosis,
XX prevention and/or treatment of autoimmune disorders; diseases and
XX disorders of haematopoietic cells (e.g., leukaemia, neutropenia, anaemia
XX and thrombocytopenia); allergic reactions such as allergic asthma,
XX anaphylaxis, IgE-mediated allergic reactions such as asthma, rhinitis and
XX eczema; inflammatory conditions e.g., inflammation associated with
XX infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,
XX nephritis, Crohn's disease, multiple sclerosis, respiratory disorders
XX (asthma and allergy), gastrointestinal disorders (inflammatory bowel
XX disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders
XX (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative
XX disorders such as Parkinson's disease, Alzheimer's disease), etc. The
XX fusion protein is also useful as an adjuvant to enhance antibacterial or
XX antifungal immune responses, antiparasitic immune responses, etc. The
XX fusion protein is also useful for treating monoclonal gammopathy of
XX undetermined significance (MGUS), Waldenstrom's disease, plasmacytomas,
XX adult respiratory distress syndrome, for stimulating wound repair, for
XX preventing or treating infections of joints, bones, skin, etc. The fusion
XX protein is also useful for treating or preventing thrombosis, myocardial
XX infarction, cancers, thrombocytopenia, sickle cell anaemia,
XX glomerulonephritis, cardiac arrest, edema, pulmonary embolism,
XX atherosclerosis, etc. In an example from the invention, a system of Tf
XX peptide display for generating peptide sequences uses the N-domain of Tf
XX incorporated into the pIII protein and the insertion of random peptides
XX within the Tf scaffold. The present sequence was used to illustrate this
XX example.
XX Sequence 371 AA;
XX
XX Query Match 100.0%; Score 86; DB 8; Length 371;
XX
XX DE

Best Local Similarity 100.0%; Pred. No. 8.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
Db 274 VVARSNGKEDLIWELL 290

RESULT 5
AAU02980

ID AAU02980 standard; protein; 539 AA.

XX AAU02980;

DT 12-SEP-2001 (first entry)

DE Angiotensin converting enzyme (ACEV) splice variant protein #80.

XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW noncardioidic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; atherosclerosis.

XX Homo sapiens.

PN WO200136632-A2.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000WO-IL000766.

XX 17-NOV-1999; 99IL-00132978.

XX 10-DEC-1999; 99IL-00133455.

XX (COMP-) COMPUGEN LTD.

XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;

XX MPI; 2001-336004/35.

XX N-PSDB; AAS06080.

XX Novel alternative splicing variants e.g. variant of angiotensin
PT converting enzyme (ACEV), useful in identifying candidate compounds
PT capable of binding to the variant and to detect anti-variant antibodies.

XX Claim 4; Fig 80; 519pp; English.

XX The sequence represents an angiotensin converting enzyme splice variant
CC (ACEV) polypeptide. The polypeptides of the invention include variants of
CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
CC inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
CC polypeptide receptor 2. The polypeptides and their associated nucleic
CC acids are useful for identification of variant sequences and detection of
CC candidate compounds capable of binding the molecules. The sequences of
CC the invention can be used in the treatment and diagnosis of various
CC disorders including cardiovascular diseases such as arteriosclerosis,
CC myocardial infarction and coronary arterial thrombosis, renal diseases
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
CC immune disorders such as immune complex nephritis, multiple sclerosis,
CC cancer, sarcoidosis, noncardioidic pulmonary granulomatous diseases such
CC as atherosclerosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis

XX Sequence 539 AA;

XX Query Match 100.0%; Score 86; DB 4; Length 539;

Best Local Similarity 100.0%; Pred. No. 1.3e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
Db 143 VVARSNGKEDLIWELL 159

RESULT 6
ABR82321

ID ABR82321 standard; protein; 575 AA.

XX ABR82321;

DT 06-NOV-2003 (first entry)

DE Human metalloprotein (MEPR) polypeptide (Id-7509328CD1).

XX MEPR; metalloprotein; anti-HIV; antiallergic; antiinflammatory; human;
KW antianemic; antiparkinsonian; noctropic; anticonvulsant; cytostatic;
KW antiatherosclerotic; antiasthmatic; immunosuppressive; antithyroid;
KW hepatocarcinoma; dermatological; antidiabetic; nephrotoxic; antigen;
KW thymometric; neuroprotective; osteopathic; antiarthritic; uterine;
KW antiparasitic; antihelminthic; antipsoriatic; ophthalmological; virucide;
KW antirheumatic; haemostatic; antibacterial; protozoacide; fungicide;
KW gene therapy; transgenic.

XX Homo sapiens.

PN WO2003060089-A2.

XX 24-JUL-2003.

XX 14-JAN-2003; 2003WO-US001485.

XX 14-JAN-2002; 2002US-0348769P.

XX 18-JAN-2002; 2002US-0350701P.

XX 19-MAR-2002; 2002US-0366059P.

XX 10-MAY-2002; 2002US-0379907P.

XX (INCY-) INCYTE GENOMICS INC.

XX Kable AE, Griffin JA, Gorvad AE, Becha SD, Richardson TW;

XX Emerling BM, Chien D, Jin P, Chawla NK, Yue H, Khare R, Margulis JP;

XX Tang YF;

XX MPI; 2003-598523/56.

XX N-PSDB; ACP35812.

XX New human metalloproteins and polynucleotides, useful for diagnosing,
PT treating or preventing autoimmune or inflammatory disorders (e.g. AIDS,
PT allergy or anemia), multiple sclerosis, osteoarthritis, cancer or
PT hepatitis.

XX Claim 1; Page 146-148; 153pp; English.

XX The invention relates to novel human metalloproteins (MEPR) and encoding
CC polynucleotides. The human MEPR polypeptides, polynucleotides and
CC modulators are useful for diagnosing, treating or preventing disorders
CC associated with aberrant expression of MEPR, particularly cell
CC proliferative disorders (e.g. arteriosclerosis, atherosclerosis,
CC cirrhosis, hepatitis, paroxysmal nocturnal hemoglobinuria, polycythemia
CC vera, psoriasis, primary thrombocytopenia or cancer), developmental
CC disorders (e.g. renal tubular acidosis, anemia or mental retardation),
CC neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or
CC epilepsy), autoimmune/inflammatory disorders (e.g. AIDS, allergies,
CC asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease,
CC diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout,
CC Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome,
CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
CC bacterial, fungal, parasitic, protozoan or helminthic infections. The
CC polynucleotides encoding MEPR are useful for creating transgenic animals

CC to model human disease. Sequences ABR82316-323 represent the human MEPR
CC polypeptides of the invention
XX
SQ Sequence 575 AA;
Query Match 100.0%; Score 86; DB 6; Length 575;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVARSWGKEDLIWELL 17
DB 147 VVARSWGKEDLIWELL 163
RESULT 7
ABM83778
ID ABM83778 standard; protein; 643 AA.
XX
AC ABM83778;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4027.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dittp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Hartshorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;
PI Mooney EM, Deleagane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX MPI; 2004-329368/30.
DR N-PSDB; ACN42430.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page: 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dittp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dittp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dittp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly

CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 643 AA;
Query Match 100.0%; Score 86; DB 8; Length 643;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVARSWGKEDLIWELL 17
DB 251 VVARSWGKEDLIWELL 267
RESULT 8
ABM83783
ID ABM83783 standard; protein; 645 AA.
XX
AC ABM83783;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4032.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dittp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Hartshorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;
PI Mooney EM, Deleagane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX MPI; 2004-329368/30.
DR N-PSDB; ACN42435.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page: 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dittp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dittp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dittp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

```
XX SQ Sequence 645 AA;
Query Match 100.0%; Score 86; DB 8; Length 645;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVARSNGKEDLIWELL 17
   |||||
Db 217 VVARSNGKEDLIWELL 233

RESULT 9
AAU02938
ID AAU02938 standard; protein; 646 AA.
XX
AC AAU02938;
XX
DT 12-SEP-2001 (first entry)
XX
DE Angiotensin converting enzyme (ACEV) splice variant protein #38.
XX
KM Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KM granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KM platelet-derived endothelial cell growth factor; cardiovascular disease;
KM cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KM vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KM myocardial infarction; coronary arterial thrombosis; renal disease;
KM diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KM multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KM noncarcinoidic pulmonary granulomatous disease; endothelial abnormality;
KM vascular disorder; asbestosis.
XX
OS Homo sapiens.
XX
PN WO200136632-A2.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000MO-IL000766.
XX
PR 17-NOV-1999; 99IL-00132978.
XX
PR 10-DEC-1999; 99IL-00133455.
XX
PA (COMP-) COMPUGEN LTD.
XX
PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;
XX
DR WPI; 2001-336004/35.
XX
DR N-PSDB; AAS06038.
XX
PT Novel alternative splicing variants e.g. variant of angiotensin
PT converting enzyme (ACEV), useful in identifying candidate compounds
PT capable of binding to the variant and to detect anti-variant antibodies.
XX
PS Claim 4; Fig 38; 519pp; English.
XX
XX
The sequence represents an angiotensin converting enzyme splice variant
(ACEV) polypeptide. The polypeptides of the invention include variants of
granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
platelet-derived endothelial cell growth factor, cyclin-dependent kinase
inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
polypeptide receptor 2. The polypeptides and their associated nucleic
acids are useful for identification of variant sequences and detection of
candidate compounds capable of binding the molecules. The sequences of
the invention can be used in the treatment and diagnosis of various
disorders including cardiovascular diseases such as arteriosclerosis,
myocardial infarction and coronary arterial thrombosis, renal diseases
such as diabetic nephropathy, muscular diseases such as hypertrophy,
immune disorders such as immune complex nephritis, multiple sclerosis,
cancer, sarcoidosis, noncarcinoidic pulmonary granulomatous diseases such
as asbestosis and vascular pathologies involving an endothelial
abnormality such as deep vein thrombosis
```

```
XX SQ Sequence 646 AA;
Query Match 100.0%; Score 86; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVARSNGKEDLIWELL 17
   |||||
Db 270 VVARSNGKEDLIWELL 286

RESULT 10
AAU02937
ID AAU02937 standard; protein; 665 AA.
XX
AC AAU02937;
XX
DT 12-SEP-2001 (first entry)
XX
DE Angiotensin converting enzyme (ACEV) splice variant protein #37.
XX
KM Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KM granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KM platelet-derived endothelial cell growth factor; cardiovascular disease;
KM cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KM vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KM myocardial infarction; coronary arterial thrombosis; renal disease;
KM diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KM multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KM noncarcinoidic pulmonary granulomatous disease; endothelial abnormality;
KM vascular disorder; asbestosis.
XX
OS Homo sapiens.
XX
PN WO200136632-A2.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000MO-IL000766.
XX
PR 17-NOV-1999; 99IL-00132978.
XX
PR 10-DEC-1999; 99IL-00133455.
XX
PA (COMP-) COMPUGEN LTD.
XX
PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;
XX
DR WPI; 2001-336004/35.
XX
DR N-PSDB; AAS06037.
XX
PT Novel alternative splicing variants e.g. variant of angiotensin
PT converting enzyme (ACEV), useful in identifying candidate compounds
PT capable of binding to the variant and to detect anti-variant antibodies.
XX
PS Claim 4; Fig 37; 519pp; English.
XX
XX
The sequence represents an angiotensin converting enzyme splice variant
(ACEV) polypeptide. The polypeptides of the invention include variants of
granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
platelet-derived endothelial cell growth factor, cyclin-dependent kinase
inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
polypeptide receptor 2. The polypeptides and their associated nucleic
acids are useful for identification of variant sequences and detection of
candidate compounds capable of binding the molecules. The sequences of
the invention can be used in the treatment and diagnosis of various
disorders including cardiovascular diseases such as arteriosclerosis,
myocardial infarction and coronary arterial thrombosis, renal diseases
such as diabetic nephropathy, muscular diseases such as hypertrophy,
immune disorders such as immune complex nephritis, multiple sclerosis,
cancer, sarcoidosis, noncarcinoidic pulmonary granulomatous diseases such
as asbestosis and vascular pathologies involving an endothelial
abnormality such as deep vein thrombosis
```

```

XX Sequence 665 AA;
SO Query Match 100.0%; Score 86; DB 4; Length 665;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17
DB 270 VVARSWGKEDLIWELL 286

RESULT 11
ABP72820
ID ABP72820 standard; protein; 679 AA.
AC ABP72820;
XX
XX
XX 11-AUG-2003 (first entry)
DE Human transferrin (mature polypeptide).
XX
XX Human; transferrin; neuroprotective; cerebroprotective; vasotropic;
KW antiparkinsonian; nootropic; anti-HIV; antiaesthetic; antiallergic;
KW cytostatic; immunosuppressive; antiatherosclerotic; cardiac;
KW gynaecological; immunostimulant; antinaemic; haemostatic;
KW antiinflammatory; dermatological; antibacterial; virucide; antiparasitic;
KW fungicide; hepatotropic; antirheumatic; antiarthritic; antigout;
KW tranquilizer; vulnery; antidiabetic; nephrotropic; antipyretic;
KW gastrointestinal; gene therapy; transgenic animal.
XX
XX Homo sapiens.
OS

FH Location/Qualifiers
FT Binding-site 63
FT /note= "Iron binding site"
FT Region 94..96
FT /note= "Hinge region"
FT Binding-site 95
FT /note= "Iron binding site"
FT Binding-site 120
FT /note= "Carbonate ion binding site"
FT Binding-site 124
FT /note= "Carbonate ion binding site"
FT Binding-site 126
FT /note= "Carbonate ion binding site"
FT Binding-site 127
FT /note= "Carbonate ion binding site"
FT Binding-site 188
FT /note= "Iron binding site"
FT Region 245..247
FT /note= "Hinge region"
FT Binding-site 249
FT /note= "Iron binding site"
FT Region 316..318
FT /note= "Hinge region"
FT Binding-site 392
FT /note= "Iron binding site"
FT Modified-site 413
FT /note= "N-glycosylated"
FT Region 425..427
FT /note= "Hinge region"
FT Binding-site 426
FT /note= "Iron binding site"
FT Binding-site 452
FT /note= "Carbonate ion binding site"
FT Binding-site 456
FT /note= "Carbonate ion binding site"
FT Binding-site 458
FT /note= "Carbonate ion binding site"
FT Binding-site 459
FT /note= "Carbonate ion binding site"
FT Binding-site 514

```

```

FT Binding-site 517 /note= "Iron binding site"
FT /note= "Iron binding site"
FT Region 581..582
FT /note= "Hinge region"
FT Binding-site 585
FT /note= "Iron binding site"
FT Modified-site 611 /note= "N-glycosylated"
FT Region 652..658
FT /note= "Hinge region"
XX
XX MO2003020746-A1.
XX
XX 13-MAR-2003.
XX
XX 30-AUG-2002; 2002WC-US027637.
XX
XX 30-AUG-2001; 2001US-0315745P.
XX 30-NOV-2001; 2001US-0334059P.
XX
XX (BIOR-) BIOREXIS PHARM CORP.
XX
XX Prior CP;
XX
XX MPI; 2003-332916/31.
XX
XX New fusion protein, useful in the diagnosis and treatment of diseases or
PT disorders relating to the respiratory, cardiovascular and digestive
PT systems, comprises a transferrin protein fused to a therapeutic protein.
XX
XX Disclosure; Page 280-281, 298pp; English.
XX
XX The present sequence is the protein sequence of human transferrin (TF),
CC minus the signal peptide. The invention relates to modified TF fusion
CC proteins comprising at least one therapeutic protein, polypeptide or
CC peptide, in which the TF portion is engineered to extend the serum half-
CC life or bioavailability of the molecule. The modified TF fusion protein
CC preferably comprises a human TF moiety that has been modified to reduce
CC or prevent glycosylation, iron binding and/or transferrin receptor
CC binding, having at least one amino acid substitution, deletion or
CC addition in the hinge region, or at residues Asp-63, Gly-65, Tyr-95, Tyr-
CC 188, Lys-206, His-207, His-249, Asp-392, Tyr-426, Tyr-514, Tyr-517, His-
CC 585, Thr-120, Arg-124, Ala-126, Gly-127, Thr-452, Arg-456, Ala-458 and
CC Gly-459, or a mutation which prevents glycosylation at Asn-413 or Asn-611
CC (all claimed). Nucleic acids encoding such fusion proteins, vectors, host
CC cells and transgenic animals which produce the fusion protein in their
CC serum or milk are also claimed. The modified fusion protein is useful for
CC treating a disease or disease symptom, or for delivering a therapeutic
CC agent complexed to the ferric iron of transferrin to the inside of a cell
CC or across the blood-brain barrier. The modified fusion protein, or a
CC nucleic acid encoding it, can be used in the diagnosis, prognosis,
CC prevention and/or treatment of diseases and/or disorders of the
CC endocrine, nervous, immune, respiratory, cardiovascular, reproductive and
CC digestive systems, diseases and/or disorders relating to the blood or to
CC cell proliferation, inflammatory conditions, and to treat viral, fungal,
CC bacterial or parasitic infection
XX
XX Sequence 679 AA;
SQ
Query Match 100.0%; Score 86; DB 6; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17
DB 251 VVARSWGKEDLIWELL 267

RESULT 12
ADH89360
ID ADH89360 standard; protein; 679 AA.
XX

```

AC ADH89360;
XX
XX 15-APR-2004 (first entry)
XX
DE Human transferrin protein mature amino acid sequence.
XX
XX fusion protein; transferrin protein; glycosylation;
XX antibody variable region; cytostatic; antibacterial; virucide;
XX antiparasitic; immunosuppressive; antiarthritic; gene therapy;
XX septic shock; endotoxic shock; cachexia syndrome; bacterial infection;
XX viral infection; parasitic infection; neoplasm; autoimmune disease;
XX arthritis; graft rejection; human.
XX
XX Homo sapiens.
XX
XX US2003226155-A1.
XX
XX 04-DEC-2003.
XX
XX 10-MAR-2003; 2003US-00384060.
XX
XX 30-AUG-2001; 2001US-0315745P.
XX 30-NOV-2001; 2001US-0334059P.
XX 30-AUG-2002; 2002US-00231494.
XX 30-AUG-2002; 2002US-0406977P.
XX
XX (BIOR-) BIOREXIS PHARM CORP.
XX
XX Sadeghi H, Prior CP, Turner A;
XX
XX WPI, 2004-022093/02.
XX N-PSDB; ADH89358.
XX
XX New fusion protein comprising a transferrin protein exhibiting reduced
XX glycosylation fused to at least one antibody variable region, useful for
XX preparing a composition for treating e.g., septic shock, neoplasm or
XX autoimmune disease.
XX
XX Disclosure; SEQ ID NO 3; 82pp; English.
XX
XX This invention relates to a novel fusion protein which comprises a
XX transferrin protein exhibiting reduced glycosylation fused to at least
XX one antibody variable region. The invention may be useful for the
XX development of compounds with cytostatic, antibacterial, virucide,
XX antiparasitic, immunosuppressive or antiarthritic activity. In addition,
XX the sequences disclosed may be useful for gene therapy. The fusion
XX protein is useful for preparing a composition for treating a disease or
XX disease symptom in a patient for example septic shock, endotoxic shock,
XX cachexia syndrome associated with bacterial, viral or parasitic
XX infections, neoplasm, autoimmune disease, arthritis or adverse effects
XX associated with treatment for preventing graft rejection. The present
XX sequence is that of the mature human transferrin protein which is related
XX to the invention.
XX
XX
SQ Sequence 679 AA;

Query Match 100.0%; Score 86; DB 8; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVARMGKEDLIWELL 17
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 251 VVARMGKEDLIWELL 267

RESULT 13
ADK15869
ID ADK15869 standard; protein; 679 AA.
XX
XX ADK15869;
XX
XX 06-MAY-2004 (first entry)
XX
XX

DE Mature human transferrin (Tf) protein.
XX
XX fusion protein; transferrin; Tf; beta-interferon; beta-IFN;
XX glucagons-like peptide; GLP-1; erythropoietin mimetic peptide; EMP1,
XX T-20; soluble toxin receptor; epitope tagging; human.
XX
XX Homo sapiens.
XX
XX US2003221201-A1.
XX
XX 27-NOV-2003.
XX
XX 04-MAR-2003; 2003US-00378094.
XX
XX 30-AUG-2001; 2001US-0315745P.
XX 30-NOV-2001; 2001US-0334059P.
XX 30-AUG-2002; 2002US-00231494.
XX 30-AUG-2002; 2002US-0406977P.
XX
XX (BIOR-) BIOREXIS PHARM CORP.
XX
XX Prior CP, Lai C, Sadeghi H, Turner A;
XX
XX WPI, 2004-010899/01.
XX
XX New fusion protein comprising a modified transferrin (Tf) protein fused
XX to a therapeutic protein or peptide, useful for epitope tagging.
XX
XX Example 5; SEQ ID NO 3; 70pp; English.
XX
XX The invention comprises a fusion protein that contains a modified
XX transferrin (Tf) protein fused to a therapeutic protein/peptide (e.g.,
XX beta-interferon - IFN, glucagons-like peptide - GLP-1, erythropoietin
XX mimetic peptide - EMP1, T-20 and soluble toxin receptor). The fusion
XX protein of the invention is useful for epitope tagging. The present amino
XX acid sequence represents the mature human Tf protein.
XX
XX
SQ Sequence 679 AA;

Query Match 100.0%; Score 86; DB 8; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VVARMGKEDLIWELL 17
| | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | | | | | | | |
Db 251 VVARMGKEDLIWELL 267

RESULT 14
ADL70732
ID ADL70732 standard; protein; 679 AA.
XX
XX ADL70732;
XX
XX 03-JUN-2004 (first entry)
XX
XX Human transferrin, Tf, mature protein SEQ ID 3.
XX
XX
XX Immunosuppressive; Haemostatic; Antiallergic; Antiasthmatic;
XX Dermatological; Antiinflammatory; Antibacterial; Vasoregic;
XX Nephrotoxic; Neuroprotective; Cytostatic; Cerebroprotective; Vlnary;
XX Antiparkinsonian; Neurotropic; Cardiant; Antianemic; Antiatherosclerotic;
XX Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;
XX Tf; transferrin fusion protein; Tf fusion protein; human.
XX
XX
XX Homo sapiens.
XX
XX WO2004020588-A2.
XX
XX 11-MAR-2004.
XX
XX 28-AUG-2003; 2003WO-US026779.
XX
XX

PR 30-AUG-2002; 2002US-0406977P.
PR 10-MAR-2003; 2003US-00384060.
PR 09-JUL-2003; 2003US-0485404P.
XX
XX
XX (BIOR-) BIOREXIS PHARM CORP.
PI Prior CP, Turner AJ, Sadeghi H,
DR WPI, 2004-239175/22.
DR N-PSDB; ADL70730.
XX
XX Novel library containing several fusion proteins each of which comprises
PT first transferrin polypeptide fused to at least one second peptide,
PT useful for screening for transferrin fusion protein having the particular
PT activity.
XX
XX
PS Claim 44; SEQ ID NO 3; 243pp; English.
XX
XX The present invention relates to a library (I) of modified fusion
CC proteins of transferrin (Tf) and therapeutic proteins with increased
CC serum half-life or serum stability. Preferred fusion proteins include
CC those modified so that the Tf moiety exhibits no or reduced
CC glycosylation, iron binding and/or Tf receptor binding. The transferrin
CC fusion proteins are useful for treating, preventing or ameliorating
CC disorders or diseases of endocrine system, nervous system, immune system,
CC respiratory system, cardiovascular system, diseases and/or disorders
CC relating to cell proliferation, and/or diseases or disorders relating to
CC blood. The modified fusion proteins are useful in diagnosis, prognosis,
CC prevention and/or treatment of autoimmune disorders; diseases and
CC disorders of hematopoietic cells (e.g., leukopenia, neutropenia, anaemia
CC and thrombocytopenia); allergic reactions such as allergic asthma,
CC anaphylaxis, IgE-mediated allergic reactions such as asthma, rhinitis and
CC eczema; inflammatory conditions e.g., inflammation associated with
CC infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,
CC neutritis, Crohn's disease, multiple sclerosis, respiratory disorders
CC (asthma and allergy), gastrointestinal disorders (inflammatory bowel
CC disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders
CC (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative
CC disorders such as Parkinson's disease, Alzheimer's disease), etc. The
CC fusion protein is also useful as an adjuvant to enhance antibacterial or
CC antifungal immune responses, antiparasitic immune responses, etc. The
CC fusion protein is also useful for treating monoclonal gammopathy of
CC undetermined significance (MGUS), Waldenstrom's disease, plasmacytomas,
CC adult respiratory distress syndrome, for stimulating wound repair, for
CC preventing or treating infections of joints, bones, skin, etc. The fusion
CC protein is also useful for treating or preventing thrombosis, myocardial
CC infarction, cancers, thrombocytopenia, sickle cell anaemia,
CC glomerulonephritis, cardiac arrest, edema, pulmonary embolism,
CC atherosclerosis, etc. The present sequence is human Tf mature protein,
CC used to make the modified Tf fusion proteins of the invention.
XX
SQ Sequence 679 AA;
Query Match 100.0%; Score 86; DB 8; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVARSWGKEDLIWELL 17
DB 251 VVARSWGKEDLIWELL 267
RESULT 15
ADL24413
ID ADL24413 standard; protein; 679 AA.
XX
XX ADL24413,
AC
XX
XX
DT 03-JUN-2004 (first entry)
XX
XX Human transferrin protein #2.
DE
XX
XX human; transferrin; oral delivery; glycosylation; cancer;

KW cardiovascular disease; gastrointestinal disease;
KW neurodegenerative disease; inflammatory disease; autoimmune disease;
KW diabetes; respiratory disease; multiple sclerosis; metabolic disease.
XX
XX Homo sapiens.
OS
XX
XX WO2004019872-A2.
PN
XX 11-MAR-2004.
PD
XX
XX 28-AUG-2003; 2003WO-US026778.
PF
XX
XX 30-AUG-2002; 2002US-0406977P.
PR 04-MAR-2003; 2003US-00378094.
PR 08-APR-2003; 2003US-0460829P.
XX
XX (BIOR-) BIOREXIS PHARM CORP.
PA
XX
XX
PI Prior CP, Sadeghi H, Turner A;
DR WPI, 2004-239108/22.
XX
XX
XX Pharmaceutical composition useful for treating diabetes, obesity,
PT multiple sclerosis, comprising transferrin protein exhibiting reduced
PT glycosylation and fused to therapeutic protein or peptide.
XX
XX disclosure; Page 325-327; 356pp; English.
PS
XX
XX The present invention relates to a pharmaceutical composition formulated
CC for oral, nasal or pulmonary delivery, comprising a transferrin (Tf)
CC protein exhibiting reduced glycosylation and fused to a therapeutic
CC protein or peptide. The composition is effective to treat a human
CC disease, preferably chronic human disease. The chronic disease is chosen
CC from viral disease, cancer, metabolic disease, obesity, autoimmune
CC disease, inflammatory disease, allergy, graft-vs.-host disease, systemic
CC microbial infection, anaemia, cardiovascular disease, neurodegenerative
CC disease, disorder of haematopoietic cells, diseases of the endocrine
CC system or reproductive systems, gastrointestinal disease, respiratory
CC disease, diabetes and multiple sclerosis. The present sequence is a
XX polypeptide shown in the exemplification of the invention.
SQ Sequence 679 AA;
Query Match 100.0%; Score 86; DB 8; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VVARSWGKEDLIWELL 17
DB 251 VVARSWGKEDLIWELL 267
Search completed: November 1, 2005, 12:48:51
Job time : 100.25 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: November 1, 2005, 12:37:09 ; Search time 25 Seconds
(without alignments)
50.761 Million cell updates/sec

Title: US-10-612-162A-1

Sequence: 1 VVARSNGKEDLIWELL 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
- 4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
- 5: /cgn2_6/prodata/1/1aa/6CTUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	# Match	Query Length	DB ID	Description
1	86	100.0	696	5262177-4	Patent No. 5262177
2	86	100.0	696	5262177-4	Patent No. 5262177
3	86	100.0	698	US-08-175-158A-2	Sequence 2, Appl
4	86	100.0	698	US-09-439-740-2	Sequence 2, Appl
5	86	100.0	1074	US-08-470-058-2	Sequence 2, Appl
6	86	100.0	1074	US-09-037-188-2	Sequence 2, Appl
7	86	100.0	1074	US-09-285-310-2	Sequence 2, Appl
8	86	100.0	1410	US-08-470-058-4	Sequence 4, Appl
9	86	100.0	1410	US-09-037-188-4	Sequence 4, Appl
10	86	100.0	1410	US-09-285-310-4	Sequence 4, Appl
11	71	82.6	708	US-08-145-681-4	Sequence 4, Appl
12	71	82.6	708	US-08-453-703-4	Sequence 4, Appl
13	71	82.6	708	US-08-456-106-4	Sequence 4, Appl
14	71	82.6	708	US-08-456-108-4	Sequence 4, Appl
15	71	82.6	708	US-09-265-577-4	Sequence 4, Appl
16	71	82.6	708	US-09-633-739-4	Sequence 4, Appl
17	67	77.9	697	US-09-724-864-54	Sequence 5, Appl
18	66	76.7	694	US-08-724-586-2	Sequence 2, Appl
19	66	76.7	694	US-09-421-632-2	Sequence 2, Appl
20	66	76.7	705	US-09-332-190-2	Sequence 2, Appl
21	66	76.7	705	US-08-655-640-2	Sequence 2, Appl
22	66	76.7	708	US-08-655-640-4	Sequence 2, Appl
23	66	76.7	709	US-08-154-019-2	Sequence 2, Appl
24	66	76.7	709	US-08-461-333-2	Sequence 2, Appl
25	66	76.7	709	US-08-464-167-2	Sequence 2, Appl
26	66	76.7	709	US-09-158-313-2	Sequence 2, Appl
27	66	76.7	709	US-08-476-798-2	Sequence 2, Appl

28	66	76.7	711	1	US-08-145-681-2	Sequence 2, Appl
29	66	76.7	711	1	US-08-250-308-2	Sequence 2, Appl
30	66	76.7	711	1	US-08-154-013-4	Sequence 4, Appl
31	66	76.7	711	1	US-08-461-333-4	Sequence 4, Appl
32	66	76.7	711	1	US-08-453-703-2	Sequence 2, Appl
33	66	76.7	711	2	US-08-456-106-2	Sequence 2, Appl
34	66	76.7	711	3	US-08-464-167-4	Sequence 4, Appl
35	66	76.7	711	3	US-09-158-313-4	Sequence 4, Appl
36	66	76.7	711	3	US-08-456-108-2	Sequence 2, Appl
37	66	76.7	711	3	US-08-476-798-4	Sequence 4, Appl
38	66	76.7	711	3	US-09-265-577-2	Sequence 2, Appl
39	66	76.7	711	4	US-09-633-739-2	Sequence 2, Appl
40	66	76.7	711	5	PCT-US93-03614-2	Sequence 2, Appl
41	65	75.6	703	1	US-08-145-681-6	Sequence 6, Appl
42	65	75.6	703	1	US-08-453-703-6	Sequence 6, Appl
43	65	75.6	703	2	US-08-456-106-6	Sequence 6, Appl
44	65	75.6	703	3	US-08-456-108-6	Sequence 6, Appl
45	65	75.6	703	3	US-09-265-577-6	Sequence 6, Appl

ALIGNMENTS

```
RESULT 1
5262177-4
; Patent No. 5262177
; APPLICANT: BROWN, J OSEPH P.; ESTIN, CHARLES D.; PLOWMAN, GREGORY
; D.; HELLSTROM, KARL E.; ROSE, TIMOTHY M.; HELLSTROM, INGEGERD;
; PURCHIO, ANTHONY F.; HU, SHIU-LOK; PENNATHUR, SRIDHAR
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 827,313
; FILING DATE: 07-FEB-1986
; SEQ ID NO:4
; LENGTH: 696
5262177-4
; Patent No. 5262177
; APPLICANT: BROWN, J OSEPH P.; ESTIN, CHARLES D.; PLOWMAN, GREGORY
; D.; HELLSTROM, KARL E.; ROSE, TIMOTHY M.; HELLSTROM, INGEGERD;
; PURCHIO, ANTHONY F.; HU, SHIU-LOK; PENNATHUR, SRIDHAR
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 827,313
; FILING DATE: 07-FEB-1986
; SEQ ID NO:4
; LENGTH: 696
Query Match          100.0%; Score 86; DB 6; Length 696;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 VVARSNGKEDLIWELL 17
      |||||
Db      270 VVARSNGKEDLIWELL 286
RESULT 2
5262177-4
; Patent No. 5262177
; APPLICANT: BROWN, J OSEPH P.; ESTIN, CHARLES D.; PLOWMAN, GREGORY
; D.; HELLSTROM, KARL E.; ROSE, TIMOTHY M.; HELLSTROM, INGEGERD;
; PURCHIO, ANTHONY F.; HU, SHIU-LOK; PENNATHUR, SRIDHAR
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 827,313
; FILING DATE: 07-FEB-1986
; SEQ ID NO:4
; LENGTH: 696
Query Match          100.0%; Score 86; DB 6; Length 696;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

	QY	1 VVARSMGKEDLIWELL	17
Dd		270 VVARSMGKEDLIWELL	286

```

1      RESULT 3
2      US-08-175-158A-2
3      Sequence 2, Application US/08175158A
4      Patent No. 5986067
5      GENERAL INFORMATION:
6      APPLICANT: FUNK, Walter D.
7      APPLICANT: MACGILLIVRAY, Ross T.A.
8      APPLICANT: MASON, Anne B.
9      APPLICANT: WOODWORTH, Robert C.
10     TITLE OF INVENTION: RECOMBINANT TRANSFERRIN, TRANSFERRIN HALF-
11     NUMBER OF SEQUENCES: 7
12     CORRESPONDENCE ADDRESS:
13     ADDRESSEE: LAHIVE & COCKFIELD
14     STREET: 60 State Street, suite 510
15     CITY: Boston
16     STATE: Massachusetts
17     COUNTRY: USA
18     ZIP: 02109
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: Floppy disk
21     COMPUTER: IBM PC compatible
22     OPERATING SYSTEM: PC-DOS/MS-DOS
23     SOFTWARE: ASCII text
24     CURRENT APPLICATION DATA:
25     APPLICATION NUMBER: US/08/175,158A
26     FILING DATE: 28-DEC-1993
27     CLASSIFICATION: 530
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: US 07/832,029
30     FILING DATE: 06-FEB-1992
31     ATTORNEY/AGENT INFORMATION:
32     NAME: DeConti, Giulio A.
33     REGISTRATION NUMBER: 31,503
34     REFERENCE/DOCKET NUMBER: UVI-005CP2
35     TELECOMMUNICATION INFORMATION:
36     TELEPHONE: (617) 227-7400
37     TELEFAX: (617) 227-5941
38     INFORMATION FOR SEQ ID NO: 2:
39     SEQUENCE CHARACTERISTICS:
40     LENGTH: 698 amino acids
41     TYPE: amino acid
42     TOPOLOGY: linear
43     MOLECULE TYPE: protein
44     US-08-175-158A-2

```

```

Query Match          100.0% ; Score 86 ; DB 2 ; Length 698 ;
Best Local Similarity 100.0% ; Pred. No. 1.5e-06 ;
Matches 17 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;

QY          1 VVARSMGKEDLIWELL 17
             |||||
Db           270 VVARSMGKEDLIWELL 286

RESULT 4
US-09-439-740-2
; Sequence 2, Application US/09439740
; Patent No. 6825037
; GENERAL INFORMATION:
; APPLICANT: FUNK, Walter D.
; APPLICANT: MAGGILLIVRAY, Ross T. A.
; APPLICANT: MASON, Anne B.
; APPLICANT: WOODWORTH, Robert C.
; TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
; TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF
; NUMBER OF SEQUENCES: 7

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/439,740
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/175,158
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: UVI-005CFP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 698 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

```

Query Match	100.0%	Score 86	DB 4	Length 698
Best Local Similarity	100.0%	Pred. No.	1.5e-06	
Matches	17	Conservative	0	Mismatches 0; Indels 0; Gaps 0
Oy	1	VVARSWGKEDLIWELL	17	
Db	270	VVARSWGKEDLIWELL	286	

RESULT 5
 US-08-470-058-2
 Sequence 2, Application US/08470058
 Patent No. 5817789
 GENERAL INFORMATION:
 APPLICANT: Heartlein, Michael W.
 APPLICANT: Lemont, Jeffrey F.
 TITLE OF INVENTION: Chimeric Proteins For Use in Transport
 TITLE OF INVENTION: of a Selected Substance Into Cells
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02173
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,058
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: TK193-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-2

Query Match 100.0%; Score 86; DB 2; Length 1074;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
|||||
646 VVARSMGKEDLIWELL 662

Db 646 VVARSMGKEDLIWELL 662

RESULT 6
US-09-037-188-2
Sequence 2, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-2

Query Match 100.0%; Score 86; DB 3; Length 1074;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
|||||
646 VVARSMGKEDLIWELL 662

Db 646 VVARSMGKEDLIWELL 662

RESULT 7
US-09-285-310-2
Sequence 2, Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-2

Query Match 100.0%; Score 86; DB 3; Length 1074;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
|||||
646 VVARSMGKEDLIWELL 662

Db 646 VVARSMGKEDLIWELL 662

RESULT 8
US-08-470-058-4
Sequence 4, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
of a Selected Substance into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millicia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA

ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-4

Query Match 100.0%; Score 86; DB 2; Length 1410;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17
DB 982 VVARSWGKEDLIWELL 998

RESULT 9
US-09-037-188-4
Sequence 4, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-4

Query Match 100.0%; Score 86; DB 3; Length 1410;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17
DB 982 VVARSWGKEDLIWELL 998

RESULT 10
US-09-285-310-4
Sequence 4, Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-4

Query Match 100.0%; Score 86; DB 3; Length 1410;
Best Local Similarity 100.0%; Pred. No. 3.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17
DB 982 VVARSWGKEDLIWELL 998

RESULT 11
US-08-145-681-4
Sequence 4, Application US/08145681

Patent No. 5571691
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Heaton, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
TITLE OF INVENTION: Various Organisms
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Baker & Botts, L.L.P.
STREET: 910 Louisiana St
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,681
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McGregor, Martin L.
REGISTRATION NUMBER: 29,329
REFERENCE/DOCKET NUMBER: 19928-0125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/229/1874
TELEFAX: 713/229/1522
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bos taurus
US-08-145-681-4

Query Match 82.6%; Score 71; DB 1; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.0006;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
DB 274 VVARSYDGKEDLIWKL 290

RESULT 12
US-08-453-703-4
Sequence 4, Application US/08453703
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Heaton, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,703
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bos taurus
US-08-453-703-4

Query Match 82.6%; Score 71; DB 1; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.0006;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
DB 274 VVARSYDGKEDLIWKL 290

RESULT 13
US-08-456-106-4
Sequence 4, Application US/08456106
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Heaton, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,106
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993

ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halliwin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bos taurus
US-08-456-106-4

Query Match 82.6%; Score 71; DB 2; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.0006;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VVARSWGKEDLIWELL 17
||||:|||||:
Db 274 VVARSVDGKEDLIWKL 290

RESULT 14
US-08-456-108-4
Sequence 4, Application US/08456108
Patent No. 6100054
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cdna Sequences in
TITLE OF INVENTION: Various Organisms
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,108
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halliwin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 708 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bos taurus
US-08-456-108-4

Query Match 82.6%; Score 71; DB 3; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.0006;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VVARSWGKEDLIWELL 17
||||:|||||:
Db 274 VVARSVDGKEDLIWKL 290

RESULT 15
US-09-265-577-4
Sequence 4, Application US/09265577
Patent No. 6228614
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT LACTOFERRIN
TITLE OF INVENTION: AND LACTOFERRIN POLYPEPTIDES USING CDNA SEQUENCES IN VARIOUS
TITLE OF INVENTION: ORGANISMS
FILE REFERENCE: 01380023US01
CURRENT APPLICATION NUMBER: US/09/265,577
CURRENT FILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 708
TYPE: PRT
ORGANISM: Bos taurus
US-09-265-577-4

Query Match 82.6%; Score 71; DB 3; Length 708;
Best Local Similarity 82.4%; Pred. No. 0.0006;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VVARSWGKEDLIWELL 17
||||:|||||:
Db 274 VVARSVDGKEDLIWKL 290

Search completed: November 1, 2005, 12:57:29
Job time : 26 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:54:52, Search time 86 Seconds

(without alignments)
82,636 Million cell updates/sec

Title: US-10-612-162a-1

Sequence: 86
1 VVARSNGKEDLIWELL 17

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 1865214

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	17	US-10-612-162-1	Sequence 1, Appli
2	86	100.0	220	US-10-384-060-76	Sequence 76, Appli
3	86	100.0	679	US-10-378-094-3	Sequence 3, Appli
4	86	100.0	679	US-10-384-060-3	Sequence 3, Appli
5	86	100.0	679	US-10-231-494-3	Sequence 3, Appli
6	86	100.0	679	US-10-429-482-4	Sequence 4, Appli
7	86	100.0	679	US-10-429-497-4	Sequence 4, Appli
8	86	100.0	679	US-10-429-515-4	Sequence 4, Appli
9	86	100.0	679	US-10-429-598-4	Sequence 4, Appli
10	86	100.0	679	US-10-429-635-4	Sequence 4, Appli
11	86	100.0	679	US-10-429-653-4	Sequence 4, Appli

12	86	100.0	679	US-10-429-659-4	Sequence 4, Appli
13	86	100.0	679	US-10-429-661-4	Sequence 4, Appli
14	86	100.0	679	US-10-429-660-4	Sequence 4, Appli
15	86	100.0	679	US-10-429-662-4	Sequence 4, Appli
16	86	100.0	679	US-10-429-655-4	Sequence 4, Appli
17	86	100.0	679	US-10-429-654-4	Sequence 4, Appli
18	86	100.0	698	US-09-935-642-6	Sequence 6, Appli
19	86	100.0	698	US-10-378-094-2	Sequence 2, Appli
20	86	100.0	698	US-10-384-060-2	Sequence 2, Appli
21	86	100.0	698	US-10-231-494-2	Sequence 2, Appli
22	86	100.0	698	US-10-383-201-10	Sequence 10, Appli
23	86	100.0	698	US-10-383-201-14	Sequence 14, Appli
24	86	100.0	698	US-10-887-711-2	Sequence 2, Appli
25	86	100.0	698	US-10-513-523-3	Sequence 3, Appli
26	86	100.0	1074	US-09-753-385-2	Sequence 2, Appli
27	86	100.0	1410	US-09-753-385-4	Sequence 2, Appli
28	86	100.0	1410	US-10-473-127-805	Sequence 805, App
29	86	100.0	1418	US-10-473-127-804	Sequence 804, App
30	76	88.4	704	US-10-513-523-4	Sequence 8, Appli
31	71	82.6	708	US-10-169-297-8	Sequence 8, Appli
32	71	82.6	708	US-10-620-256-4	Sequence 4, Appli
33	69	80.2	708	US-10-513-523-2	Sequence 2, Appli
34	69	80.2	22	US-10-801-990-183	Sequence 183, App
35	66	76.7	100	US-09-864-408A-5324	Sequence 5324, Ap
36	66	76.7	333	US-10-408-765A-241	Sequence 241, App
37	66	76.7	359	US-10-169-297-49	Sequence 49, Appli
38	66	76.7	690	US-10-076-816-4	Sequence 4, Appli
39	66	76.7	690	US-10-077-381-4	Sequence 4, Appli
40	66	76.7	690	US-10-639-835-4	Sequence 4, Appli
41	66	76.7	694	US-10-023-056-2	Sequence 2, Appli
42	66	76.7	695	US-10-316-253-273	Sequence 273, App
43	66	76.7	698	US-10-316-253-275	Sequence 275, App
44	66	76.7	698	US-10-205-331-55	Sequence 55, Appli
45	66	76.7	709	US-10-170-221-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-10-612-162-1
; Sequence 1, Application US/10612162
; Publication No. US20040014145A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
; FILE REFERENCE: 2002/8001
; CURRENT APPLICATION NUMBER: US/10/612,162
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-162-1

Query Match 100.0%; Score 86; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
| | | | | | | | | | | | | | | | | |
DB 1 VVARSNGKEDLIWELL 17

RESULT 2
US-10-384-060-76

Sequence 76, Application US/10384060
Publication No. US20030226155A1
GENERAL INFORMATION:
APPLICANT: SADEGH, Homayoun
APPLICANT: PRIOR, Christopher P.
TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
FILE REFERENCE: 54710-5004-US
CURRENT APPLICATION NUMBER: US/10/384,060
CURRENT FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US 10/231,494
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/334,059
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/315,745
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/406,977
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.2
SEQ ID NO 76
LENGTH: 220
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: mtf sequence in PREX0080
US-10-384-060-76

Query Match 100.0%; Score 86; DB 15; Length 220;
Best Local Similarity 100.0%; Pred. No. 2.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
|||||

Db 183 VVARSNGKEDLIWELL 199

RESULT 3
US-10-378-094-3
Sequence 3, Application US/10378094
Publication No. US20030221201A1
GENERAL INFORMATION:
APPLICANT: PRIOR, Christopher P.
APPLICANT: LAI, Char-Huei
APPLICANT: SADEGH, Homayoun
APPLICANT: TURNER, Andrew
TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
FILE REFERENCE: 54710-5001-01-US
CURRENT APPLICATION NUMBER: US/10/378,094
CURRENT FILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: US 10/231,494
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/334,059
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/315,745
PRIOR FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: Mature Transferrin Protein
US-10-378-094-3

Query Match 100.0%; Score 86; DB 15; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
|||||

Db 251 VVARSNGKEDLIWELL 267

RESULT 4
US-10-384-060-3
Sequence 3, Application US/10384060
Publication No. US20030226155A1
GENERAL INFORMATION:
APPLICANT: SADEGH, Homayoun
APPLICANT: PRIOR, Christopher P.
TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
FILE REFERENCE: 54710-5004-US
CURRENT APPLICATION NUMBER: US/10/384,060
CURRENT FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US 10/231,494
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/334,059
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/315,745
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/406,977
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: Mature Transferrin Protein
US-10-384-060-3

Query Match 100.0%; Score 86; DB 15; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
|||||

Db 251 VVARSNGKEDLIWELL 267

RESULT 5
US-10-231-494-3
Sequence 3, Application US/10231494
Publication No. US20040023334A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
TITLE OF INVENTION: Modified Transferrin Fusion Proteins
FILE REFERENCE: 54710-5001-US
CURRENT APPLICATION NUMBER: US/10/231,494
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/315,745
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/334,059
PRIOR FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Mature transferrin protein
US-10-231-494-3

Query Match 100.0%; Score 86; DB 15; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
|||||

Db 251 VVARSMGKEDLIWELL 267

RESULT 6
US-10-429-482-4

; Sequence 4, Application US/10429482
; Publication No. US20040219097A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For The Diagnosis, Imaging and Treatment Of Tu
; FILE REFERENCE: 2537.000001
; CURRENT APPLICATION NUMBER: US/10/429,482
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-482-4

Query Match 100.0%; Score 86; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 9,6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 251 VVARSMGKEDLIWELL 267

RESULT 7
US-10-429-497-4

; Sequence 4, Application US/10429497
; Publication No. US20040219098A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For The Treatment Of Tumors
; FILE REFERENCE: 2537.000006
; CURRENT APPLICATION NUMBER: US/10/429,497
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-497-4

Query Match 100.0%; Score 86; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 9,6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 251 VVARSMGKEDLIWELL 267

RESULT 8
US-10-429-515-4

; Sequence 4, Application US/10429515
; Publication No. US20040219099A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For The Treatment Of Tumors
; FILE REFERENCE: 2537.000005
; CURRENT APPLICATION NUMBER: US/10/429,515
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-429-515-4

Query Match 100.0%; Score 86; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 9,6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 251 VVARSMGKEDLIWELL 267

RESULT 9
US-10-429-598-4

; Sequence 4, Application US/10429598
; Publication No. US20040219100A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For The Treatment Of Tumors
; FILE REFERENCE: 2537.000003
; CURRENT APPLICATION NUMBER: US/10/429,598
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-598-4

Query Match 100.0%; Score 86; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 9,6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 251 VVARSMGKEDLIWELL 267

RESULT 10
US-10-429-635-4

; Sequence 4, Application US/10429635
; Publication No. US20040219101A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For Treatment Of Tumors
; FILE REFERENCE: 2537.000007
; CURRENT APPLICATION NUMBER: US/10/429,635
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-635-4

Query Match 100.0%; Score 86; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 9,6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 251 VVARSMGKEDLIWELL 267

RESULT 11
US-10-429-653-4

; Sequence 4, Application US/10429653
; Publication No. US20040219102A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Compositions For Drug Delivery
; FILE REFERENCE: 2537.000009

```
; CURRENT APPLICATION NUMBER: US/10/429,653
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-653-4
```

```
Query Match          100.0%; Score 86; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VVARSMSGKEDLIWELL 17
         |||
Db       251 VVARSMSGKEDLIWELL 267
```

```
RESULT 12
US-10-429-659-4
; Sequence 4, Application US/10429659
; Publication No. US20040219103A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods Useful For The Diagnosis, Imaging and Treatment Of Tumors
; FILE REFERENCE: 2537.000004
; CURRENT APPLICATION NUMBER: US/10/429,659
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-659-4
```

```
Query Match          100.0%; Score 86; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VVARSMSGKEDLIWELL 17
         |||
Db       251 VVARSMSGKEDLIWELL 267
```

```
RESULT 13
US-10-429-661-4
; Sequence 4, Application US/10429661
; Publication No. US20040219104A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For Treatment Of Tumors
; FILE REFERENCE: 2537.000008
; CURRENT APPLICATION NUMBER: US/10/429,661
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-661-4
```

```
Query Match          100.0%; Score 86; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VVARSMSGKEDLIWELL 17
         |||
Db       251 VVARSMSGKEDLIWELL 267
```

```
RESULT 14
US-10-429-660-4
; Sequence 4, Application US/10429660
; Publication No. US20040220084A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For Nucleic Acid Delivery
; FILE REFERENCE: 2537.000012
; CURRENT APPLICATION NUMBER: US/10/429,660
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-660-4
```

```
Query Match          100.0%; Score 86; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VVARSMSGKEDLIWELL 17
         |||
Db       251 VVARSMSGKEDLIWELL 267
```

```
RESULT 15
US-10-429-662-4
; Sequence 4, Application US/10429662
; Publication No. US20040220085A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Compositions For Nucleic Acid Delivery
; FILE REFERENCE: 2537.000010
; CURRENT APPLICATION NUMBER: US/10/429,662
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-662-4
```

```
Query Match          100.0%; Score 86; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 9.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 VVARSMSGKEDLIWELL 17
         |||
Db       251 VVARSMSGKEDLIWELL 267
```

Search completed: November 1, 2005, 13:26:06
Job time : 88 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:35:39 ; Search time 17.25 Seconds

(without alignments)
94.822 Million cell updates/sec

Title: US-10-612-162a-1

Perfect score: 86
Sequence: 1 VVARSMGKEDLIMELL 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database :

1: PIR 79: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	698	1	TFHNP
2	75	87.2	694	1	TFHNP
3	75	87.2	704	2	carbonic anhydrase
4	71	82.6	708	1	TFHNP
5	70	81.4	708	2	lactotransferrin p
6	68	79.1	706	2	transferrin - goat
7	66	76.7	695	2	transferrin precu
8	66	76.7	711	1	transferrin precu
9	65	75.6	696	1	transferrin - pig
10	65	75.6	703	2	lactotransferrin
11	55	64.0	707	1	transferrin precu
12	52	60.5	311	2	transferrin - mous
13	49.5	57.6	459	2	hypothetical prote
14	47.5	55.2	510	2	hypothetical prote
15	45	52.3	2958	2	probable membrane
16	44	51.2	885	2	probable fad34 pr
17	44	51.2	885	2	alantane-cRNA ligas
18	43	50.0	210	1	gene 55.10 protein
19	43	50.0	439	2	hypothetical prote
20	43	50.0	2140	2	probable cell-adhe
21	42	48.8	164	2	hypothetical prote
22	42	48.8	882	2	hypothetical prote
23	42	48.8	970	2	receptor protein-t
24	42	48.8	995	2	embryo kinase 5 -
25	41	47.7	99	2	hypothetical ORF-1
26	41	47.7	324	2	guanine oxidoreduc
27	41	47.7	326	2	ABC-type transpor
28	41	47.7	346	2	ABC transporter, A
29	41	47.7	451	2	hypothetical prote

30	41	47.7	452	2	E71154	hypothetical prote
31	41	47.7	559	2	A99237	hypothetical prote
32	41	47.7	559	2	UC8616	group II chaperoni
33	41	47.7	560	2	S59859	rosellatase alpha
34	41	47.7	853	2	A95269	probable sensory t
35	41	47.7	1502	2	T42216	multidrug resistan
36	41	47.7	1677	2	T46095	hypothetical prote
37	41	47.7	1938	1	S06005	myosin alpha heavy
38	40.5	47.1	201	2	S75047	drga protein - Syn
39	40	46.5	98	2	T14691	hypothetical prote
40	40	46.5	103	2	A10259	hypothetical phage
41	40	46.5	136	2	T15031	hypothetical prote
42	40	46.5	169	2	AD1293	hypothetical prote
43	40	46.5	307	2	D36868	copd homolog - Xan
44	40	46.5	374	2	D81937	probable ribosomal
45	40	46.5	403	2	H83477	conserved hypochet

ALIGNMENTS

RESULT 1

transferrin precursor [validated] - human

N:Alternate names: siderophilin

C:Species: Homo sapiens (man)

C>Date: 15-Oct-1982 #sequence, revision 30-Sep-1993 #ext change 09-Jul-2004

C/Accession: A20981; A92417; A94044; A29090; A32739; I51959; I63133; I54011; I68160; A0

R/Yang, F.; Lum, J.B.; McGill, J.R.; Moore, C.M.; Naylor, S.L.; van Bragt, P.H.; Baldwin

Proc. Natl. Acad. Sci. U.S.A. 81, 2752-2756, 1984

A>Title: Human transferrin: cDNA characterization and chromosomal localization.

A/Reference number: A20981; PMID:84194084; PMID:6585826

A/Contents: variant C

A/Accession: A20981

A/Molecule type: mRNA

A/Residues: 1-698 <YAN>

A/Cross-references: UNIPROT:P02787; EMBL:M12530; NID:G339452; PIDN:AAA61140.1; PID:G339

A/Note: the authors translated the codon CAA for residue 203 as Glu

R/MacGillivray, R.T.A.; Mendez, E.; Shevale, J.G.; Sinha, S.K.; Linebeck-Zins, J.; Brew,

U. Biol. Chem. 258, 3543-3553, 1983

A>Title: The primary structure of human serum transferrin. The structures of seven cyan

A/Reference number: A92417; PMID:83160878; PMID:6833213

A/Accession: A92417

A/Molecule type: protein

A/Residues: 20-263, 'E', 265-328, 'N', 330-379, 'SD', 382-435, 'D', 437-557, 'T', 559-560, 'P', 562

A/Note: the sequence shown is the predominant electrophoretic genetic variant (C or T/C)

R/Park, I.; Schaeffer, E.; Sidoli, A.; Baralle, F.E.; Cohen, G.N.; Zakin, M.M.

Proc. Natl. Acad. Sci. U.S.A. 82, 3149-3153, 1985

A>Title: Organization of the human transferrin gene: direct evidence that it originated

A/Reference number: A94044; PMID:85216459; PMID:3858812

A/Accession: A94044

A/Molecule type: DNA

hypothetical prote

hypothetical prote

group II chaperoni

rosellatase alpha

probable sensory t

multidrug resistan

hypothetical prote

myosin alpha heavy

drga protein - Syn

hypothetical prote

hypothetical phage

hypothetical prote

copd homolog - Xan

probable ribosomal

conserved hypochet

A>Title: The complete amino acid sequence of human serum transferrin.
 A.Reference number: A93911; PMID:82223166; PMID:6953407
 A.Contents: annotation; disulfide bonds
 R.Hershenberger, C.L.; Larson, J.L.; Arnold, B.; Roatbeck, P.R.
 Ann. N.Y. Acad. Sci. 646, 140-154, 1991
 A>Title: A cloned gene for human transferrin.
 A.Reference number: 151959; PMID:92231399; PMID:1809186
 A.Accession: 151959
 A>Status: translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-698 <RES>
 A.Cross-references: GB:S95936; NID:9248647; PIDN:AA822049.1; PID:9248648
 R.Duguid, J.R.; Bonmont, C.W.; Liu, N.G.; Tourtelotte, W.W.
 Proc. Natl. Acad. Sci. U.S.A. 86, 7260-7264, 1989
 A>Title: Changes in brain gene expression shared by scrapie and Alzheimer disease.
 A.Reference number: 148174; PMID:89386721; PMID:2780570
 A.Accession: 163133
 A>Status: translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 636-696 <RB2>
 A.Cross-references: GB:M26641; NID:9339988; PIDN:AAA61233.1; PID:9339989
 R.Schaeffer, E.; Lucero, M.A.; Jeltch, J.M.; Py, M.C.; Levin, M.J.; Chambon, P.; Cohen, Gene 56, 109-116, 1987
 A>Title: Complete structure of the human transferrin gene. Comparison with analogous chi
 A.Reference number: 154011; PMID:8805305; PMID:3678832
 A.Accession: 154011
 A>Status: translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 1-72 <RB3>
 A.Cross-references: GB:M17611; NID:9339480; PIDN:AAA6147.1; PID:9339485
 A.Accession: 168160
 A>Status: translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Residues: 564-698 <RB4>
 A.Cross-references: GB:M17614; NID:9339483; PIDN:AAA61148.1; PID:9339486
 C.Comment: Each of the two repetitive domains binds a ferric ion and a bicarbonate anion
 C.Genetics:
 A.Gene: GDB:TF
 A.Cross-references: GDB:120432; OMIM:190000
 A.Map position: 3q21-3q21
 A.Intron: 15/1; 72/3; 119/1; 166/1; 212/2; 231/1; 290/3; 350/1; 401/3; 433/1; 444/1; 49
 C.Function:
 A.Description: binds iron for delivery into cells
 A.Superfamily: transferrin; transferrin repeat homology
 C.Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
 F.1-19/Domain: signal sequence #status predicted <SIG>
 F.20-698/Product: transferrin #status experimental <MAT>
 F.20-350/Domain: transferrin repeat homology <TRH1>
 F.356-686/Domain: transferrin repeat homology <TRH2>
 F.28-67,38-58,137-213,156-350,177-193,180-196,190-198,246-260,358-615,364-396,374-387,42
 F.432,630/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 100.0%; Score 86; DB 1; Length 698;
 Best Local Similarity 100.0%; Pred. No. 1.6e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
 |||||
 DB 270 VVARSNGKEDLIWELL 286

RESULT 2

TFRBP
 transferrin precursor - rabbit
 C.Species: Oryctolagus cuniculus (domestic rabbit)
 C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
 C.Accession: S16246; A61239; S00335; S02694; A24504; S14853
 R.Banfield, D.K.; Chow, B.K.C.; Funk, W.D.; Robertson, K.A.; Umels, T.M.; Woodworth, R.
 Biochim. Biophys. Acta 1089, 262-265, 1991
 A>Title: The nucleotide sequence of rabbit liver transferrin cDNA.
 A.Reference number: S16246; PMID:91274362; PMID:2054387
 A.Accession: S16246
 A.Molecule type: mRNA

A.Residues: 1-694 <BAN>
 A.Cross-references: EMBL:X59533; NID:91750; PIDN:CAA41424.1; PID:91751
 R.Pierpaoli, W.; Dalli'Aré, A.; Yi, C.; Neri, P.; Santucci, A.; Choay, J.
 Cell. Immunol. 134, 225-234, 1991
 A>Title: Iron carrier proteins facilitate engraftment of allogeneic bone marrow and endu
 A.Reference number: A61239; PMID:91191584; PMID:2013104
 A.Accession: A61239
 A.Molecule type: protein
 A.Residues: 19-36 <PIR>
 R.Chung, M.C.M.; Chan, S.L.; Shimizu, S.
 Int. J. Biochem. 23, 609-616, 1991
 A>Title: Purification of transferrins and lactoferrin using DEAE Affi-Gel Blue.
 A.Reference number: A61573; PMID:91293379; PMID:2065820
 A.Accession: C61573
 A.Molecule type: protein
 A.Residues: 19-26, 'X', 28-36, 'X', 38-53 <CHU>
 R.Godovac-Zimmermann, J.
 Biol. Chem. Hoppe-Seyler 369, 93-96, 1988
 A>Title: Isolation, characterization and N-terminal amino-acid sequence of rabbit transf
 A.Reference number: S00335; PMID:88209278; PMID:3365331
 A.Accession: S00335
 A.Molecule type: protein
 A.Residues: 19-45, 'S', 47-48, 'Y', 50 <GOD>
 R.Evans, R.W.; Aitken, A.; Patel, K.J.
 FEBS Lett. 238, 39-42, 1988
 A>Title: Evidence for a single glycan moiety in rabbit serum transferrin and location of
 A.Reference number: S02694; PMID:89005676; PMID:3169252
 A.Accession: S02694
 A.Molecule type: protein
 A.Residues: 482-515, 'V', 517-544 <EVA>
 A.Note: 516-116 was also found
 R.Heaphy, S.; Williams, J.
 Biochem. J. 205, 611-617, 1982
 A>Title: The preparation and partial characterization of N-terminal and C-terminal iron-
 A.Reference number: A26504; PMID:83074540; PMID:6816218
 A.Accession: A26504
 A.Molecule type: protein
 A.Residues: 19-24, 'N', 26, 'X', 28-29, 'S' <HRA>
 C.Superfamily: transferrin; transferrin repeat homology
 C.Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
 F.1-18/Domain: signal sequence #status predicted <SIG>
 F.19-694/Product: transferrin #status experimental <MAT>
 F.19-349/Domain: transferrin repeat homology <TRH1>
 F.355-682/Domain: transferrin repeat homology <TRH2>
 F.27-66,37-57,136-212,155-349,176-192,179-195,189-197,245-259,357-611,363-395,373-386,42
 F.508/Binding site: carbohydrate (asn) (covalent) #status experimental

Query Match 87.2%; Score 75; DB 1; Length 694;
 Best Local Similarity 88.2%; Pred. No. 0.00012;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
 |||||
 DB 269 VVARSNGKEDLIWELL 285

RESULT 3

147228
 carbonic anhydrase II inhibitor (transferrin homolog) precursor - pig
 C.Species: Sus scrofa domestica (domestic pig)
 C.Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C.Accession: 147228
 R.Roush, E.D.; Fierke, C.A.
 Biochemistry 31, 12536-12542, 1992
 A>Title: Purification and characterization of a carbonic anhydrase II inhibitor from por
 A.Reference number: 147228; PMID:93099129; PMID:1463741
 A.Accession: 147228
 A.Status: preliminary;
 A.Molecule type: translated from GB/EMBL/DBJ
 A.Molecule type: mRNA
 A.Residues: 1-704 <ROU>
 A.Cross-references: UNIPROT:Q29545; EMBL:U36916; NID:91016329; PIDN:AA858956.1; PID:9101
 C.Genetics:
 A.Gene: PICA

C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication
 F:20-350/Domain: transferrin repeat homology <TRH1>
 Query Match 87.2%; Score 75; DB 2; Length 704;
 Best Local Similarity 88.2%; Pred. No. 0.00013;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

1 VVARSMGKEDLIWELL 17
 |||||:|||||
 Db 270 VVARSDGKEDLIWELL 286

RESULT 4
 TFEBOL
 Lactotransferrin precursor - bovine
 N:Alternate names: lactoferrin
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 09-Jul-2004
 C:Accession: I45919; S14674; S14110; S18517; J05959; S13057; S18518; S13881; P10148; S21
 R;Fhang, T.C.; Burne, D.K.; Wang, F.; Pan, Y.
 FASEB J. 6, 233, 1991
 A:Title: Cloning of a 80-kD advanced glycosylation end product (AGE) binding protein frc
 A:Reference number: I45919
 A:Accession: I45919
 A:Status: translated from GB/EMBL/DBD
 A:Molecule type: mRNA
 A:Residues: 1-708 <TSA>
 A:Cross-references: UNIPROT:P24627; GB:L08604; NID:G13269; PIDN:AAA30609.1; PID:G163270
 R:Pierce, A.
 submitted to the EMBL Data Library, November 1990
 A:Reference number: S14674
 A:Accession: S14674
 A:Molecule type: mRNA
 A:Residues: 1-144, 'V', 146-163, 'P', 166-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <PI1>
 A:Cross-references: EMBL:X57084; NID:G505; PIDN:CAA40366.1; PID:G506
 R:Pierce, A.; Colavizza, D.; Benalissa, M.; Maes, P.; Tartar, A.; Montreuil, J.; Spik, G.
 Eur. J. Biochem. 196, 177-184, 1991
 A:Title: Molecular cloning and sequence analysis of bovine lactotransferrin.
 A:Reference number: S14110; MUID:9160550; PMID:2001696
 A:Accession: S14110
 A:Molecule type: mRNA
 A:Residues: 3-144, 'V', 146-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <PI2>
 A:Cross-references: EMBL:X57084
 A:Accession: S18517
 A:Molecule type: protein
 A:Residues: 20-35;82-114;148-163, 'P', 166-178, 'V', 'P', 183-190;205-212;230-239;304-339;59
 R:Goodman, R.E.; Schanbacher, F.L.
 Biochem. Biophys. Res. Commun. 180, 75-84, 1991
 A:Title: Bovine lactoferrin mRNA: sequence, analysis, and expression in the mammary glar
 A:Reference number: J05955; MUID:92028986; PMID:1718281
 A:Accession: J05955
 A:Molecule type: mRNA
 A:Residues: 1-65, 'P', 68-296, 'S', 298-339, 'A', 341-708 <GOO>
 A:Cross-references: GB:M63502
 R:Head, P.E.; Tweedle, J.W.
 Nucleic Acids Res. 18, 7167, 1990
 A:Title: cDNA and protein sequence of bovine lactoferrin.
 A:Reference number: S13097; MUID:91088328; PMID:2263492
 A:Accession: S13097
 A:Molecule type: mRNA
 A:Residues: 28-33, 'DS', 36-38, 'P', 40-708 <MEA>
 A:Cross-references: EMBL:X54801
 A:Accession: S18518
 A:Molecule type: protein
 A:Residues: 20-47;59-66;132-139;256-277;278,305-332;343-351;361-363;586;587-589;598-619
 R:Head, P.E.
 submitted to the EMBL Data Library, October 1990
 A:Reference number: S13881
 A:Accession: S13881
 A:Molecule type: mRNA
 A:Residues: 28-38, 'P', 40-86, 'C', 88-708 <ME3>

A:Cross-references: EMBL:X54801
 R:Rejman, J.U.; Hegarty, H.M.; Hurley, W.L.
 Comp. Biochem. Physiol. B 93, 929-934, 1989
 A:Title: Purification and characterization of bovine lactoferrin from secretions of the
 A:Reference number: P10148; MUID:90011466; PMID:2805645
 A:Accession: P10148
 A:Molecule type: protein
 A:Residues: 20-27, 'X', 29-37, 'X', 39-54, 'X', 56-59 <REJ>
 R:Belilamy, W.; Takase, M.; Yamachi, K.; Wakabayashi, H.; Kawase, K.; Tomita, M.
 Biochim. Biophys. Acta 1121, 130-136, 1992
 A:Title: Identification of the bactericidal domain of lactoferrin.
 A:Reference number: S21756; MUID:92287941; PMID:1599934
 A:Accession: S21756
 A:Molecule type: protein
 A:Residues: 36-60 <BEL>
 R:Shimazaki, K.; Tanaka, T.; Kon, H.; Oota, K.; Kawaguchi, A.; Maki, Y.; Sato, T.
 J. Dairy Sci. 76, 946-955, 1993
 A:Title: Separation and characterization of the C-terminal half molecule of bovine lact
 A:Reference number: A56659; MUID:93253156; PMID:8486845
 A:Accession: A56659
 A:Molecule type: protein
 A:Residues: 20-25;302-308;359-366, 'X', 368-376, 'X', 378 <SHI>
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-708/Product: lactotransferrin #status experimental <MAT>
 F:20-355/Domain: transferrin repeat homology <TRH1>
 F:36-60/Region: antimicrobial
 F:359-696/Domain: transferrin repeat homology <TRH2>
 F:26-64;134-217;176-192;179-200;189-202;250-264;367-399;377-390;424-703;444-666;476-551
 P:38-55/Disulfide bonds: #status predicted
 F:79,111,211,272/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
 F:140/Binding site: carbonate (Arg) #status experimental
 F:252,300,387,495,564/Binding site: carboxylate (Asn) (covalent) #status predicted
 F:414,452,545,611/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
 F:482/Binding site: carbonate (Arg) #status experimental

Query Match 82.6%; Score 71; DB 1; Length 708;
 Best Local Similarity 82.4%; Pred. No. 0.00061;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 VVARSMGKEDLIWELL 17
 |||||:|||||
 Db 274 VVARSDGKEDLIWELL 290

RESULT 5
 J02323
 Lactoferrin - goat
 C:Species: Capra aegagrus hircus (domestic goat)
 C>Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text change 07-May-1999
 C:Accession: J02323
 R:Le Provost, F.; Nocard, M.; Guerin, G.; Martin, P.
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A:Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locu
 A:Reference number: J02323; MUID:94380047; PMID:8093048
 A:Accession: J02323
 A:Molecule type: mRNA
 A:Residues: 1-708 <LEP>
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:359-696/Domain: transferrin repeat homology
 F:252,300,387,495,564/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 81.4%; Score 70; DB 2; Length 708;
 Best Local Similarity 82.4%; Pred. No. 0.00091;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

1 VVARSMGKEDLIWELL 17
 |||||:|||||
 Db 274 VVARSDGKEDLIWELL 290

```

RESULT 6
transferrin precursor - horse
S33761
N/Alternate names: growth-promoting factor
C/Species: Equus caballus (domestic horse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S33761; S02145
R/Carpenter, M.A.; Broad, T.E.
Biochim. Biophys. Acta 1173, 230-232, 1993
A/Title: The cDNA sequence of horse transferrin.
A/Reference number: S33761; MUID:93277958; PMID:6504171
A/Accession: S33761
A/Molecule type: mRNA
A/Status: preliminary
A/Residues: 1-706 <CAR>
A/Cross-references: UNIPROT:P27425; EMBL:ME9020; NID:g164242; PIDN:AAA30958.1; PID:g1642
A/Experimental source: liver; developmental stage adult
R/Yoshinari, K.; Yuasa, K.; Iga, F.; Minura, A.
Biochim. Biophys. Acta 1010, 28-34, 1989
A/Title: A growth-promoting factor for human myeloid leukemia cells from horse serum ide
A/Reference number: S02145; MUID:89076897; PMID:2909248
A/Accession: S02145
A/Molecule type: protein
A/Residues: 20-35, 'X', 37, 'X', 39-40, 'X', 43-44 <YOS>
C/Complex: monomer
C/Suprafamily: transferrin; transferrin repeat homology
C/Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
F.1-19/Domain: signal sequence #status predicted <Sig>
F.20-706/Product: transferrin #status experimental <MAT>
F.358-694/Domain: transferrin repeat homology <TRH2>
F.26-64, 36-55, 134-215, 174-190, 177-198, 187-200, 248-262, 360-623, 366-398, 376-389, 423-701, 44
Query Match 79.1%; Score 68; DB 2; Length 706;
Best Local Similarity 82.4%; Pred. No. 0.002;
Matches 14; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 272 VVARSVGKEDLIWGL 288

RESULT 7
S49163
transferrin precursor - rat
N/Alternate names: lung-derived growth factor; siderophilin
C/Species: Rattus norvegicus (Norway rat)
C/Date: 16-Feb-1995 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C/Accession: S49163; S54980; A30014; A4679; A53289; A30512; 152203
R/Esquivia, H.; Pierce, A.; Codderville, B.; Gonzalez, F.; Benalissa, M.; Leger, D.; Wierus
submitted to the EMBL Data Library, January 1994
A/Description: Rat mammary gland transferrin: glycan structure, nucleotide sequence and
A/Reference number: S49163
A/Accession: S49163
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-695 <ESC>
A/Cross-references: UNIPROT:P12346; UNIPROT:Q63602; EMBL:X77158; NID:g510195; PIDN:CA54
R/Esquivia, H.; Pierce, A.; Codderville, B.; Gonzalez, F.; Benalissa, M.; Leger, D.; Wierus
Biochem. J. 307, 47-55, 1995
A/Title: Rat mammary-gland transferrin: nucleotide sequence, phylogenetic analysis and g
A/Reference number: S54980; MUID:95234054; PMID:7717992
A/Accession: S54980
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-695 <ES2>
A/Cross-references: EMBL:X77158; NID:g510195; PIDN:CA54403.1; PID:g510196
R/Hugueny, J.L.; Idzerda, R.L.; Haywood, L.; Lee, D.C.; McKnight, G.S.; Griswold, M.D.
Endocrinology 120, 332-340, 1987
A/Title: Transferrin messenger ribonucleic acid: molecular cloning and hormonal regulati
A/Reference number: A30014; MUID:87053639; PMID:3023031
A/Accession: A30014
A/Molecule type: mRNA
A/Residues: 518-687, 'D', 689-692, 'TA', 695 <HUG>
A/Cross-references: GB:M27966; NID:g207439; PIDN:AAA42267.1; PID:g207440

```

```

R/Schreiber, G.; Dryburgh, H.; Millerhip, A.; Matsuda, Y.; Inglis, A.; Phillips, J.; Ed
J. Biol. Chem. 254, 12013-12019, 1979
A/Title: The synthesis and secretion of rat transferrin.
A/Reference number: A14679; MUID:80049855; PMID:500689
A/Accession: A14679
A/Molecule type: protein
A/Residues: 20-47 <SCH>
R/Cavanaugh, P.G.; Nicolson, G.L.
J. Cell. Biochem. 47, 261-271, 1991
A/Title: Lung-derived growth factor that stimulates the growth of lung-metastasizing tum
A/Reference number: A53289; MUID:92165927; PMID:1791188
A/Accession: A53289
A/Status: preliminary
A/Molecule type: protein
A/Residues: 89, 'Y', 91, 'A', 93-99, 'V', 101-102, 'N', 233, 'AN', 236-243, 401-406, 'N', 408 <CAV>
A/Experimental source: lung
A/Note: sequence modified after extraction from NCBI backbone
A/Note: sequence extracted from NCBI backbone (NCBI:86115, NCBI:86116, NCBI:86114)
R/Purves, L.R.; Purves, M.; Linton, N.; Brandt, W.; Johnson, G.; Jacobs, P.
Biochim. Biophys. Acta 966, 318-327, 1988
A/Title: Properties of the transferrin associated with rat intestinal mucosa.
A/Reference number: A30512; MUID:88327006; PMID:304665
A/Accession: A30512
A/Molecule type: protein
A/Residues: 20-30; 639-643, 'KD', 646, 'LXACD' <PUR>
R/Alfred, A.R.; Howlett, G.J.; Schreiber, G.
Biochem. Biophys. Res. Commun. 122, 960-965, 1984
A/Title: Synthesis of rat transferrin in Escherichia coli containing a recombinant bacte
A/Reference number: 152203; MUID:84307580; PMID:6236811
A/Accession: 152203
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 7-25, 'X', 27-56, 'A', 58-64, 267-295 <RES>
A/Cross-references: GB:M6113; NID:g207437; PIDN:AAA42266.1; PID:g207438
C/Genetics:
A/Genes: TF
C/Suprafamily: transferrin; transferrin repeat homology
C/Keywords: duplication
F.20-348/Domain: transferrin repeat homology <TRH1>

Query Match 76.7%; Score 66; DB 2; Length 695;
Best Local Similarity 76.5%; Pred. No. 0.0043;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
Db 270 VVARSGKEDLIWGL 286

RESULT 8
TFHUL
lactotransferrin precursor [validated] - human
N/Alternate names: lactoferrin
C/Species: Homo sapiens (man)
C/Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 08-Dec-2000
C/Accession: G01394; S11228; A45401; S10324; S18553; S20841; S07160; A61169; A31000; S74
R/Cho, Y.
submitted to the EMBL Data Library, March 1994
A/Reference number: G06820
A/Accession: G01394
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-711 <CHO>
A/Cross-references: EMBL:U07643; NID:g467236; PIDN:AAB60324.1; PID:g467237
R/Rey, M.W.; Moloshuk, S.L.; deBoer, H.A.; Pieper, F.R.
Nucleic Acids Res. 18, 5288, 1990
A/Title: Complete nucleotide sequence of human mammary gland lactoferrin.
A/Reference number: S11228; MUID:90384839; PMID:2402455
A/Accession: S11228
A/Molecule type: mRNA
A/Residues: 1-148, 'T', 150-423, 'C', 424-711 <REY>
A/Cross-references: EMBL:X5361; NID:g34415; PIDN:CA37914.1; PID:g34416
R/Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Pannella, T.

```

Mol. Endocrinol. 6, 1969-1981, 1992
 A>Title: Differential molecular mechanism of the estrogen action that regulates lactoferrin
 A/Reference number: A45401; PMID:93125571; PMID:1480183
 A/Accession: A45401
 A/Molecule type: DNA
 A/Residues: 1-15 <TRN>
 A/Cross-references: GB:852659; NID:9263311; PIDN:AAB24877.1; PID:9263312
 A/Experimental source: placenta (NCBI backbone (NCBI:P:122202))
 A/Note: sequence extracted from NCBI backbone (NCBI:P:122202)
 R/Powell, M.O.; Ogden, J.E.
 Nucleic Acids Res. 18, 4013, 1990
 A>Title: Nucleotide sequence of human lactoferrin cDNA.
 A/Reference number: S10324; PMID:90326549; PMID:2374724
 A/Accession: S10324
 A/Molecule type: mRNA
 A/Residues: 3-711 <POW>
 A/Cross-references: EMBL:X52941; NID:934411; PIDN:CAA37116.1; PID:934412
 R/Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
 Biochem. J. 276, 349-355, 1991
 A>Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
 A/Reference number: S15853; PMID:91264786; PMID:2049066
 A/Accession: S15853
 A/Status: nucleic acid sequence not shown; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 20-31 <ST1>
 A/Accession: S20841
 A/Molecule type: protein
 A/Residues: 20-28, 'X', 30-31 <ST2>
 R/Rado, T.A.; Wei, X.; Benz Jr., E.J.
 Blood 70, 989-993, 1987
 A>Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
 A/Reference number: S07160; PMID:88001031; PMID:3477300
 A/Accession: S07160
 A/Molecule type: mRNA
 A/Residues: 436-487, 'A', 489-711 <RAD>
 A/Cross-references: EMBL:M8642; NID:916815; PIDN:AA86665.1; PID:936885
 R/Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
 Cancer Res. 51, 3037-3043, 1991
 A>Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
 A/Reference number: A61169; PMID:91235214; PMID:1674448
 A/Accession: A61169
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 3-701, 'SMKPNV' <PAN>
 A/Experimental source: normal breast tissue
 R/Wiet-Boutique, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.; Eur. J. Biochem. 145, 659-666, 1984
 A>Title: Human lactoferrin: amino acid sequence and structural comparisons with other
 A/Reference number: A31000; PMID:85076667; PMID:6510420
 A/Accession: A31000
 A/Molecule type: protein
 A/Residues: 20-140, 142-169, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-400
 A/Note: this is the final paper in a series
 R/Houen, G.; Hoegdall, E.V.; Barkholt, V.; Nørskov, L.
 Eur. J. Biochem. 241, 303-308, 1996
 A>Title: Lactoferrin: similarity to diamine oxidase and purification by aminoethyl affinity chromatography
 A/Reference number: S74119; PMID:97054624; PMID:8898921
 A/Accession: S74119
 A/Molecule type: protein
 A/Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>
 A/Experimental source: neutrophil granulocytes
 C/Genetic:
 A/Genes: GDB:119368; OMIM:150210
 A/Cross-references: GDB:119368; OMIM:150210
 A/Map position: 3q21-3q23
 C/Superfamily: transferrin, transferrin repeat homology
 C/Keywords: duplication; glycoprotein; iron binding; milk
 F:1-13/Domain: signal sequence #status predicted <Sig>
 F:20-711/Product: lactoferrin #status experimental <MAT>
 F:21-356/Domain: transferrin repeat homology <TRH1>
 F:360-699/Domain: transferrin repeat homology <TRH2>
 F:59-65, 39-55, 135-218, 177-193, 190-201, 251-265, 503-697, 595-609/disulfide bonds: #status experimental
 F:157, 498/Binding site: carbohydrate (Agn) (covalent) #status experimental

F:368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/disulfide bonds: #status experimental
 Query Match 76.7%; Score 66; DB 1; Length 711;
 Best Local Similarity 76.5%; Pred. No. 0.0044;
 Matches 13; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 VVARSNGKEDLIWELL 17
 DB 275 VVARSNGKEDLIWELL 291
 RESULT 9
 S01384
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: S01384; A60520; A61573
 R/Baldwin, G.S.; Weinstein, J.
 Nucleic Acids Res. 16, 8720, 1988
 A>Title: Nucleotide sequence of porcine liver lactoferrin.
 A/Reference number: S01384; PMID:88335629; PMID:3419934
 A/Accession: S01384
 A/Status: translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-696 <BAL>
 A/Cross-references: UNIPROT:P09571; EMBL:X12386; NID:92126; PIDN:CAA30943.1; PID:9833800
 A/Note: 308-Arg was also found
 R/Baldwin, G.S.; Baci, T.; Chandler, R.; Grego, B.; Pedersen, J.; Simpson, R.J.; Toh, E.
 Comp. Biochem. Physiol. B 95, 261-268, 1990
 A>Title: Isolation of transferrin from porcine gastric mucosa: comparison with porcine
 A/Reference number: A60520; PMID:90227903; PMID:2328566
 A/Accession: A60520
 A/Molecule type: protein
 A/Residues: 1-8, 'X', 10-11, 'X', 13-15 <BA2>
 A/Experimental source: gastric mucosa
 A/Note: the authors suggest transferrin from gastric mucosa may act in dietary iron uptake
 R/Chung, M.C.M.; Chan, S.L.; Shih, S.
 Int. J. Biochem. 23, 609-616, 1991
 A>Title: Purification of transferrin and lactoferrin using DEAE Affi-Gel Blue.
 A/Reference number: A61573; PMID:91293379; PMID:2065820
 A/Accession: A61573
 A/Molecule type: protein
 A/Residues: 1-8, 'X', 10-18, 'XX' <CHU>
 C/Superfamily: transferrin, transferrin repeat homology
 C/Keywords: duplication; glycoprotein; iron transport; plasma
 F:1-656/Product: transferrin #status predicted <MAT>
 F:1-335/Domain: transferrin repeat homology <TRH1>
 Query Match 75.6%; Score 65; DB 1; Length 696;
 Best Local Similarity 76.5%; Pred. No. 0.0064;
 Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 VVARSNGKEDLIWELL 17
 DB 255 VVARSVDGEDSIWELL 271
 RESULT 10
 A45543
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
 C/Accession: A45543; S24173
 R/Alexander, L.O.; Levine, W.B.; Teng, C.T.; Beattie, C.W.
 Anim. Genet. 23, 251-256, 1992
 A>Title: Cloning and sequencing of the porcine lactoferrin cDNA.
 A/Reference number: A45543; PMID:92367939; PMID:1503259
 A/Accession: A45543
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-703 <ALE>
 A/Cross-references: UNIPROT:P14632
 A/Experimental source: mammary gland

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:34:09 / Search time 83.25 Seconds

(without alignments)
104.569 Million cell updates/sec

Title: US-10-612-162a-1

Sequence: 1 VVARSWGKEDLIWELL 17

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	80	2	09GL90
2	86	100.0	81	2	09GL95
3	86	100.0	698	1	TRE_HUMAN
4	82	95.3	81	2	09GL91
5	82	93.0	81	2	09GL92
6	80	93.0	81	2	09GL94
7	79	91.9	81	2	09GL93
8	76	88.4	704	1	TRE_BOVIN
9	75	87.2	695	1	TRE_RABBIT
10	75	87.2	704	1	ICA_PIG
11	72	83.7	694	2	07TSX8
12	72	83.7	708	1	TRFL_CAMDR
13	71	82.6	117	2	06LC78
14	71	82.6	681	2	06LBN7
15	71	82.6	708	1	TRFL_BOVIN
16	71	82.6	708	1	TRFL_BUBBU
17	71	82.6	708	2	06LEC7
18	71	82.6	711	2	09XT72
19	70	81.4	708	1	TRFL_CAPHI
20	68	79.1	189	2	09TQV8
21	68	79.1	706	1	TRE_HORSE
22	67	77.9	79	2	09GL89
23	67	77.9	695	1	TRFL_HORSE
24	67	77.9	697	1	TRE_MOUSE
25	66	76.7	698	1	TRE_RAT
26	66	76.7	698	2	07TNX0
27	66	76.7	711	1	TRFL_HUMAN
28	66	76.7	979	2	07TMG7
29	66	76.7	980	2	07TP24
30	65	75.6	696	1	TRE_PIG
31	65	75.6	704	1	TRFL_PIG

32	65	75.6	704	2	08WMN8	08WMN8 sus scrofa
33	65	75.6	704	2	06TY39	06TY39 sus scrofa
34	60	69.8	704	2	07YS20	07YS20 sus scrofa
35	56	65.1	462	2	06Q147	06Q147 rattus norv
36	56	65.1	700	2	08VC96	08VC96 mus musculi
37	56	65.1	700	2	09DBD0	09DBD0 mus musculi
38	55	64.0	707	1	TRFL_MOUSE	P08071 mus musculi
39	55	64.0	707	2	08CBH0	08CBH0 mus musculi
40	49.5	57.6	459	2	09UZH9	09UZH9 pyrococcus
41	47.5	55.2	510	2	09Y9C5	09Y9C5 aetopyrum p
42	47	54.7	199	2	07RTV6	07RTV6 homo sapien
43	47	54.7	464	2	07XH23	07XH23 oryza sativ
44	47	54.7	464	2	09AY12	09AY12 oryza sativ
45	46	53.5	154	2	06XHD0	06XHD0 drosophila

ALIGNMENTS

RESULT 1	ID	Q9GL90	PRELIMINARY;	PRT;	80 AA.
AC	Q9GL90;				
DT	01-MAR-2001 (TREMBLrel. 16, Created)				
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)				
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)				
DE	Transferrin (Fragment).				
OS	Balaena mysticetus (bowhead whale).				
OC	Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti; Balaenidae;				
OC	Balaena.				
OX	NCBI_Taxid=27602;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=20481910; PubMed=11027333; DOI=10.1073/pnas.97.21.11343;				
RA	Cassens I., Vicario S., Maddell V.G., Balchowsky H., Van Belle D.,				
RA	Ding W., Fan C., Mohan L., Simoes-Lopes P.C., Bastida R., Meyer A.,				
RA	Stanhope M.J., Milinkovitch M.C.;				
RT	ancient cetacean lineages."				
RT	Independent adaptation to riverine habitats allowed survival of				
CC	Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000).				
CC	-1- FUNCTION: Transferrins are iron binding transport proteins which				
CC	bind ferric iron in association with the binding of an anion,				
CC	usually bicarbonate (By similarity).				
CC	-1- SIMILARITY: Belongs to the transferrin family.				
DR	EMBL; AF304105; AAC32047.1; -.				
DR	HSSP; P02787; 1A8E.				
DR	GO; GO:0005576; C:extracellular; IEA.				
DR	GO; GO:0008199; F:ferric iron binding; IEA.				
DR	GO; GO:0006879; P:iron ion homeostasis; IEA.				
DR	GO; GO:0006810; P:iron ion transport; IEA.				
DR	InterPro; IPR001156; Peptidase_S60.				
DR	Pfam; PF00405; Transferrin; 1.				
DR	PRINTS; PR00422; TRANSFERRIN.				
DR	PROSITE; PS00207; TRANSFERRIN_3; 1				
KW	Iron transport; Metal-binding; Transport.				
FT	NON_TER				
FT	NON_TER				
FT	NON_TER				
SQ	SEQUENCE 80 AA; 9115 MW; 8FEDB3A5F2FAE675 CRC64;				
Query Match	100.0%;	Score 86;	DB 2;	Length 80;	
Best Local Similarity	100.0%;	Pred. No. 6.4e-07;			
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1 VVARSWGKEDLIWELL 17				
Db	39 VVARSWGKEDLIWELL 55				
RESULT 2					
Q9GL95	PRELIMINARY;	PRT;	81 AA.		

```

AC Q9GL95;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transferrin (Fragment).
OS Phocoenoides phocoena (Harbor porpoise).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Phocoenidae;
OC Phocoena.
OX NCBI_TaxID=9742;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20481910; PubMed=11027333; DOI=10.1073/pnas.97.21.11343;
RA Casares I., Valcarlos S., Maddell V.G., Balchowsky H., Van Belle D.,
RA Ding M., Pan C., Mohan L., Simoes-Lopes P.C., Bastida R., Meyer A.,
RA Stahope M.J., Mlinkovitch M.C.;
RT "Independent adaptation to riverine habitats allowed survival of
RT ancient cetacean lineages."
RL Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000).
DR EMBL; AF304100; MAG32042.1; -.
DR HSSP; P09571; 1H76.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin_1.
DR PRINTS; PR00422; TRANSFERRIN.
FT NON_TER
FT 1
FT 81
FT NON_TER
SQ SEQUENCE 81 AA; 9379 MW; 785DE6D52445A45 CRC64;

Query Match 100.0%; Score 86; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 6,4e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWEIL 17
Db 39 VVARSMGKEDLIWEIL 55

RESULT 3
TFPE_HUMAN STANDARD; PRT; 698 AA.
AC P02787; O43890; Q9NQB8; Q9UHV0;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serotransferrin precursor (transferrin) (Siderophilin) (beta-1-metal
DE binding globulin) (PRO1400).
GN Name=TF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS TF*B2; TF*CHI AND TF*DI.
RX MEDLINE=84194084; PubMed=6585826;
RA Yang F., Lum J.B., McGill J.R., Moore C.M., Naylor S.L.,
RA van Bregt P.H., Baldwin W.D., Bowman B.H.;
RT "Human transferrin: cDNA characterization and chromosomal
RT localization."
RL Proc. Natl. Acad. Sci. U.S.A. 81:2752-2756(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88056305; PubMed=3678832; DOI=10.1016/0378-1119(87)90163-6;
RA Schaeffer E., Lucero M.A., Jeltsch J.-M., Py M.-C., Levin M.J.,
RA Chanbon P., Cohen G.N., Zakim M.M.;
RT "Complete structure of the human transferrin gene. Comparison with
RT analogous chicken gene and human pseudogene."
RL Gene 56:109-116(1987).
RN [3]
RP SEQUENCE FROM N.A.

```

```

RC TISSUE=Liver;
RX MEDLINE=992231399; PubMed=1809186;
RA Herberberger C.L., Larson J.L., Arnold B., Rostock P.R., Jr.;
RA Williams P., Dehoff B., Dunn P., O'Neal K.L., Riemen M.W., Rice P.A.;
RT "A cloned gene for human transferrin."
RL Ann. N. Y. Acad. Sci. 646:140-154(1991).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT ATRANSFERRINEMIA PRO-477.
RX MEDLINE=20563920; PubMed=1110675;
RA Beutler E., Gelbart T., Lee P.L., Trevino R., Fernandez M.A.,
RA Fairbanks V.P.;
RT "Molecular characterization of a case of atransferrinemia."
RL Blood 96:4071-4074(2000).
RN [5]
RP SEQUENCE FROM N.A.
RX Rieder M.J., Carrington D.P., da Ponte S.H., Hastings N.C.,
RA Ahearn M.O., Kulaneck S.A., Rajkumar N., Toch E.J., Yi Q.,
RA Nickerson D.A.;
RT "SeattleSNPs: NHLBI HL66682 program for genomic applications, UW-
RT FHCR, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Collins F.S., Wagner L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Bask S.S., Louellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Rohak S.A., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.D., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.T., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 99-698 FROM N.A.
RC TISSUE=Fetal liver;
RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
RA He F.;
RT "Functional prediction of the coding sequences of 33 new genes deduced
RT by analysis of cDNA clones from human fetal liver."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE OF 422-698 FROM N.A.
RX MEDLINE=84153910; PubMed=6322780;
RA Uzan G., Frain M., Park I., Besmond C., Maessen G., Trepas J.S.,
RA Zakim M.M., Kahn A.;
RT "Molecular cloning and sequence analysis of cDNA for human
RT transferrin."
RL Biochem. Biophys. Res. Commun. 119:273-281(1984).
RN [9]
RP SEQUENCE OF 20-698.
RX MEDLINE=83160878; PubMed=6833213;
RA McGilivray R.T.A., Mendez E., Shewale J.G., Sinha S.K.,
RA Linback-Jins J., Brew K.;
RT "The primary structure of human serum transferrin. The structures of
RT seven cyanogen bromide fragments and the assembly of the complete
RT structure."
RL J. Biol. Chem. 258:3543-3553(1983).
RN [10]
RP SEQUENCE OF 73-698 FROM N.A.
RX MEDLINE=85216459; PubMed=3858812;

```

RA Park I., Schaeffer E., Sidoli A., Baralle F.E., Cohen G.N.,
 RA Zakin M.M.;
 RT "Origination of the human transferrin gene: direct evidence that it
 RT originated by gene duplication.";
 RL Proc. Natl. Acad. Sci. U.S.A. 82:3149-3153(1985).
 RN [11]
 RP SEQUENCE OF 1-14 FROM N.A.
 RX MEDLINE=87066744; PubMed=786138;
 RA Lucero M.A., Schaeffer E., Cohen G.N., Zakin M.M.;
 RT "The 5' region of the human transferrin gene: structure and potential
 RT regulatory sites.";
 RL Nucleic Acids Res. 14:8692-8692(1986).
 RN [12]
 RP SEQUENCE OF 1-72 AND 291-300 FROM N.A.
 RX MEDLINE=87192006; PubMed=3106157; DOI=10.1016/0378-1119(86)90277-5;
 RA Adelman G.S., Korinek B.W., Bowman B.H., Yang F.;
 RT "The human transferrin gene: 5' region contains conserved sequences
 RT which match the control elements regulated by heavy metals,
 RT glucocorticoids and acute phase reaction.";
 RL Gene 49:167-175(1986).
 RN [13]
 RP SEQUENCE OF 45-72 FROM N.A.
 RX MEDLINE=20392111; PubMed=10931525;
 RA DOI=10.1002/1097-4547(200008)5:6:1<4388::AID-JNRS>3.0.CO;2-Q;
 RA de Arriba Zepa G.A., Saleh M.-C., Fernandez P.M., Guillou F.,
 RA Espinosa de los Monteros A., de Vellis J., Zakin M.M., Baron B.;
 RT "Alternative splicing prevents transferrin secretion during
 RT differentiation of a human oligodendrocyte cell line.";
 RL J. Neurosci. Res. 61:388-395(2000).
 RN [14]
 RP SEQUENCE OF 564-624 FROM N.A., AND VARIANT TF+C2.
 RC TISSUE=Brain;
 RX MEDLINE=97418135; PubMed=9272172;
 RA Namekata K., Oyama F., Imagawa M., Ihara Y.;
 RT "Human transferrin (TF): a single mutation at codon 570 determines TF
 RT C1 or TF C2 variant.";
 RL Hum. Genet. 100:457-458(1997).
 RN [15]
 RP SEQUENCE OF 564-624 FROM N.A.
 RA Teuchida S., Ikemoto S., Kajii E.;
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 RN [16]
 RP SEQUENCE OF 636-696 FROM N.A.
 RX MEDLINE=89386721; PubMed=2780570;
 RA Duguid J.R., Bohmont C.W., Liu N.G., Tourtellotte W.W.;
 RT "Changes in brain gene expression shared by scrapie and Alzheimer
 RT disease.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7260-7264(1989).
 RN [17]
 RP SEQUENCE OF 263-266; 454-458; 531-538 AND 589-595.
 RC TISSUE=Heart;
 RX MEDLINE=96007936; PubMed=7498159;
 RA Kovalyov L.I., Shlekhin S.S., Efimochkin A.S., Kovalyova M.A.,
 RA Erekhova E.S., Egorov T.A., Musalyamov A.K.;
 RT "The major protein expression profile and two-dimensional protein
 RT database of human heart.";
 RL Electrophoresis 16:1160-1169(1995).
 RN [18]
 RP DISULFIDE BONDS.
 RX MEDLINE=8222216; PubMed=6953407;
 RA McGillivray R.T.A., Mendez E., Simha S.K., Sutton M.R.,
 RA Lineback-Zins J., Brew K.;
 RT "The complete amino acid sequence of human serum transferrin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2504-2508(1982).
 RN [19]
 RP MUTAGENESIS.
 RX MEDLINE=92031536; PubMed=1932003;
 RA Woodworth R.C., Mason A.B., Funk W.D., McGillivray R.T.A.;
 RT "Expression and initial characterization of five site-directed mutants
 RT of the N-terminal half-molecule of human transferrin.";
 RL Biochemistry 30:10824-10829(1991).
 RN [20]
 RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 22-350.

RX MEDLINE=98272665; PubMed=9609685; DOI=10.1021/b19803551;
 RA McGillivray R.T.A., Moore S.A., Chen J., Anderson B.F., Baker H.,
 RA Luo Y., Bewley M.C., Smith C.A., Murphy M.E.P., Wang Y., Mason A.B.,
 RA Woodworth R.C., Brayer G.D., Baker E.N.;
 RT "Two high-resolution crystal structures of the recombinant N-lobe of
 RT human transferrin reveal a structural change implicated in iron
 RT release.";
 RL Biochemistry 37:7919-7928(1998).
 RN [21]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-350.
 RX MEDLINE=98434369; PubMed=9760232; DOI=10.1021/b19812064;
 RA Jeffrey P.D., Bewley M.C., McGillivray R.T.A., Mason A.B.,
 RA Woodworth R.C., Baker E.N.;
 RT "Ligand-induced conformational change in transferrin: crystal
 RT structure of the open form of the N-terminal half-molecule of human
 RT transferrin.";
 RL Biochemistry 37:13978-13986(1998).
 RN [22]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 23-352.
 RX MEDLINE=99155227; PubMed=10029548; DOI=10.1021/b19824543;
 RA Bewley M.C., Tam B.M., Grewal J., He S., Shewry S., Murphy M.E.P.,
 RA Mason A.B., Woodworth R.C., Baker E.N., McGillivray R.T.A.;
 RT "X-ray crystallography and mass spectroscopy reveal that the N-lobe of
 RT human transferrin expressed in *Pichia pastoris* is folded correctly but

Query Match 100.0%; Score 86; DB 1; Length 698;
 Best Local Similarity 100.0%; Pred. No. 5.8e-06;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17
 DB 270 VVARSMGKEDLIWELL 286

RESULT 4
 O9GL91
 ID O9GL91 PRELIMINARY; PRT; 81 AA.
 AC O9GL91;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Transferrin (Fragment).
 OS Ziphilus cavirostris (Goose-beaked whale).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Ziphiidae;
 OC Ziphius.
 OX NCBI_TaxID=9760;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20481910; PubMed=11027333; DOI=10.1073/pnas.97.21.11343;
 RA Casensu I., Vicario S., Maddell V.G., Balchowsky H., Van Belle D.,
 RA Ding W., Fan C., Mohan L., Simoes-Lopes P.C., Bastida R., Meyer A.,
 RA Stanhope M.J., Milinkovitch M.C.;
 RT "Independent adaptation to riverine habitats allowed survival of
 RT ancient cetacean lineages.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000).
 DR EMBL; AF304104; AAC32046.1; -.
 DR HSSP; P02787; IABE.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008199; F:feric iron binding; IEA.
 DR GO; GO:0006879; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR InterPro; IPR001156; Peptidase_S60.
 DR Pfam; PF00405; Transferrin; 1.
 DR PRINTS; PR00422; TRANSFERRIN.
 FT NON TER 1
 FT NON TER 81
 SO SEQUENCE 81 AA; 9243 MW; D6EE22B822C8B33 CRC64;

Query Match 95.3%; Score 82; DB 2; Length 81;
 Best Local Similarity 94.1%; Pred. No. 3.2e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 VVARSNGKEDLIWELL 17
Db 39 VVARSVGKEDLIWELL 55

RESULT 5
Q9GL92 PRELIMINARY; PRT; 81 AA.
ID 09GL92;
AC 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DS Transferrin (Fragment).
OS Mesoplodon peruvianus (Peruvian beaked whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Ziphiidae;
OC Mesoplodon.
OX NCBI_TaxID=27617;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20481910; PubMed=11027333; DOI=10.1073/pnas.97.21.11343;
RA Casens I., Vicario S., Maddell V.G., Balchowsky H., Van Belle D.,
RA Ding W., Fan C., Mohan L., Simoes-Lopes P.C., Bastida R., Meyer A.,
RA Stanhope M.J., Mlinkovitch M.C.;
RT "Independent adaptation to riverine habitats allowed survival of
RT ancient cetacean lineages."
RU Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000).
DR EMBL; AF304103; AAC32045.1; -.
DR HSSP; P02787; IJOF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 1.
DR PRINTS; PR00422; TRANSFERRIN.
FT NON_TER 1
SQ SEQUENCE 81 AA; 9138 MW; 1DC9418BF5FAC3 CRC64;

Query Match
Best Local Similarity 95.3%; Score 82; DB 2; Length 81;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
Db 39 VVARSVGKEDLIWELL 55

RESULT 6
Q9GL94 PRELIMINARY; PRT; 81 AA.
ID 09GL94;
AC 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DS Transferrin (Fragment).
OS Inia geoffrensis (Amazon dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Iniidae;
OC Inia.
OX NCBI_TaxID=9725;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20481910; PubMed=11027333; DOI=10.1073/pnas.97.21.11343;
RA Casens I., Vicario S., Maddell V.G., Balchowsky H., Van Belle D.,
RA Ding W., Fan C., Mohan L., Simoes-Lopes P.C., Bastida R., Meyer A.,
RA Stanhope M.J., Mlinkovitch M.C.;
RT "Independent adaptation to riverine habitats allowed survival of
RT ancient cetacean lineages."
RU Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000).
DR EMBL; AF304101; AAC32043.1; -.
DR HSSP; P19134; IJNF.

```

```

DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 1.
DR PRINTS; PR00422; TRANSFERRIN.
FT NON_TER 1
SQ SEQUENCE 81 AA; 9220 MW; 49BD4339D3F1B52A CRC64;

Query Match
Best Local Similarity 93.0%; Score 80; DB 2; Length 81;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
Db 39 VVARSVGKEDLIWELL 55

RESULT 7
Q9GL93 PRELIMINARY; PRT; 81 AA.
ID 09GL93;
AC 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DS Transferrin (Fragment).
OS Physeter catodon (Sperm whale) (Physeter macrocephalus).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Physeteridae; Physeter.
OX NCBI_TaxID=9755;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20481910; PubMed=11027333; DOI=10.1073/pnas.97.21.11343;
RA Casens I., Vicario S., Maddell V.G., Balchowsky H., Van Belle D.,
RA Ding W., Fan C., Mohan L., Simoes-Lopes P.C., Bastida R., Meyer A.,
RA Stanhope M.J., Mlinkovitch M.C.;
RT "Independent adaptation to riverine habitats allowed survival of
RT ancient cetacean lineages."
RU Proc. Natl. Acad. Sci. U.S.A. 97:11343-11347(2000).
DR EMBL; AF304102; AAC32044.1; -.
DR HSSP; P19134; IJNF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 1.
DR PRINTS; PR00422; TRANSFERRIN.
FT NON_TER 1
SQ SEQUENCE 81 AA; 9219 MW; 8B9DEA2153941BA6 CRC64;

Query Match
Best Local Similarity 91.9%; Score 79; DB 2; Length 81;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSNGKEDLIWELL 17
Db 39 VVARSMDKEDLIWELL 55

RESULT 8
TRFE_BOVIN STANDARD; PRT; 704 AA.
ID TRFE_BOVIN;
AC Q29443;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 05-UNL-2004 (Rel. 44, Last annotation update)
DS Sero-transferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal
binding globulin).

```


RC TISSUE=Plasma;
RX MEDLINE=89026775; PubMed=3179277;
RA Bailey S., Evans R.W., Garrate R.C., Gorinsky B., Hasnain S.,
RA Horeburg C., Jhori H., Lindley P.F., Mydin A., Sarra R., Watson J.L.;
RT "Molecular structure of serum transferrin at 3.3-A resolution.";
RL Biochemistry 27:5804-5812(1988).
RP [6]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS)
RA Sarra R., Garrate R.C., Gorinsky B., Jhori H., Lindley P.F.;
RT "High-resolution X-ray studies on rabbit serum transferrin:
RT preliminary structure analysis of the N-terminal half-molecule at 2.3-
RT A resolution.";
RL Acta Crystallogr. B 46:763-771(1990).
CC -I- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate. It is responsible for the
CC transport of iron from sites of absorption and heme degradation to
CC those of storage and utilization. Serum transferrin may also have
CC a further role in stimulating cell proliferation.
CC -I- SUBUNIT: Monomer.
CC -I- SUBCELLULAR LOCATION: Secreted.
CC -I- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -I- DOMAIN: Composed of two homologous domains.
CC -I- SIMILARITY: Belongs to the transferrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC
DR EMBL, X58533, CAA41424.1; -;
DR EMBL, AF031625, AAB94136.1; -;
DR EMBL, AF031611, AAB94136.1; JOINED.
DR EMBL, AF031612, AAB94136.1; JOINED.
DR EMBL, AF031613, AAB94136.1; JOINED.
DR EMBL, AF031614, AAB94136.1; JOINED.
DR EMBL, AF031615, AAB94136.1; JOINED.
DR EMBL, AF031616, AAB94136.1; JOINED.
DR EMBL, AF031617, AAB94136.1; JOINED.
DR EMBL, AF031618, AAB94136.1; JOINED.
DR EMBL, AF031619, AAB94136.1; JOINED.
DR EMBL, AF031620, AAB94136.1; JOINED.
DR EMBL, AF031621, AAB94136.1; JOINED.
DR EMBL, AF031622, AAB94136.1; JOINED.
DR EMBL, AF031623, AAB94136.1; JOINED.
DR EMBL, AF031624, AAB94136.1; JOINED.
DR PDB, 1UNF; X-ray; A=20-695.
DR PDB, 1TFD; X-ray; @=20-323.
DR InterPro: IPR001156; Peptidase_S60.
DR Pfam: PF00405; Transferrin; 2.
DR PRINTS: PRO0422; TRANSFERRIN.
DR SMART; SMO0094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW 3D-structure; Direct protein sequencing; Glycoprotein; Iron transport;
KW Metal-binding; Repeat; Signal; Transport.
FT SIGNAL 1 19
FT CHAIN 20 695 Serotransferrin.
FT REPEAT 20 355 1.
FT REPEAT 356 695 2.
FT DISULFID 28 67
FT DISULFID 38 58
FT DISULFID 137 213
FT DISULFID 156 350
FT DISULFID 177 193
FT DISULFID 180 196
FT DISULFID 190 198
FT DISULFID 246 260
FT DISULFID 358 612

FT DISULFID 364 396
FT DISULFID 374 387
FT DISULFID 421 690
FT DISULFID 436 653
FT DISULFID 468 539
FT DISULFID 492 681
FT DISULFID 502 516
FT DISULFID 513 522
FT DISULFID 579 593
FT DISULFID 611 606
FT CARBOHYD 509 509
FT METAL 82 82
FT METAL 114 114
FT METAL 207 207
FT METAL 268 268
FT METAL 411 411
FT METAL 444 444
FT METAL 533 533
FT METAL 601 601
FT BINDING 139 139
FT BINDING 143 143
FT BINDING 145 145
FT BINDING 146 146
FT BINDING 470 470
FT BINDING 474 474
FT BINDING 476 476
FT BINDING 477 477
FT VARIANT 517 517
FT CONFLICT 7 7
FT CONFLICT 47 47
FT CONFLICT 50 50
FT STRAND 24 30
FT HELIX 31 48
FT TURN 51 52
FT STRAND 55 61
FT HELIX 64 72
FT TURN 73 74
FT STRAND 78 81
FT HELIX 83 90
FT TURN 92 94
FT STRAND 96 104
FT STRAND 111 111
FT STRAND 113 121
FT TURN 122 123
FT HELIX 128 130
FT TURN 132 133
FT STRAND 136 138
FT TURN 141 142
FT TURN 144 147
FT HELIX 148 154
FT HELIX 155 157
FT HELIX 165 172
FT STRAND 176 177
FT TURN 179 180
FT TURN 183 185
FT HELIX 187 190
FT TURN 191 192
FT TURN 194 195
FT TURN 200 201
FT TURN 203 204
FT HELIX 206 215
FT TURN 216 217
FT STRAND 221 225
FT TURN 226 227
FT HELIX 232 232
FT HELIX 236 239
FT TURN 240 241
FT STRAND 242 245
FT TURN 247 248
FT STRAND 251 253
FT HELIX 254 256
FT TURN 257 258
FT STRAND 263 266

N-linked (GlcNAc. . .).
Iron 1.
Iron 1.
Iron 1.
Iron 1.
Iron 2.
Iron 2.
Iron 2.
Carbonate 1.
Carbonate 1 (via amide nitrogen).
Carbonate 1 (via amide nitrogen).
Carbonate 2.
Carbonate 2.
Carbonate 2 (via amide nitrogen).
Carbonate 2 (via amide nitrogen).
V-> I. (in Ref. 1).
Missing (in Ref. 3).
K-> S (in Ref. 3).
P-> Y (in Ref. 3).

```

FT STRAND 269 273
FT HELIX 279 293
FT TURN 303 304
FT TURN 307 308
FT TURN 316 317
FT STRAND 320 323
FT TURN 326 327
FT HELIX 330 334
FT HELIX 336 346
FT TURN 347 348

Query Match 87.2%; Score 75; DB 1; Length 695;
Best Local Similarity 88.2%; Pred. No. 0.00047;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VVARSMGKEDLIWELL 17
Db 270 VVARSDGKEDLIWELL 286

RESULT 10
ICA_PIG STANDARD; PRT; 704 AA.
AC Q29545;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Inhibitor of carbonic anhydrase precursor.
GN Name=ICA;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sue.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RA MEDLINE:97254619; PubMed:9100029; DOI=10.1021/b19627424;
RA Muebbers M.W., Roush E.D., Decastro C.M., Fierke C.A.;
RT "Cloning, sequencing, and recombinant expression of the porcine
RT inhibitor of carbonic anhydrase: a novel member of the transferrin
RT family."
RL Biochemistry 36:4327-4336(1997).
RN [2]
RA CHARACTERIZATION.
RA MEDLINE:93099129; PubMed:1463741;
RA Roush E.D., Fierke C.A.;
RT "Purification and characterization of a carbonic anhydrase II
RT inhibitor from porcine plasma."
RL Biochemistry 31:12536-12542(1992).
CC -1- FUNCTION: Specifically binds and inhibits carbonic anhydrase II
CC with nanomolar affinity.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Plasma.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- PTM: N-glycosylated.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U36916; AAB58956.1; -.
CC PIR: I47228; I47228.
CC HSSP: P09571; 1H76.
CC InterPro: IPR001156; Peptidase_S60.
CC Pfam: PF00405; Transferrin_2.
CC PRINTS: PR00422; TRANSFERRIN.
CC SMART: SM00094; TR_FER_2.
CC PROSITE: PS00205; TRANSFERRIN_1; 2.

```

```

DR PROSITE: PS00206; TRANSFERRIN_2; 1.
DR PROSITE: PS00207; TRANSFERRIN_3; 2.
KW Direct protein sequencing; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19
FT CHAIN 20 704
FT REPEAT 20 351
FT REPEAT 352 704
FT DISULFID 28 67
FT DISULFID 38 58
FT DISULFID 137 213
FT DISULFID 172 188
FT DISULFID 175 196
FT DISULFID 185 198
FT DISULFID 246 260
FT DISULFID 360 392
FT DISULFID 370 383
FT DISULFID 417 699
FT DISULFID 440 662
FT DISULFID 472 549
FT DISULFID 496 690
FT DISULFID 506 520
FT DISULFID 517 532
FT DISULFID 589 603
FT CARBOHYD 491 491
SQ SEQUENCE 704 AA; 77634 MW; 16B80E5191EB36 CRC64;

Query Match 87.2%; Score 75; DB 1; Length 704;
Best Local Similarity 88.2%; Pred. No. 0.00048;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VVARSMGKEDLIWELL 17
Db 270 VVARSDGKEDLIWELL 286

RESULT 11
Q7TSX8 PRELIMINARY; PRT; 694 AA.
AC Q7TSX8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transferrin.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Rinaudo J.A.S., Gerin J.L.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
CC EMBL: AY288100; AAP37129.1; -.
CC HSSP: P19134; 1UNF.
CC GO: GO:0005576; C:extracellular; IEA.
CC GO: GO:0008199; F:ferric iron binding; IEA.
CC GO: GO:0006879; P:iron ion homeostasis; IEA.
CC GO: GO:0006826; P:iron ion transport; IEA.
CC GO: GO:0006810; P:iron ion transport; IEA.
CC InterPro: IPR001156; Peptidase_S60.
CC Pfam: PF00405; Transferrin_2.
CC SMART: SM00094; TR_FER_2.
CC PROSITE: PS00205; TRANSFERRIN_1; 2.
CC PROSITE: PS00206; TRANSFERRIN_2.
CC PROSITE: PS00207; TRANSFERRIN_3; 2.
CC Itron transport; Metal-binding; Transport.
SQ SEQUENCE 694 AA; 76466 MW; 40053F7DC1CFC8A7 CRC64;

```

Query Match 83.7%; Score 72; DB 2; Length 694;
 Best Local Similarity 82.4%; Pred. No. 0.0016;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARGMGKEDLIWELL 17
 ||||:|||||||
 DB 270 VVARTVDGKEDLIWELL 286

RESULT 12
 TRFL CAMDR STANDARD; PRT; 708 AA.
 ID TRFL CAMDR STANDARD; PRT; 708 AA.
 AC Q9TUM0; Q9WZS5; Rel. 40; Created)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 25-OCT-2004 (Rel. 45; Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin).
 GN Name=LTF;
 OS Camelus dromedarius (Dromedary) (Arabian camel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
 NCBI_taxid=9838;
 OK NCBI_taxid=9838;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Somali; TISSUE=Lactating mammary gland;
 RA Kappel S.R., Ackermann M., Farah Z., Puhan Z.;
 RT "Sequence analysis of camel (Camelus dromedarius) lactoferrin";
 RL Int. Dairy J. 9:481-486(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
 RT Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Transferrins are iron binding transport proteins which
 can bind two atoms of ferric iron in association with the binding
 of an anion, usually bicarbonate (By similarity).
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to license@sib.ch).
 CC -----
 CC EMBL: AJ131674; CAB53387.1; -;
 CC EMBL: AF165879; AAF83241.1; -;
 CC PDB: 1DTZ; X-ray; A=20-708.
 CC InterPro: IPR001156; Peptidase_S60.
 CC Pfam: PF00405; Transferrin; 2.
 CC PRINTS: PR00422; TRANSFERRIN.
 CC SMART: SMO0094; TR_PFR; 2.
 CC PROSITE: PS00305; TRANSFERRIN_1; 2.
 CC PROSITE: PS00206; TRANSFERRIN_2; 2.
 CC PROSITE: PS00207; TRANSFERRIN_3; 2.
 CC 3D-structure: Glycoprotein; Iron transport; Metal-binding; Repeat;
 CC Signal; Transport.
 CC -----
 CC SIGNAL 1 19 By similarity.
 CC CHAIN 20 708 Lactotransferrin.
 CC REPEAT 20 363 1.
 CC REPEAT 364 708 2.
 CC DISULFID 28 64 By similarity.
 CC DISULFID 38 55 By similarity.
 CC DISULFID 134 217 By similarity.
 CC DISULFID 176 192 By similarity.
 CC DISULFID 189 200 By similarity.
 CC DISULFID 250 264 By similarity.

FT DISULFID 367 399 By similarity.
 FT DISULFID 377 390 By similarity.
 FT DISULFID 424 703 By similarity.
 FT DISULFID 444 666 By similarity.
 FT DISULFID 476 551 By similarity.
 FT DISULFID 500 694 By similarity.
 FT DISULFID 510 524 By similarity.
 FT DISULFID 521 534 By similarity.
 FT DISULFID 592 606 By similarity.
 FT DISULFID 644 649 By similarity.
 FT METAL 79 79 Iron 1 (By similarity).
 FT METAL 111 111 Iron 1 (By similarity).
 FT METAL 211 211 Iron 1 (By similarity).
 FT METAL 272 272 Iron 1 (By similarity).
 FT METAL 414 414 Iron 2 (By similarity).
 FT METAL 452 452 Iron 2 (By similarity).
 FT METAL 545 545 Iron 2 (By similarity).
 FT METAL 614 614 Iron 2 (By similarity).
 FT BINDING 136 136 Carbonate 1 (By similarity).
 FT BINDING 140 140 Carbonate 1 (By similarity).
 FT BINDING 142 142 Carbonate 1 (via amide nitrogen) (By similarity).
 FT BINDING 143 143 Carbonate 1 (via amide nitrogen) (By similarity).
 FT BINDING 478 478 Carbonate 2 (By similarity).
 FT BINDING 482 482 Carbonate 2 (By similarity).
 FT BINDING 484 484 Carbonate 2 (via amide nitrogen) (By similarity).
 FT BINDING 485 485 Carbonate 2 (via amide nitrogen) (By similarity).
 FT CARBOHYD 252 252 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 385 385 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 537 537 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 594 594 N-linked (GlcNAc...) (potential).
 FT CONFLICT 261 261 F -> S (in Ref. 2).
 FT CONFLICT 304 304 G -> A (in Ref. 2).
 FT CONFLICT 330 330 S -> P (in Ref. 2).
 FT CONFLICT 492 494 LUS -> PLF (in Ref. 2).
 FT CONFLICT 506 506 L -> F (in Ref. 2).
 FT CONFLICT 609 609 A -> P (in Ref. 2).
 FT CONFLICT 642 642 R -> Q (in Ref. 2).
 FT STRAND 25 29
 FT HELIX 32 46
 FT TURN 47 49
 FT STRAND 53 57
 FT HELIX 61 69
 FT TURN 70 71
 FT STRAND 75 78
 FT HELIX 80 87
 FT TURN 89 91
 FT STRAND 93 99
 FT STRAND 101 101
 FT STRAND 108 108
 FT STRAND 118 118
 FT HELIX 125 127
 FT TURN 129 130
 FT STRAND 132 135
 FT TURN 138 139
 FT TURN 141 144
 FT HELIX 145 150
 FT TURN 151 151
 FT HELIX 152 154
 FT TURN 155 155
 FT TURN 160 161
 FT HELIX 164 171
 FT STRAND 174 176
 FT TURN 178 179
 FT TURN 182 184
 FT HELIX 186 189
 FT TURN 190 191
 FT HELIX 196 198
 FT TURN 199 200
 FT TURN 204 205

```

FT TURN 207 208
FT HELIX 210 219
FT STRAND 225 229
FT TURN 230 231
FT HELIX 232 236
FT HELIX 240 243
FT TURN 244 245
FT STRAND 246 250
FT TURN 251 253
FT STRAND 254 256
FT HELIX 258 260
FT TURN 261 263
FT STRAND 267 270
FT TURN 273 277
FT TURN 279 280
FT HELIX 283 297
FT TURN 299 300
FT TURN 321 322
FT STRAND 326 328
FT TURN 331 332
FT HELIX 335 339
FT HELIX 341 348
FT TURN 349 351
FT HELIX 354 362
FT STRAND 364 369
FT HELIX 371 384
FT TURN 385 386
FT STRAND 388 393
FT HELIX 396 404
FT TURN 405 406
FT STRAND 410 413
FT HELIX 415 422
FT TURN 423 425
FT STRAND 427 434
FT TURN 437 438
FT STRAND 444 446
FT TURN 453 459
FT STRAND 467 472
FT TURN 474 477
FT TURN 480 481
FT TURN 483 493
FT TURN 502 503
FT STRAND 508 510
FT TURN 512 513
FT TURN 516 517
FT TURN 519 520
FT STRAND 521 521
FT STRAND 527 527
FT TURN 528 530
FT STRAND 531 531
FT TURN 538 539
FT TURN 541 542
FT HELIX 544 553
FT TURN 554 555
FT STRAND 559 563
FT HELIX 564 567
FT TURN 568 569
FT TURN 579 580
FT TURN 586 587
FT STRAND 588 589
FT TURN 593 594
FT HELIX 600 605
FT STRAND 610 610
FT STRAND 615 618
FT TURN 620 622
FT HELIX 623 637

```

Query Match 83.7%; Score 72; DB 1; Length 708;

Best Local Similarity: 82.4%; Pred. No. 0.0016; 1; Indels 0; Gaps 0;

Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17

|||||:|||||:|

DB 274 VVARSMGKEDLIWKL 290

RESULT 13

06LC78 PRELIMINARY; PRT; 117 AA.

AC 06LC78;

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, last annotation update)

DE Lactoferrin (Fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovinae; Bos.

OX NCBI_TaxID=9913;

RP [1] SEQUENCE FROM N.A.

RC STRAIN=Holstein;

RA Noble M.S., Hurley W.L.;

Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Transferrins are iron binding transport proteins which

bind ferric iron in association with the binding of an anion,

usually bicarbonate (By similarity).

-1- SIMILARITY: Belongs to the transferrin family.

EMBL: U82254; AAB62030.1; -.

DR HSSP; Q29477; JMW.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0008199; F:ferric iron binding; IEA.

DR GO; GO:0003700; F:transcription factor activity; IEA.

DR GO; GO:0006879; P:iron ion homeostasis; IEA.

DR GO; GO:0006826; P:iron ion transport; IEA.

DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

DR GO; GO:0006810; P:transport; IEA.

DR InterPro; IPR002197; HTH_F15.

DR Pfam; PF00405; Transferrin; 1.

DR PRINTS; PRO1590; HTHFRS.

DR PRINTS; PRO0422; TRANSFERRIN.

DR SMART; SM00094; TR_FER; 1.

DR PROSITE; PS00207; TRANSFERRIN_3; 1.

KW Iron transport; Metal-binding; Transport.

FT NON_TER 1 1

FT NON_TER 117 117

SQ SEQUENCE 117 AA; 13206 MW; FD344261D8D56B66 CRC64;

Query Match 82.6%; Score 71; DB 2; Length 117;

Best Local Similarity: 82.4%; Pred. No. 0.00038; 1; Indels 0; Gaps 0;

Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMGKEDLIWELL 17

|||||:|||||:|

DB 39 VVARSVGKEDLIWKL 55

RESULT 14

06LBN7 PRELIMINARY; PRT; 681 AA.

AC 06LBN7;

DT 05-JUL-2004 (TREMBlrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)

DT 05-JUL-2004 (TREMBlrel. 27, last annotation update)

DE Lactoferrin (Fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovinae; Bos.

OX NCBI_TaxID=9913;

RP [1] SEQUENCE FROM N.A.

RC TISSUE=Mammary;

MEADLINE=9108328; PubMed=2263492;

RA Mead P.E., Tweedie J.W.;

```

RT "cDNA and protein sequence of bovine lactoferrin.";
RT Nucleic Acids Res. 18:7167-7167(1990).
RU [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary;
RA Tweedie J.;
RU Submitted (JAN-1991) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL; X54801; CAA38572.1; -.
DR HSSP; 029477; JMW1.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR01156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FRR; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
DR Iron transport; Metal-binding; Transport.
KW NON TER
FT CHAIN 1 681 Bovine lactoferrin.
FT SEQUENCE 681 AA; 75181 MW; 4927DE88144D99BA CRC64;
SQ
Query Match 82.6%; Score 71; DB 2; Length 681;
Best Local Similarity 82.4%; Pred. No. 0.0023;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 VVARSNGKEDLIWELL 17
Db 247 VVARSVDGKEDLIWKL 263
RESULT 15
TRFL_BOVIN STANDARD; PRT; 708 AA.
ID TRFL_BOVIN P24627; Q29629; Q9MZY3;
AC P24627; Q29629; Q9MZY3;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferricin B
DE (Lifcin B)].
GN Name=LTF;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos
OC NCBI_TaxId=9913;
OX NCBI_TaxId=9913;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Submaxillary gland;
RX MEDLINE=91160550; PubMed=2001696;
RA Pierce A., Colavizza D., Benaissa M., Mace P., Tatar A.,
RA Montreuil J., Spik G.;
RT "Molecular cloning and sequence analysis of bovine lactotransferrin.";
RT Eur. J. Biochem. 196;177-184(1991).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE=92028986; PubMed=1718281;
RA Goodman R.E., Schanbacher F.L.;
RA "Bovine lactoferrin mRNA: sequence, analysis, and expression in the
RA mammary gland.";
RT Biochem. Biophys. Res. Commun. 180;75-84(1991).
RN (3)
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Teang T.C., Burns D.K., Wang F., Pan Y.C.E., Schmidt A.M., Stern D.;

```

```

RT "Cloning of a 80-kD advanced glycosylation end product (AGE) binding
RT protein from bovine lung.";
RT FASEB J. 6;233-233(1991).
RN (4)
RP SEQUENCE FROM N.A.
RC TISSUE=Blood, and Mammary gland;
RX MEDLINE=94266164; PubMed=8206385; DOI=10.1016/0378-1119(94)90108-2;
RA Seyfert H.-M., Tuckorick A., Interthal H., Koczan D., Hobom G.;
RT "Structure of the bovine lactoferrin-encoding gene and its promoter.";
RT Gene 143;265-269(1994).
RN (5)
RP SEQUENCE FROM N.A.
RA Nakamura I., Shinazaki K., Yagi Y., Watanabe A.;
RU Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
RN (6)
RP SEQUENCE OF 20-59.
RX MEDLINE=90031466; PubMed=2805645;
RA Rejman J.U., Hegarty H.M., Hurley W.L.;
RT "Purification and characterization of bovine lactoferrin from
RT secretions of the involuting mammary gland: identification of multiple
RT molecular weight forms";
RT Comp. Biochem. Physiol. 93B;929-934(1989).
RN (7)
RP FUNCTION OF LACTOFERRICIN.
RX PubMed=8980754;
RA Hoek K.S., Milne J.M., Griewe P.A., Dionysius D.A., Smith R.;
RT "Antibacterial activity in bovine lactoferrin-derived peptides.";
RT Antimicrob. Agents Chemother. 41;54-59(1997).
RN (8)
RP ANTIMICROBIAL ACTIVITY.
RX PubMed=14650542;
RA Kutila T., Pyorala S., Saloniemi H., Kaartinen L.;
RT "Antibacterial effect of bovine lactoferrin against udder pathogens.";
RT Acta Vet. Scand. 44;35-42(2003).
RN (9)
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE=98062367; PubMed=9398529; DOI=10.1006/jmbi.1997.1386;
RA Moore S.A., Anderson B.F., Groom C.R., Haridas M., Baker E.N.;
RT "Three-dimensional structure of dimeric bovine lactoferrin at 2.8-A
RT resolution.";
RT J. Mol. Biol. 274;222-236(1997).
RN (10)
RP STRUCTURE BY NMR OF 36-60.
RX MEDLINE=98190007; PubMed=9521752; DOI=10.1021/b1972323m;
RA Hwang P.M., Zhou N., Shan X., Arrowsmith C.H., Vogel H.J.;
RT "Three-dimensional solution structure of lactoferricin B, an
RT antimicrobial peptide derived from bovine lactoferrin.";
RT Biochemistry 37;4288-4298(1998).
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate.
CC -1- FUNCTION: Lactotransferrin has antimicrobial activity. The most
CC effective inhibitory activity was seen against E.coli and
CC P.aeruginosa.
CC -1- FUNCTION: Lactoferricin B is an antimicrobial peptide. Inhibits
CC the growth of Gram-negative and Gram-positive bacteria.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-ch).
DR EMBL; X57084; CAA40366.1; -.
DR EMBL; M63502; AAA30617.1; -.
DR EMBL; U08604; AAA30609.1; -.
DR EMBL; U19933; AAA21722.1; -.

```

DR EMBL; L19983; AAA21722.1; JOINED.
 DR EMBL; L19983; AAA21722.1; JOINED.
 DR EMBL; L19983; AAA21722.1; JOINED.
 DR EMBL; L19985; AAA21722.1; JOINED.
 DR EMBL; L19986; AAA21722.1; JOINED.
 DR EMBL; L19986; AAA21722.1; JOINED.
 DR EMBL; L19989; AAA21722.1; JOINED.
 DR EMBL; L19991; AAA21722.1; JOINED.
 DR EMBL; L19992; AAA21722.1; JOINED.
 DR EMBL; AB046664; BAB03470.1; -.
 DR PIR; I45919; TFEOL.
 DR PDB; 1BLF; X-ray; @=20-708.
 DR PDB; 1LFC; NMR; @=36-60.
 DR PDB; 1NKC; X-ray; A=361-708.
 DR GlycoSuiteDB; P24627; -.
 DR InterPro; IPR001156; Peptidase_S60.
 DR Pfam; PF00405; Transferrin; 2.
 DR PRINTS; PR00422; TRANSFERRIN.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 2.
 DR 3D-structure; Antibiotic; Direct protein sequencing; Glycoprotein;
 KM Iron transport; Metal-binding; Repeat; Signal; Transport.
 FT SIGNAL 1 19
 FT CHAIN 20 708 Lactotransferrin.
 FT PEPTIDE 36 60 Lactoferricin B.
 FT REPEAT 20 363 1.
 FT REPEAT 364 708 2.
 FT DISULFID 28 64 By similarity.
 FT DISULFID 38 55 By similarity.
 FT DISULFID 134 217 By similarity.
 FT DISULFID 176 192 By similarity.
 FT DISULFID 189 200 By similarity.
 FT DISULFID 250 264 By similarity.
 FT DISULFID 367 399 By similarity.
 FT DISULFID 377 390 By similarity.
 FT DISULFID 424 703 By similarity.
 FT DISULFID 444 666 By similarity.
 FT DISULFID 476 551 By similarity.
 FT DISULFID 500 694 By similarity.
 FT DISULFID 510 524 By similarity.
 FT DISULFID 521 534 By similarity.
 FT DISULFID 592 606 By similarity.
 FT DISULFID 644 649 By similarity.
 FT METAL 79 79 Iron 1.
 FT METAL 111 111 Iron 1.
 FT METAL 211 211 Iron 1.
 FT METAL 272 272 Iron 1.
 FT METAL 414 414 Iron 2.
 FT METAL 452 452 Iron 2.
 FT METAL 545 545 Iron 2.
 FT METAL 614 614 Iron 2.
 FT BINDING 136 136 Carbonate 1.
 FT BINDING 140 140 Carbonate 1 (via amide nitrogen).
 FT BINDING 142 142 Carbonate 1 (via amide nitrogen).
 FT BINDING 143 143 Carbonate 1 (via amide nitrogen).
 FT BINDING 147 148 Carbonate 2.
 FT BINDING 148 148 Carbonate 2.
 FT BINDING 148 148 Carbonate 2 (via amide nitrogen).
 FT BINDING 148 148 Carbonate 2 (via amide nitrogen).
 FT BINDING 148 148 Carbonate 2 (via amide nitrogen).
 FT CARBOHYD 252 252 N-linked (GlcNAc...).
 FT CARBOHYD 387 387 /FTid=CAR_000186.
 FT CARBOHYD 495 495 N-linked (GlcNAc...).
 FT CARBOHYD 495 495 N-linked (GlcNAc...).
 FT CARBOHYD 564 564 /FTid=CAR_000197.
 FT CARBOHYD 564 564 N-linked (GlcNAc...).
 FT CARBOHYD 564 564 /FTid=CAR_000198.
 FT CARBOHYD 564 564 E->A (in Ref. 4).
 FT CARBOHYD 564 564 RA->PG (in Ref. 2).
 FT CARBOHYD 564 564 I->V (in Ref. 1 and 4).
 FT CARBOHYD 564 564 LQ->PP (in Ref. 1).

FT CONFLICT 264 264 C -> Y (in Ref. 4).
 FT CONFLICT 273 273 A -> P (in Ref. 4).
 FT CONFLICT 281 281 G -> R (in Ref. 4).
 FT CONFLICT 291 291 S -> A (in Ref. 4).
 FT CONFLICT 297 297 F -> S (in Ref. 2).
 FT CONFLICT 340 340 G -> A (in Ref. 1).
 FT CONFLICT 418 418 I -> V (in Ref. 4).
 FT CONFLICT 439 439 H -> Y (in Ref. 1).
 FT CONFLICT 459 459 K -> R (in Ref. 4).
 FT CONFLICT 514 514 A -> R (in Ref. 1).
 FT CONFLICT 632 632 H -> R (in Ref. 5).
 FT STRAND 25 29
 FT HELIX 32 45
 FT HELIX 46 48
 FT STRAND 53 57
 FT HELIX 61 69
 FT TURN 70 71
 FT STRAND 75 78
 FT HELIX 80 87
 FT TURN 89 91
 FT STRAND 93 102
 FT STRAND 107 108

Query Match 82.6%; Score 71; DB 1; Length 708;
 Best Local Similarity 82.4%; Pred. No. 0.0024; 1; Indels 0; Gaps 0;
 Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VVARSMGKEDLIWELL 17
 Db 274 VVARSVGKEDLIWKL 290

Search completed: November 1, 2005, 12:54:29
 Job time : 85.25 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: November 1, 2005, 12:56:01 ; Search time 162 Seconds
(without alignments)
40.586 Million cell updates/sec

Title: US-10-612-162a-1

Sequence: 1 VVARSMGKEDLIWELL 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 664154

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980a:***
2: geneseqp1990a:***
3: geneseqp2000a:***
4: geneseqp2001a:***
5: geneseqp2002a:***
6: geneseqp2003a:***
7: geneseqp2003b:***
8: geneseqp2004a:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	86	100.0	17 8 ADG46075	Adg46075 Human CDT
2	70	81.4	13 8 ADG46088	Adg46088 Human CDT
3	69	80.2	13 8 ADG46089	Adg46089 Human CDT
4	43	50.0	17 8 ADRI5903	Adri5903 Transferr
5	43	50.0	17 8 ADRI5963	Adri5963 Transferr
6	43	50.0	17 8 ADRI5963	Adri5963 Transferr
7	35	40.7	13 2 AAR49486	Aar49486 Bovine tr
8	35	40.7	13 2 AAR47038	Aar47038 Bovine tr
9	35	40.7	15 2 AAR49426	Aar49426 Immunomod
10	34	39.5	15 6 ABR30177	Abri30177 Human can
11	33	38.4	9 8 ADRI9363	Adri9363 TRPI derl
12	33	38.4	13 5 ABP63629	Abp63629 Human MHC
13	33	38.4	13 5 ABP63628	Abp63628 Human MHC
14	33	38.4	13 5 ABP63627	Abp63627 Human MHC
15	33	38.4	13 5 AAE27219	AAe27219 Human obe
16	33	38.4	13 5 AAE27218	AAe27218 Human obe
17	33	38.4	13 5 AAE27220	AAe27220 Human obe
18	32	37.2	6 8 ADRI5892	Adri5892 Transferr
19	32	37.2	10 7 ADLI7482	Adli7482 Human INA
20	32	37.2	14 4 ABB56643	Abb56643 Human SNP
21	32	37.2	15 6 ABR33637	Abri33637 Human can
22	32	37.2	15 6 ABR33654	Abri33654 Human can
23	32	37.2	15 6 ABR33753	Abri33753 Human can
24	32	37.2	15 6 ABR33660	Abri33660 Human can
25	32	37.2	15 8 ADR68334	Adr68334 Androgen

26	31	36.0	6 8 ADO85220	Ado85220 Milk proc
27	31	36.0	6 8 ADO67999	Ado67999 TNF-alpha
28	31	36.0	9 4 AAG99695	Aag99695 ERA bindi
29	31	36.0	9 4 AAG99702	Aag99702 ERA bindi
30	31	36.0	15 7 ADM75931	Adm75931 Human MHC
31	31	34.9	9 7 ADE66590	Ade66590 Human 161
32	30	34.9	9 7 ADE67321	Ade67321 Human 161
33	30	34.9	9 7 ADE67550	Ade67550 Human 161
34	30	34.9	9 7 ADE67775	Ade67775 Human 161
35	30	34.9	9 7 ADE69001	Ade69001 Human 161
36	30	34.9	9 7 ADE66352	Ade66352 Human 161
37	30	34.9	9 7 ADE66836	Ade66836 Human 161
38	30	34.9	9 7 ADE67558	Ade67558 Human 161
39	30	34.9	9 7 ADE66106	Ade66106 Human 161
40	30	34.9	9 7 ADE66111	Ade66111 Human 161
41	30	34.9	9 7 ADE68044	Ade68044 Human 161
42	30	34.9	9 7 ADE66593	Ade66593 Human 161
43	30	34.9	9 7 ADE67316	Ade67316 Human 161
44	30	34.9	9 7 ADE68899	Ade68899 Human 161
45	30	34.9	9 7 ADE66345	Ade66345 Human 161

ALIGNMENTS

RESULT 1
ID ADG46075 standard; peptide, 17 AA.
XX
AC ADG46075;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human CDT peptide fragment #1.
XX
KW antibody; carbohydrate-deficient transferrin; CDT;
KM non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.
XX
OS Homo sapiens.
XX
PN EP1378521-A1.
XX
PD 07-JAN-2004.
XX
PF 19-MAY-2003; 2003EP-00011334.
XX
PR 05-JUL-2002; 2002DE-01030550.
XX
PA (DADE-) DADE BEHRING MAREBURG GMBH.
XX
PI Althaus H;
XX
DR WPI; 2004-073743/08.
XX
PT New antibody specific for carbohydrate-deficient transferrin, useful for
PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.
XX
PS Claim 4; SEQ ID NO 1; 21pp; German.
XX
XX
XX This invention describes a novel antibody that, in aqueous solution,
XX binds selectively to carbohydrate-deficient transferrin (CDT) without
XX having to bind CDT to a solid phase. The invention also describes an
XX antibody that binds selectively to CDT at regions containing the
XX sequences VVARSMGKEDLIWELL, TTEDSIATKINGEADAMSIDGAF, SKLSMGSLNISEPN and
XX YEKLYGEYVAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
XX using the antibodies of the invention. The antibodies of the invention
XX are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
XX antibodies are obtained by immunisation with non-glycosylated
XX transferrin, or a fragment, then generation of hybridomas by standard
XX fusion of spleen and myeloma cells. Hybridomas are then selected for
XX production of antibodies that specifically bind CDT from the aqueous
XX phase. The antibodies are useful for diagnosis of alcoholism, CDT, which

CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
 CC alcohols. The antibodies allow direct detection of CDT in solution,
 CC eliminating the need for immobilising it on a solid phase (as required
 CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
 CC fragments used in the method of the invention.

XX Sequence 17 AA;

Query Match 100.0%; Score 86; DB 8; Length 17;
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17
 |||||
 DB 1 VVARSWGKEDLIWELL 17

RESULT 2

ADG46088 standard; peptide; 13 AA.

XX ADG46088;

XX 25-MAR-2004 (first entry)

XX Human CDT peptide fragment #14.

XX antibody; carbohydrate-deficient transferrin; CDT;

XX non-glycosylated transferrin; alcoholic; diagnosis; human.

OS Homo sapiens.

XX EPI378521-A1.

XX 07-JAN-2004.

XX 19-MAY-2003; 2003EP-00011334.

XX 05-JUL-2002; 2002DE-01030550.

XX (DADE-) DADE BEHRING MARBURG GMBH.

XX Althaus H;

XX WPI; 2004-073743/08.

XX New antibody specific for carbohydrate-deficient transferrin, useful for
 PT diagnosis of alcoholism, can bind its target in solution, eliminating
 PT need for immobilization.

XX Example 7; Page 15; 21pp; German.

XX This invention describes a novel antibody that, in aqueous solution,
 CC binds selectively to carbohydrate-deficient transferrin (CDT) without
 CC having to bind CDT to a solid phase. The invention also describes an
 CC antibody that binds selectively to CDT at regions containing the
 CC sequences VVARSWGKEDLIWELL, TTEDSIKIMNGEADAMSLDGSF, SKUSMSGGLNLSBN and
 CC YEKYLGEYVAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
 CC using the antibodies of the invention. The antibodies of the invention
 CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
 CC antibodies are obtained by immunisation with non-glycosylated
 CC transferrin, or a fragment, then generation of hybridomas by standard
 CC fusion of spleen and myeloma cells. Hybridomas are then selected for
 CC production of antibodies that specifically bind CDT from the aqueous
 CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
 CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
 CC alcohols. The antibodies allow direct detection of CDT in solution,
 CC eliminating the need for immobilising it on a solid phase (as required
 CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
 CC fragments used in the method of the invention.

XX Sequence 13 AA;

Query Match 81.4%; Score 70; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9.9e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ARSWGKEDLIWE 15
 |||||
 DB 1 ARSWGKEDLIWE 13

RESULT 3

ADG46089 standard; peptide; 13 AA.

XX ADG46089;

XX 25-MAR-2004 (first entry)

XX Human CDT peptide fragment #15.

XX antibody; carbohydrate-deficient transferrin; CDT;

XX non-glycosylated transferrin; alcoholic; diagnosis; human.

OS Homo sapiens.

XX EPI378521-A1.

XX 07-JAN-2004.

XX 19-MAY-2003; 2003EP-00011334.

XX 05-JUL-2002; 2002DE-01030550.

XX (DADE-) DADE BEHRING MARBURG GMBH.

XX Althaus H;

XX WPI; 2004-073743/08.

XX New antibody specific for carbohydrate-deficient transferrin, useful for
 PT diagnosis of alcoholism, can bind its target in solution, eliminating
 PT need for immobilization.

XX Example 7; Page 15; 21pp; German.

XX This invention describes a novel antibody that, in aqueous solution,
 CC binds selectively to carbohydrate-deficient transferrin (CDT) without
 CC having to bind CDT to a solid phase. The invention also describes an
 CC antibody that binds selectively to CDT at regions containing the
 CC sequences VVARSWGKEDLIWELL, TTEDSIKIMNGEADAMSLDGSF, SKUSMSGGLNLSBN and
 CC YEKYLGEYVAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
 CC using the antibodies of the invention. The antibodies of the invention
 CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
 CC antibodies are obtained by immunisation with non-glycosylated
 CC transferrin, or a fragment, then generation of hybridomas by standard
 CC fusion of spleen and myeloma cells. Hybridomas are then selected for
 CC production of antibodies that specifically bind CDT from the aqueous
 CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
 CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
 CC alcohols. The antibodies allow direct detection of CDT in solution,
 CC eliminating the need for immobilising it on a solid phase (as required
 CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
 CC fragments used in the method of the invention.

XX Sequence 13 AA;

Query Match 80.2%; Score 69; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00015;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SMGKEDLIWELL 17
 |||||
 DB 1 SMGKEDLIWELL 13

RESULT 4
ID ADR15903 standard; peptide; 17 AA.
XX
AC ADR15903;
XX
DT 04-NOV-2004 (first entry)
XX
DE Transferrin peptide fragment #61.
XX
KM glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.
XX
OS Synthetic.
XX
PN WO2004070389-A1.
XX
PD 19-AUG-2004.
XX
PF 06-FEB-2004; 2004WO-GB000480.
XX
PR 06-FEB-2003; 2003GB-00002740.
XX
PA (AXIS-) AXIS-SHIELD ASA.
XX
PI Rye PD;
XX
DR WPI; 2004-625547/60.
XX
XX
PT Assay for differentiating protein isoforms to determine their
PT concentrations in sample e.g. blood, involves contacting the sample with
PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
PT detecting.
XX
XX
PS Disclosure; Page 15; 30pp; English.
XX
CC The present invention describes an assay for a protein having at least
CC two isoforms with different glycosylation patterns. The assay involves
CC contacting a sample containing the protein with a proteolytic enzyme,
CC followed by detecting the content or relative content of at least one
CC peptide fragment produced by proteolysis. Also described is a kit for the
CC assay method comprising the proteolytic enzyme and a substrate bound
CC specific binding partner (SI) for at least 2 of the isoforms of the
CC proteins. The method can be used for assaying isoforms of proteins
CC according to their glycosylation pattern to determine their concentration
CC or relative concentration in the sample or material (e.g. blood). The
CC method avoids use of antibodies for distinguishing between glycosylated
CC isoforms of the proteins. The present sequence represents a transferrin
CC peptide fragment which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 17 AA;
XX
Query Match 50.0%; Score 43; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 EDLIWELL 17
DB 1 EDLIWELL 8
XX
RESULT 5
ID ADR15963 standard; peptide; 17 AA.
XX
AC ADR15963;
XX
DT 04-NOV-2004 (first entry)
XX
DE Transferrin peptide fragment #121.
XX
KM glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.
XX

XX
OS Synthetic.
XX
PN WO2004070389-A1.
XX
PD 19-AUG-2004.
XX
PF 06-FEB-2004; 2004WO-GB000480.
XX
PR 06-FEB-2003; 2003GB-00002740.
XX
PA (AXIS-) AXIS-SHIELD ASA.
XX
PI Rye PD;
XX
DR WPI; 2004-625547/60.
XX
PT Assay for differentiating protein isoforms to determine their
PT concentrations in sample e.g. blood, involves contacting the sample with
PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
PT detecting.
XX
XX
PS Disclosure; Page 17; 30pp; English.
XX
CC The present invention describes an assay for a protein having at least
CC two isoforms with different glycosylation patterns. The assay involves
CC contacting a sample containing the protein with a proteolytic enzyme,
CC followed by detecting the content or relative content of at least one
CC peptide fragment produced by proteolysis. Also described is a kit for the
CC assay method comprising the proteolytic enzyme and a substrate bound
CC specific binding partner (SI) for at least 2 of the isoforms of the
CC proteins. The method can be used for assaying isoforms of proteins
CC according to their glycosylation pattern to determine their concentration
CC or relative concentration in the sample or material (e.g. blood). The
CC method avoids use of antibodies for distinguishing between glycosylated
CC isoforms of the proteins. The present sequence represents a transferrin
CC peptide fragment which is used in the exemplification of the present
CC invention.
XX
SQ Sequence 17 AA;
XX
Query Match 50.0%; Score 43; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 10 EDLIWELL 17
DB 1 EDLIWELL 8
XX
RESULT 6
ID ADS13216 standard; peptide; 17 AA.
XX
AC ADS13216;
XX
DT 16-DEC-2004 (first entry)
XX
DE Human rheumatoid arthritis marker peptide - SEQ ID 7.
XX
KM rheumatoid arthritis; marker; antiinflammatory; antiarthritic.
XX
OS Homo sapiens.
XX
PN WO2004082617-A2.
XX
PD 30-SEP-2004.
XX
PF 15-MAR-2004; 2004WO-US007880.
XX
PR 14-MAR-2003; 2003US-0455037P.
XX
PA (SURR-) SURROMED INC.
XX

```
XX XX Kantor AB, Becker CH, Schulman H;
PI XX
XX XX WPI; 2004-690929/67.
DR XX
XX XX New isolated marker for rheumatoid arthritis, useful in preparing a
PT XX composition for diagnosing or treating rheumatoid arthritis.
XX PS
XX PS Claim 1, SEQ ID NO 7, 184pp; English.
CC XX
CC XX The invention relates to a novel isolated marker for rheumatoid arthritis
CC XX selected from one of many (around 400) markers defined in the
CC XX specification. Rheumatoid arthritis is a chronic inflammatory disorder of
CC XX the small joints which is estimated to affect 2.1 million people in the
CC XX United States alone. Current approaches to treat the disease include the
CC XX use of non-steroidal antiinflammatory drugs (NSAIDs), which may reduce
CC XX pain, swelling and inflammation, and disease-modifying anti-rheumatic
CC XX drugs (DMARDs), which act to slow the progression of the disease and
CC XX avoid further joint injury. These drugs are associated with a number of
CC XX serious side effects and the search for improved therapeutics is a
CC XX subject of active research. The marker of the invention demonstrates
CC XX antirheumatic activity and may be useful in preparing a composition for
CC XX diagnosing or treating rheumatoid arthritis. The current sequence is that
CC XX of a human rheumatoid arthritis marker peptide of the invention.
SQ XX
XX XX Sequence 17 AA;
Query Match 50.0%; Score 43; DB 8; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5; Mismatches 0; Gaps 0;
Matches 8; Conservative 0; Indels 0;
QY 10 EDLWEL 17
DB 1 EDLWEL 8
RESULT 7
AAR49486
ID AAR49486 standard; protein; 13 AA.
XX AC
XX AC AAR49486;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 16-SEP-1994 (first entry)
XX XX
XX DE Bovine transferrin position 261-273.
XX XX
XX KW Naturally-occurring; immunomodulatory protein; human; therapy; class I;
XX KW major histocompatibility complex; class II; allotype; type I diabetes;
XX KW autoimmune disease; rheumatoid arthritis; T-cell-mediated response;
XX KW multiple sclerosis; transplant rejection; vaccine; MHC.
XX OS
XX OS Bos taurus.
XX XX
XX XX WO9404171-A1.
XX XX
XX PD 03-MAR-1994.
XX XX
XX PF 11-AUG-1993; 93WO-US007545.
XX XX
XX PR 11-AUG-1992; 92US-00925460.
XX PR 15-JUN-1993; 93US-00077255.
XX XX
XX PA (HARD ) HARVARD COLLEGE.
XX XX
XX PI Urban RG, Chicz RM, Vignali DA, Hedley ML, Stern LJ;
XX PI Strominger JL;
XX XX
XX DR WPI; 1994-082825/10.
XX XX
XX PT Novel immunomodulatory peptide(s) and nucleic acids - useful for
XX PT treatment of autoimmune diseases, transplant rejection and for
XX PT vaccination.
```

```
XX XX Disclosure; Page 49; 139pp; English.
PS XX
XX XX The sequences given in AAR49291-505 and AAR46981-7038 represent peptide
CC XX fragments of naturally-occurring immunomodulatory proteins. These
CC XX fragments are between 10-30 residues in length and bind to a human major
CC XX histocompatibility complex (MHC) class II allotype. These peptides may be
CC XX used for therapy of autoimmune diseases, such as type I diabetes,
CC XX rheumatoid arthritis and multiple sclerosis, and to reduce transplant
CC XX rejection. They may also be used for vaccination providing an exclusively
CC XX T-cell-mediated response, which can be class I or class-II based, or
CC XX both, depending on the length and character of the immunogenic peptides.
CC XX (updated on 25-MAR-2003 to correct PN field.) (updated on 25-MAR-2003 to
CC XX correct PR field.)
SQ XX
XX XX Sequence 13 AA;
Query Match 40.7%; Score 35; DB 2; Length 13;
Best Local Similarity 85.7%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 11 DLWEL 17
DB 1 DLWEL 7
RESULT 8
AAR47038
ID AAR47038 standard; protein; 15 AA.
XX AC
XX AC AAR47038;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 16-SEP-1994 (first entry)
XX XX
XX DE Bovine transferrin position 261-275.
XX XX
XX KW Naturally-occurring; immunomodulatory protein; human; therapy; class I;
XX KW major histocompatibility complex; class II; allotype; type I diabetes;
XX KW autoimmune disease; rheumatoid arthritis; T-cell-mediated response;
XX KW multiple sclerosis; transplant rejection; vaccine; MHC.
XX OS
XX OS Bos taurus.
XX XX
XX XX WO9404171-A1.
XX XX
XX PD 03-MAR-1994.
XX XX
XX PF 11-AUG-1993; 93WO-US007545.
XX XX
XX PR 11-AUG-1992; 92US-00925460.
XX PR 15-JUN-1993; 93US-00077255.
XX XX
XX PA (HARD ) HARVARD COLLEGE.
XX XX
XX PI Urban RG, Chicz RM, Vignali DA, Hedley ML, Stern LJ;
XX PI Strominger JL;
XX XX
XX DR WPI; 1994-082825/10.
XX XX
XX PT Novel immunomodulatory peptide(s) and nucleic acids - useful for
XX PT treatment of autoimmune diseases, transplant rejection and for
XX PT vaccination.
XX PS
XX PS Disclosure; Page 49; 139pp; English.
XX XX
XX XX The sequences given in AAR49291-505 and AAR46981-7038 represent peptide
CC XX fragments of naturally-occurring immunomodulatory proteins. These
CC XX fragments are between 10-30 residues in length and bind to a human major
CC XX histocompatibility complex (MHC) class II allotype. These peptides may be
CC XX used for therapy of autoimmune diseases, such as type I diabetes,
CC XX rheumatoid arthritis and multiple sclerosis, and to reduce transplant
CC XX rejection. They may also be used for vaccination providing an exclusively
```

CC T-cell-mediated response, which can be class I or class-II based, or
CC both, depending on the length and character of the immunogenic peptides.
CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to
CC correct PR field.)
XX
SQ Sequence 15 AA;

Query Match 40.7%; Score 35; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 85;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLIEWLL 17
|:|||||
Db 1 DVIWELL 7

RESULT 9
AAR49426
ID AAR49426 standard; protein; 15 AA.

AC AAR49426;
DT 25-MAR-2003 (revised)
DT 16-SEP-1994 (first entry)

XX Immunomodulatory peptide fragment #1.

XX Naturally-occurring; immunomodulatory protein; human; therapy; class I;
XX major histocompatibility complex; class II; allotype; type I diabetes;
XX autoimmune disease; rheumatoid arthritis; T-cell-mediated response;
XX multiple sclerosis; transplant rejection; vaccine; MHC.

OS Homo sapiens.

PN WO9404171-A1.

XX 03-MAR-1994.

PD 11-AUG-1993; 93WO-US007545.

XX 11-AUG-1992; 92US-00925460.

PR 15-JUN-1993; 93US-00077255.

XX (HARD) HARVARD COLLEGE.

XX Urban RG, Chicz RM, Vignali DA, Hedley ML, Stern LJ;
PI Strominger JL;

XX WPI; 1994-082825/10.

PT Novel immunomodulatory peptide(s) and nucleic acids - useful for
PT treatment of autoimmune diseases, transplant rejection and for
PT vaccination.

XX Disclosure; Page 89; 139pp; English.

XX The sequences given in AAR49291-505 and AAR46981-7038 represent peptide
CC fragments of naturally-occurring immunomodulatory proteins. These
CC fragments are between 10-30 residues in length and bind to a human major
CC histocompatibility complex (MHC) class II allotype. These peptides may be
CC used for therapy of autoimmune diseases, such as type I diabetes,
CC rheumatoid arthritis and multiple sclerosis, and to reduce transplant
CC rejection. They may also be used for vaccination providing an exclusively
CC T-cell-mediated response, which can be class I or class-II based, or
CC both, depending on the length and character of the immunogenic peptides.
CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 25-MAR-2003 to
CC correct PR field.)
XX

SO Sequence 15 AA;

Query Match 40.7%; Score 35; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 85;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLIEWLL 17
|:|||||
Db 1 DVIWELL 7

RESULT 10
ABR30177
ID ABR30177 standard; peptide; 15 AA.

AC ABR30177;

DT 19-MAY-2003 (first entry)

XX Human cancer-related protein 74P383 HLA peptide #3021.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;
XX human leukocyte antigen.

OS Homo sapiens.

PN WO200283921-A2.

XX 24-OCT-2002.

PD 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;

XX WPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.

XX Claim 13; Page 470; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX

SO Sequence 15 AA;

Query Match 39.5%; Score 34; DB 6; Length 15;
Best Local Similarity 41.7%; Pred. No. 13e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 RSMGKEDLIWE 15
|:|||||
Db 4 ROOGGAHQAWWE 15

RESULT 11
ADR19363
ID ADR19363 standard; peptide; 9 AA.

XX

AC ADR19363;
XX
DT 04-NOV-2004 (first entry)
XX
DE TRPI derived human tryptic digest peptide, SEQ ID 25.
XX
XX Tissue damage; chronic; tissue repair-associated protein isoform; TRPI;
KW antitumor; vulnerability; chronic dermal ulcer; human; tryptic digest;
XX proteolysis; trypsin.
OS Homo sapiens.
XX
PN WO2004069795-A2.
XX
PD 19-AUG-2004.
XX
PF 02-FEB-2004; 2004WO-US002881.
XX
PR 03-FEB-2003; 2003US-044600P.
XX
PA (PFIZ) PFIZER PROD INC.
XX (OXFO-) OXFORD GLXOSCSCIENCES UK LTD.
PI But R, Rumpel K, Williams-Jones BI, Herath HMA, Rohlf C,
PI Bruce JA, Patel TP;
XX
DR WPI; 2004-604404/58.
XX
PT Diagnosing, or monitoring the effect of therapy of, chronic tissue damage
PT (e.g. chronic dermal ulcer) comprises detecting and/or quantifying tissue
PT Repair-Associated protein isoform in a sample (e.g. wound exudate) from
PT the subject.
XX
PS Claim 7; SEQ ID NO 25; 107pp; English.
XX
CC The invention relates to a novel method for assessing, screening,
CC diagnosing or prognosing chronic tissue damage in a subject, identifying
CC a subject at risk of developing chronic tissue damage, or monitoring the
CC effect of therapy administered to a subject having chronic tissue damage.
CC The method comprises detecting and/or quantifying in a biological sample
CC from the subject a tissue repair-associated protein isoform (TRPI), given
CC in the specification. The invention further comprises: an isolated or
CC recombinant TRPI selected from the proteins listed in the specification;
CC screening for or identifying an agent capable of modulating the
CC expression or activity of the TRPI or a TRPI-related polypeptide; a
CC pharmaceutical composition comprising the TRPI cited above or an active
CC agent that modulates the expression and/or activity of the TRPI or a TRPI
CC -related polypeptide, and a pharmaceutical carrier, vehicle or diluent;
CC and treating chronic tissue damage. The novel compositions have antitumor
CC and vulnerability activity. The composition and methods are useful for
CC diagnosing, preventing, prognosing and treating chronic tissue damage,
CC such as a chronic dermal ulcer. These may also be used for drug screening
CC or drug development, or for screening or identifying agents capable of
CC modulating the activity of TRPI or TRPI-related polypeptides. This
CC sequence represents a TRPI derived human tryptic digest peptide. The
CC peptide was produced by proteolysis using trypsin of a tissue repair-
CC associated protein isoform of the invention.
XX
SQ Sequence 9 AA;
Query Match 38.4%; Score 33; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 10 EDLIWELL 17
DB 1 EDALWML 8
RESULT 12
ABP63629
ID ABP63629 standard; peptide; 13 AA.
XX

AC ABP63629;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human MHC class II binding peptide #50.
XX
XX Human; obesity; leptin; T-cell epitope; diabetes; high blood pressure;
KW cholesterol metabolism; MHC class II.
XX
OS Homo sapiens.
XX
PN WO200262833-A2.
XX
PD 15-AUG-2002.
XX
PF 05-FEB-2002; 2002WO-EP001188.
XX
PR 06-FEB-2001; 2001EP-00102618.
XX
PR 19-FEB-2001; 2001EP-00103954.
XX
PA (MERE) MERCK PATENT CMBH.
XX
PI Carr FJ, Carter G, Jones T, Williams S, Hamilton A;
PI WPI; 2002-643399/69.
XX
DR
XX
PT Modified forms of human obesity protein, for therapeutic use, in which
PT the immune characteristic is modified by means of reduced or removed
PT numbers of potential T-cell epitopes.
XX
PS Claim 6; Page 11; 32pp; English.
XX
CC The invention relates to a novel modified molecule with the biological
CC activity of human obesity protein (leptin) which is substantially non-
CC immunogenic or less immunogenic than any non-modified molecule with the
CC same biological activity when used in vivo. The immune characteristic of
CC the protein is modified by means of reduced/removed numbers of potential
CC T-cell epitopes. The modified proteins have therapeutic potential for the
CC treatment of diabetes, high blood pressure, and cholesterol metabolism.
CC The sequence represents a peptide of the invention contained in human
CC leptin with potential human MHC class II binding activity
XX
SQ Sequence 13 AA;
Query Match 38.4%; Score 33; DB 5; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 7 GSKEDLIWEL 16
DB 1 GSLQDMLWQL 10
RESULT 13
ABP63628
ID ABP63628 standard; peptide; 13 AA.
XX
AC ABP63628;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human MHC class II binding peptide #49.
XX
XX Human; obesity; leptin; T-cell epitope; diabetes; high blood pressure;
KW cholesterol metabolism; MHC class II.
XX
OS Homo sapiens.
XX
PN WO200262833-A2.
XX
PD 15-AUG-2002.
XX
PF 05-FEB-2002; 2002WO-EP001188.
XX

```

XX 06-FEB-2001; 2001EP-00102618.
PR 19-FEB-2001; 2001EP-00103954.
XX (MERE ) MERCK PATENT GMBH.
XX PA Carr FJ, Carter G, Jones T, Williams S, Hamilton A;
XX PI WPI; 2002-643399/69.
XX DR
XX Modified forms of human obesity protein, for therapeutic use, in which
PT the immune characteristic is modified by means of reduced or removed
XX numbers of potential T-cell epitopes.
XX
XX Claim 6; Page 11; 32pp; English.
XX
CC The invention relates to a novel modified molecule with the biological
CC activity of human obesity protein (leptin) which is substantially non-
CC immunogenic or less immunogenic than any non-modified molecule with the
CC same biological activity when used in vivo. The immune characteristic of
CC the protein is modified by means of reduced/removed numbers of potential
CC T-cell epitopes. The modified proteins have therapeutic potential for the
CC treatment of diabetes, high blood pressure, and cholesterol metabolism.
CC The sequence represents a peptide of the invention contained in human
CC leptin with potential human MHC class II binding activity
XX
SQ Sequence 13 AA;
XX
Query Match      38.4%; Score 33; DB 5; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 7 GGEKEDLIWEI 16
DB 2 GSLLQDMLWQL 11
XX
RESULT 14
ABP63627
ID ABP63627 standard; peptide; 13 AA.
XX
AC ABP63627;
XX
DT 05-NOV-2002 (first entry)
XX
DE Human MHC class II binding peptide #48.
XX
KM Human; obesity; leptin; T-cell epitope; diabetes; high blood pressure;
KW cholesterol metabolism; MHC class II.
XX
OS Homo sapiens.
XX
PN WO200262833-A2.
XX
PD 15-AUG-2002.
XX
PF 05-FEB-2002; 2002WO-EP001188.
XX
PR 06-FEB-2001; 2001EP-00102618.
XX
PR 19-FEB-2001; 2001EP-00103954.
XX
PA (MERE ) MERCK PATENT GMBH.
XX
PI Carr FJ, Carter G, Jones T, Williams S, Hamilton A;
XX
DR WPI; 2002-643399/69.
XX
PT Modified forms of human obesity protein, for therapeutic use, in which
PT the immune characteristic is modified by means of reduced or removed
XX numbers of potential T-cell epitopes.
XX
XX Claim 6; Page 11; 32pp; English.
XX

```

```

CC The invention relates to a novel modified molecule with the biological
CC activity of human obesity protein (leptin) which is substantially non-
CC immunogenic or less immunogenic than any non-modified molecule with the
CC same biological activity when used in vivo. The immune characteristic of
CC the protein is modified by means of reduced/removed numbers of potential
CC T-cell epitopes. The modified proteins have therapeutic potential for the
CC treatment of diabetes, high blood pressure, and cholesterol metabolism.
CC The sequence represents a peptide of the invention contained in human
CC leptin with potential human MHC class II binding activity
XX
SQ Sequence 13 AA;
XX
Query Match      38.4%; Score 33; DB 5; Length 13;
Best Local Similarity 30.8%; Pred. No. 1.6e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 3 ARSMGKEDLIWE 15
DB 1 SRLQGSLLQDMLWQ 13
XX
RESULT 15
AAE27219
ID AAE27219 standard; peptide; 13 AA.
XX
AC AAE27219;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human obesity protein (leptin) peptide #49.
XX
KM Human; fusion protein; immunological; major histocompatibility complex;
KW MHC; nausea; gastric upset; obesity protein; leptin.
XX
OS Homo sapiens.
XX
PN WO200266514-A2.
XX
PD 29-AUG-2002.
XX
PF 18-FEB-2002; 2002WO-EP001690.
XX
PR 19-FEB-2001; 2001EP-00103955.
XX
PR 05-APR-2001; 2001EP-00108291.
XX
PA (MERE ) MERCK PATENT GMBH.
XX
PI Gillies S, Carr FJ, Jones T, Carter G, Hamilton A, Williams S;
PI Hanlon M, Watkins J, Baker M, Way JC;
XX
DR WPI; 2002-667054/71.
XX
XX New modified fusion protein with reduced immunogenicity, useful for
PT combining favorable properties of a composition, comprises an
PT immunoglobulin molecule linked to a non-immunoglobulin target
PT polypeptide.
XX
PS Example 2; Page 46; 92pp; English.
XX
XX The invention relates to an immunogenically modified fusion protein
CC derived from a parent fusion protein, comprising first and second
CC proteins/polypeptides, where the first protein is an immunoglobulin
CC molecule or its fragment and the second protein is non-immunoglobulin
CC molecule. The immunogenically modified fusion protein is useful in
CC combining known favourable properties of a composition or in creating new
CC properties of a composition which elicits biological or pharmacological
CC efficacy without having undesirable physiological effects such as nausea
CC or gastric upset. The present sequence is human obesity protein (leptin)
CC peptide with potential major histocompatibility complex (MHC) binding
CC activity. This sequence is used in the exemplification of the invention
XX
SQ Sequence 13 AA;
XX

```

Query Match 38.4%; Score 33; DB 5; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 7 GGEKDLIMEL 16
| : : : : :
Db 2 GSLQDMLWQL 11

Search completed: November 1, 2005, 13:28:55
Job time : 165 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 13:26:23 ; Search time 41 Seconds

(Without alignments)
30,952 Million cell updates/sec

Title: US-10-612-162A-1

Sequence: 1 VVARSMGKEDLIWELL 17

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 177072

Minimum DB seq length: 0
Maximum DB seq length: 17Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	40.7	13	2	US-08-480-190-196
2	35	40.7	13	2	US-08-488-379-196
3	35	40.7	13	4	US-08-475-399A-196
4	35	40.7	13	4	US-08-077-255A-196
5	35	40.7	13	5	PCT-US93-07545-196
6	35	40.7	15	2	US-08-480-190-136
7	35	40.7	15	2	US-08-488-379-136
8	35	40.7	15	4	US-08-475-399A-136
9	35	40.7	15	4	US-08-077-255A-136
10	35	40.7	15	5	PCT-US93-07545-136
11	35	40.7	16	2	US-08-480-190-273
12	35	40.7	16	2	US-08-488-379-273
13	35	40.7	16	4	US-08-475-399A-273
14	35	40.7	16	4	US-08-077-255A-273
15	35	40.7	16	5	PCT-US93-07545-273
16	30	34.9	10	2	US-08-735-253-5
17	30	34.9	10	2	US-08-735-253-11
18	29	33.7	10	1	US-07-802-667-17
19	28	32.6	5	1	US-07-802-667-20
20	28	32.6	6	5	US-08-269-257-6
21	28	32.6	6	5	PCT-US95-04171-6
22	28	32.6	12	1	US-08-241-054-33
23	28	32.6	12	1	US-08-390-156A-47
24	28	32.6	12	1	US-08-439-817-13
25	28	32.6	12	1	US-08-485-508-33
26	28	32.6	14	4	US-09-053-611-29
27	31.4	9	2	4	US-08-765-061-6

28	27	31.4	12	2	US-08-466-860-4	Sequence 4, Appl
29	27	31.4	12	3	US-08-472-040A-4	Sequence 4, Appl
30	27	31.4	12	3	US-08-276-776-4	Sequence 4, Appl
31	27	31.4	12	3	US-08-471-209-4	Sequence 4, Appl
32	27	31.4	15	4	US-09-255-501-146	Sequence 146, App
33	27	31.4	15	4	US-09-255-501-147	Sequence 147, App
34	27	31.4	15	4	US-09-255-501-148	Sequence 148, App
35	27	31.4	15	4	US-09-255-501-149	Sequence 149, App
36	27	31.4	15	4	US-09-060-872A-146	Sequence 146, App
37	27	31.4	15	4	US-09-060-872A-147	Sequence 147, App
38	27	31.4	15	4	US-09-060-872A-148	Sequence 148, App
39	27	31.4	15	4	US-09-060-872A-149	Sequence 149, App
40	27	31.4	15	4	US-09-500-135C-146	Sequence 146, App
41	27	31.4	15	4	US-09-500-135C-147	Sequence 147, App
42	27	31.4	15	4	US-09-500-135C-148	Sequence 148, App
43	27	31.4	15	4	US-09-500-135C-149	Sequence 149, App
44	26.5	30.8	11	1	US-08-471-058-3	Sequence 3, Appl
45	26.5	30.8	11	3	US-08-471-057-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-480-190-196
; Sequence 196, Application US/08480190
; Patent No. 5827516
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,190
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 196:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; US-08-480-190-196

Query Match 40.7%; Score 35; DB 2; Length 13;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DIWELL 17
|:|||||
Db 1 DIWELL 7

RESULT 2

US-08-488-379-196
; Sequence 196, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 MB
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 196:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-488-379-196

Query Match 40.7%; Score 35; DB 2; Length 13;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DIWELL 17
|:|||||
Db 1 DIWELL 7

RESULT 3

US-08-475-399A-196
; Sequence 196, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:

APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Vignali, Dario A.A.
APPLICANT: Hedley, Mary L.
APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 276
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/475,399A

FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/077,255

FILING DATE: 15-JUN-1993

APPLICATION NUMBER: 07/925,460

FILING DATE: 11-AUG-1992

ATTORNEY/AGENT INFORMATION:

NAME: Frazer, Janis K.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 00246/168003

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-507

TELEFAX: 617/542-890

TELEX: 200154

INFORMATION FOR SEQ ID NO: 196:

SEQUENCE CHARACTERISTICS:

LENGTH: 13 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-475-399A-196

Query Match 40.7%; Score 35; DB 4; Length 13;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DIWELL 17
|:|||||
Db 1 DIWELL 7

RESULT 4

US-08-077-255A-196
; Sequence 196, Application US/08077255A
; Patent No. 6696061
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 196:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-196

Query Match 40.7%; Score 35; DB 4; Length 13;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLIWELL 17
Db 1 DVIWELL 7

RESULT 5
PCT-US93-07545-196
Sequence 196, Application PC/TUS9307545
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 196:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-196

Query Match 40.7%; Score 35; DB 5; Length 13;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLIWELL 17
Db 1 DVIWELL 7

RESULT 6
US-08-480-190-136

Sequence 136, Application US/08480190
Patent No. 5827516

GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-136

Query Match 40.7%; Score 35; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DLIWELL 17
|:|||||
Db 1 DLIWELL 7

RESULT 7

US-08-488-379-136
; Sequence 136, Application US/08488379
; Patent No. 5880103
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,379
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/077,255
; FILING DATE: June 15, 1993
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-488-379-136

Query Match 40.7%; Score 35; DB 2; Length 15;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DLIWELL 17
|:|||||
Db 1 DLIWELL 7

RESULT 8

US-08-475-399A-136
; Sequence 136, Application US/08475399A
; Patent No. 6509033
; GENERAL INFORMATION:
; APPLICANT: Urban, Robert G.
; APPLICANT: Chicz, Roman M.
; APPLICANT: Vignali, Dario A.A.
; APPLICANT: Hedley, Mary L.

APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 276
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,399A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frazer, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 136:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-136

Query Match 40.7%; Score 35; DB 4; Length 15;
Best Local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 11 DLIWELL 17
|:|||||
Db 1 DLIWELL 7

RESULT 9

US-08-077-255A-136
; Sequence 136, Application US/08077255A
; Patent No. 6696061
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Dario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: Wordperfect (Version 5.1)

```
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/077,255A
/ FILING DATE: June 15, 1993
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 136:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/
US-08-077-255A-136

Query Match          40.7%; Score 35; DB 4; Length 15;
Best local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      11 DLIWELL 17
Db      1 DVIWELL 7

RESULT 10
PCT-US93-07545-136
/ Sequence 136, Application PC/TUS9307545
/ GENERAL INFORMATION:
/ APPLICANT: Robert G. Urban
/ APPLICANT: Roman M. Chicz
/ APPLICANT: Dario A. A. Vignali
/ APPLICANT: Mary L. Hedley
/ APPLICANT: Lawrence J. Stern
/ APPLICANT: Jack L. Strominger
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 273
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 MB
/ COMPUTER: IBM PS/2 Model 502 or 55SX
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: Wordperfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/07545
/ FILING DATE: 19930811
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 136:
/ SEQUENCE CHARACTERISTICS:
```

```
/ LENGTH: 15
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/
PCT-US93-07545-136

Query Match          40.7%; Score 35; DB 5; Length 15;
Best local Similarity 85.7%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      11 DLIWELL 17
Db      1 DVIWELL 7

RESULT 11
US-08-480-190-273
/ Sequence 273, Application US/08480190
/ Patent No. 5827516
/ GENERAL INFORMATION:
/ APPLICANT: Robert G. Urban
/ APPLICANT: Roman M. Chicz
/ APPLICANT: Dario A. A. Vignali
/ APPLICANT: Mary L. Hedley
/ APPLICANT: Lawrence J. Stern
/ APPLICANT: Jack L. Strominger
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 274
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 MB
/ COMPUTER: IBM PS/2 Model 502 or 55SX
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: Wordperfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/480,190
/ FILING DATE:
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/077,255
/ FILING DATE: June 15, 1993
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 273:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 16
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/
US-08-480-190-273

Query Match          40.7%; Score 35; DB 2; Length 16;
Best local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      11 DLIWELL 17
Db      1 DVIWELL 7
```

RESULT 12
US-08-488-379-273
Sequence 273, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 273:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-488-379-273

Query Match 40.7%; Score 35; DB 2; Length 16;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DIWELL 17
|:|||||
1 DIWELL 7

Db 1 DIWELL 7

RESULT 13
US-08-475-399A-273
Sequence 273, Application US/08475399A
Patent No. 6509033
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Vignali, Dario A.A.
APPLICANT: Hedley, Mary L.
APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 276

CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,399A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 273:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-273

Query Match 40.7%; Score 35; DB 4; Length 16;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DIWELL 17
|:|||||
1 DIWELL 7

Db 1 DIWELL 7

RESULT 14
US-08-077-255A-273
Sequence 273, Application US/08077255A
Patent No. 6696061
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 273:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-273

Query Match 40.7%; Score 35; DB 4; Length 16;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLIWELL 17
|:|||||
DB 1 DVIWELL 7

RESULT 15
PCT-US93-07545-273
Sequence 273, Application PC/TUS9307545
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chic
APPLICANT: Darlo A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 273:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

PCT-US93-07545-273

Query Match 40.7%; Score 35; DB 5; Length 16;
Best Local Similarity 85.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLIWELL 17
|:|||||
DB 1 DVIWELL 7

Search completed: November 1, 2005, 13:41:21
Job time : 42 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 13:31:57 ; Search time 164 Seconds

(Without alignments)
43.334 Million cell updates/sec

Title: US-10-612-162a-1

Perfect score: 86
Sequence: 1 VVARSWGKEDLIWELL 17Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 344634

Minimum DB seq length: 0
Maximum DB seq length: 17Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/UCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubppaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubppaa/US10E_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/1/pubppaa/US11A_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep:*
- 21: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep:*
- 22: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	17	15	US-10-612-162-1
2	43	50.0	15	16	US-10-769-514-5
3	43	50.0	17	17	US-10-801-990-7
4	33	38.4	13	15	US-10-467-114-49
5	33	38.4	13	15	US-10-467-114-51
6	33	38.4	13	15	US-10-467-114-50
7	33	38.4	13	15	US-10-468-370-52
8	33	38.4	13	15	US-10-468-370-53
9	33	38.4	13	15	US-10-468-370-54
10	32	37.2	10	14	US-10-190-082-445
11	32	37.2	14	16	US-10-813-638-1208

12	31	36.0	16	14	US-10-155-481B-17	Sequence 17, Appl
13	30	34.9	14	17	US-10-783-988-3	Sequence 3, Appl
14	30	34.9	15	10	US-09-907-965-494	Sequence 494, App
15	30	34.9	15	14	US-10-198-053-494	Sequence 494, App
16	30	34.9	15	17	US-10-860-790-494	Sequence 494, App
17	30	34.9	17	15	US-10-291-241-85	Sequence 85, Appl
18	29	33.7	7	16	US-10-714-564A-607	Sequence 607, App
19	29	33.7	13	15	US-10-467-114-52	Sequence 52, Appl
20	29	33.7	13	15	US-10-468-370-55	Sequence 55, Appl
21	29	33.7	15	16	US-10-695-155-131	Sequence 131, App
22	29	33.7	15	16	US-10-695-155-132	Sequence 132, App
23	28.5	33.1	17	15	US-10-356-257-295	Sequence 295, App
24	28	32.6	10	10	US-09-572-404B-2179	Sequence 2179, Ap
25	28	32.6	10	14	US-10-190-082-446	Sequence 446, App
26	28	32.6	14	14	US-10-215-755-13	Sequence 13, Appl
27	28	32.6	14	14	US-10-264-672-13	Sequence 13, Appl
28	28	32.6	14	15	US-10-383-999-13	Sequence 13, Appl
29	28	32.6	14	20	US-11-031-919-13	Sequence 13, Appl
30	28	32.6	15	9	US-09-853-253-17	Sequence 17, Appl
31	28	32.6	15	15	US-10-264-309-173	Sequence 173, App
32	28	32.6	15	17	US-10-921-371-173	Sequence 173, App
33	28	32.6	15	18	US-10-264-309-173	Sequence 173, App
34	28	32.6	16	9	US-09-853-253-15	Sequence 15, Appl
35	28	32.6	16	9	US-09-853-253-16	Sequence 16, Appl
36	28	32.6	16	17	US-10-808-187-1148	Sequence 1148, Ap
37	28	32.6	16	17	US-10-921-371-15	Sequence 15, Appl
38	28	32.6	16	17	US-10-921-371-16	Sequence 16, Appl
39	28	32.6	16	18	US-10-807-807-1148	Sequence 1148, Ap
40	28	32.6	17	9	US-09-853-253-14	Sequence 14, Appl
41	28	32.6	17	9	US-09-798-116-23	Sequence 23, Appl
42	28	32.6	17	17	US-10-921-371-14	Sequence 14, Appl
43	27	31.4	8	14	US-10-190-082-444	Sequence 444, App
44	27	31.4	12	17	US-10-504-726-33	Sequence 33, Appl
45	27	31.4	14	15	US-10-403-847-85	Sequence 85, Appl

ALIGNMENTS

RESULT 1
US-10-612-162-1
; Sequence 1, Application US/10612162
; Publication No. US20040014145A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
; FILE REFERENCE: 2002/B001
; CURRENT APPLICATION NUMBER: US/10/612,162
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-162-1

Query Match 100.0%; Score 86; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVARSWGKEDLIWELL 17
|||||
Db 1 VVARSWGKEDLIWELL 17

RESULT 2
US-10-769-514-5

```
; Sequence 5, Application US/10769514
; Publication No. US20040258695A1
; GENERAL INFORMATION:
; APPLICANT: Schryvers, Anthony
; TITLE OF INVENTION: Transferrin Binding Peptides and Uses Thereof
; FILE REFERENCE: 028722-001
; CURRENT APPLICATION NUMBER: US/10/769,514
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,113
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-514-5
```

```
Query Match          50.0%; Score 43; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 VVARSWGK 9
      |||||
Db      7 VVARSWGK 15
```

```
RESULT 3
US-10-801-990-7
; Sequence 7, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
; APPLICANT: Schulman, Aaron B.
; APPLICANT: Kantrow, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121
; CURRENT APPLICATION NUMBER: US/10/801,990
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-7
```

```
Query Match          50.0%; Score 43; DB 17; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      10 EDLIWELL 17
      |||||
Db      1 EDLIWELL 8
```

```
RESULT 4
US-10-467-114-49
; Sequence 49, Application US/10467114
; Publication No. US20040072219A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: MODIFIED LEPTIN WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-115
; CURRENT APPLICATION NUMBER: US/10/467,114
; CURRENT FILING DATE: 2003-08-05
```

```
; PRIOR APPLICATION NUMBER: EP 01102618.4
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01188
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MCH class II binding epitope
US-10-467-114-49
```

```
Query Match          38.4%; Score 33; DB 15; Length 13;
Best Local Similarity 30.8%; Pred. No. 1.4e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      3 ARSWGKEDLIWE 15
      |||:|:|:|
Db      1 SRLGSLQDMLWQ 13
```

```
RESULT 5
US-10-467-114-50
; Sequence 50, Application US/10467114
; Publication No. US20040072219A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: MODIFIED LEPTIN WITH REDUCED
; FILE REFERENCE: MER-115
; CURRENT APPLICATION NUMBER: US/10/467,114
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: EP 01102618.4
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01188
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 50
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MCH class II binding epitope
US-10-467-114-50
```

```
Query Match          38.4%; Score 33; DB 15; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      7 GSKEDLIWE 16
      ||:|:|
Db      2 GSLQDMLWQL 11
```

```
RESULT 6
US-10-467-114-51
; Sequence 51, Application US/10467114
; Publication No. US20040072219A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
```

```

; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: MODIFIED LEPTIN WITH REDUCED
; FILE REFERENCE: IMMUNOGENICITY
; CURRENT APPLICATION NUMBER: US/10/467,114
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: EP 01102618.4
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01188
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PaetSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MCH class II binding epitope
US-10-467-114-51

Query Match      38.4%; Score 33; DB 15; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      7 GCKEDLIWEL 16
| : : : : |
Db      1 GSIQDMLWQL 10

RESULT 7
US-10-468-370-52
; Sequence 52, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gallies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: IMMUNOGENICITY
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: PaetSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-52

Query Match      38.4%; Score 33; DB 15; Length 13;
Best Local Similarity 30.8%; Pred. No. 1.4e+02;
Matches 4; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY      3 ARSMGKEDLIWE 15
```

```

; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: MODIFIED LEPTIN WITH REDUCED
; FILE REFERENCE: IMMUNOGENICITY
; CURRENT APPLICATION NUMBER: US/10/467,114
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: EP 01102618.4
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01188
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PaetSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MCH class II binding epitope
US-10-467-114-51

Query Match      38.4%; Score 33; DB 15; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      7 GCKEDLIWEL 16
| : : : : |
Db      1 GSIQDMLWQL 10

RESULT 8
US-10-468-370-53
; Sequence 53, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gallies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: IMMUNOGENICITY
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: PaetSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-53

Query Match      38.4%; Score 33; DB 15; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      7 GCKEDLIWEL 16
| : : : : |
Db      2 GSIQDMLWQL 11

RESULT 9
US-10-468-370-54
; Sequence 54, Application US/10468370
; Publication No. US20040082039A1
; GENERAL INFORMATION:
; APPLICANT: Gallies, Stephen
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Carter, Graham
; APPLICANT: Hamilton, Anita
; APPLICANT: Williams, Stephen
; APPLICANT: Hanlon, Marian
; APPLICANT: Watkins, John
; APPLICANT: Baker, Matthew
; APPLICANT: Way, Jeffrey
; TITLE OF INVENTION: ARTIFICIAL PROTEINS WITH REDUCED
; FILE REFERENCE: IMMUNOGENICITY
; CURRENT APPLICATION NUMBER: US/10/468,370
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: EP 01103955.9
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: EP 01108291.4
; PRIOR FILING DATE: 2001-04-05
```

```

; PRIOR APPLICATION NUMBER: PCT/EP02/01690
; PRIOR FILING DATE: 2002-02-18
; NUMBER OF SEQ ID NOS: 689
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: MHC class II binding epitope
US-10-468-370-54

Query Match          38.4%; Score 33; DB 15; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 GKEDLIWEL 16
   |||:|
Db 1 GSLQDMLWQL 10

RESULT 10
US-10-190-082-445
; Sequence 445, Application US/10190082
; Publication No. US20030148264A1
; GENERAL INFORMATION:
; APPLICANT: Lasky, Lawrence A.
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Held, Heike A.
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
; FILE REFERENCE: P1905R1
; CURRENT APPLICATION NUMBER: US/10/190,082
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 445
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-190-082-445

Query Match          37.2%; Score 32; DB 14; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 KEDLIWEL 17
   |||:|
Db 1 KNSWVWEL 9

RESULT 11
US-10-813-638-1208
; Sequence 1208, Application US/10813638
; Publication No. US20040235026A1
; GENERAL INFORMATION:
; APPLICANT: Shinketo, Richard A.
; APPLICANT: Leach, Martin D.
; TITLE OF INVENTION: NUCLEIC ACIDS CONTAINING SINGLE NUCLEIC ACID POLYMORPHISMS AND ME
; FILE REFERENCE: 15966-599
; CURRENT APPLICATION NUMBER: US/10/813,638
; CURRENT FILING DATE: 2004-03-29
; PRIOR APPLICATION NUMBER: 60/163,783
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1468
; SOFTWARE: CuraGen Patent Formatter Version 0.9
; SEQ ID NO 1208
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```

; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (7)...(10)
; OTHER INFORMATION: cSNP translation
US-10-813-638-1208

Query Match          37.2%; Score 32; DB 16; Length 14;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 DLIWEL 17
   |||:|
Db 1 DLIWTL 7

RESULT 12
US-10-155-481B-17
; Sequence 17, Application US/10155481B
; Publication No. US20030113711A1
; GENERAL INFORMATION:
; APPLICANT: Stuart, J.
; APPLICANT: Bramson, H.
; APPLICANT: Moyer, Mary
; APPLICANT: Blackburn, Kevin
; TITLE OF INVENTION: PROTEIN KINASE PEPTIDE SUBSTRATE DETERMINATION USING PEPTIDE
; FILE REFERENCE: Attorney Docket No. US20030113711A1 447-76, Glaxo ID PU4253
; CURRENT APPLICATION NUMBER: US/10/155,481B
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-155-481B-17

Query Match          36.0%; Score 31; DB 14; Length 16;
Best Local Similarity 45.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GKEDLIWEL 17
   |||:|
Db 1 GGMEDYFEFM 11

RESULT 13
US-10-783-989-3
; Sequence 3, Application US/10783989
; Publication No. US20050015821A1
; GENERAL INFORMATION:
; APPLICANT: GYNNÉ, RICHARD J.
; APPLICANT: HONG, NANCY AI-HUA
; APPLICANT: NEJMS, KEATS A.
; APPLICANT: WU, HUA
; TITLE OF INVENTION: SENSIN POLYPEPTIDES, ENCODING NUCLEIC ACIDS, MUTATIONS,
; FILE REFERENCE: 022731-0402
; CURRENT APPLICATION NUMBER: US/10/783,989
; CURRENT FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/448,964
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 3
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-783-989-3

Query Match          34.9%; Score 30; DB 17; Length 14;
```

Best Local Similarity 66.7%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db :|||
4 KEDLIWEL 11

Search completed: November 1, 2005, 13:45:54
Job time : 165 secs

Qy 9 KEDLIWEL 17
|||
1 KEDLKWSSL 9

RESULT 14

US-09-907-969-494
; Sequence 494, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Hill, Paul
; APPLICANT: Albone, Earl
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C8
; CURRENT APPLICATION NUMBER: US/09/907,969
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 494
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-969-494

Query Match 34.9%; Score 30; DB 10; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 KEDLIWEL 16
:|
4 REOLYWEL 11

RESULT 15

US-10-198-053-494
; Sequence 494, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 494
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-494

Query Match 34.9%; Score 30; DB 14; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 KEDLIWEL 16

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 13:17:07 ; Search time 38 Seconds
(Without alignments)
43.044 Million cell updates/sec

Title: US-10-612-162a-1

Perfect score: 86
Sequence: 1 VVARSMGCKEDLIWELL 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2991

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	33.7	11	2	S60294
2	25	29.1	14	2	PH1769
3	25	29.1	16	2	A20190
4	24	27.9	13	2	S47383
5	24	27.9	13	2	P00700
6	24	27.9	15	4	I38031
7	23	26.7	12	2	S69123
8	23	26.7	12	2	PH1183
9	23	26.7	14	2	PH1626
10	23	26.7	15	2	S26527
11	23	26.7	15	2	PH0782
12	23	26.7	16	2	B60560
13	23	26.7	17	2	B61334
14	22	25.6	9	1	YF66
15	22	25.6	9	1	A60957
16	22	25.6	10	2	PT0310
17	22	25.6	14	2	PH0800
18	22	25.6	14	2	PH0801
19	22	25.6	14	2	P49037
20	22	25.6	16	2	A48839
21	22	25.6	16	2	A46236
22	22	25.6	16	2	A26393
23	21	24.4	6	2	PT0730
24	21	24.4	8	2	A21440
25	21	24.4	9	2	B45020
26	21	24.4	10	2	PT0289
27	21	24.4	11	2	H54346
28	21	24.4	11	2	S57575
29	21	24.4	12	1	U06W2

ALIGNMENTS

30	21	24.4	12	2	S42765	urotensin II - tel
31	21	24.4	14	2	PH1759	T cell receptor al
32	21	24.4	14	2	S58426	spemadhesin AMN h
33	21	24.4	14	2	PH1625	Ig H chain V-D-J r
34	21	24.4	14	2	PH1627	Ig H chain V-D-J r
35	21	24.4	14	2	PH0762	T-cell receptor be
36	21	24.4	15	2	S57201	basic proteinase I
37	21	24.4	17	2	B61321	histone H4 - chick
38	21	24.4	17	2	A61321	histone H4 - chick
39	20	23.3	9	2	PT0670	T-cell receptor be
40	20	23.3	10	2	PT0245	Ig heavy chain CRD
41	20	23.3	11	2	B49164	chromogranin-B - r
42	20	23.3	12	2	JS0423	urotensin II-A pep
43	20	23.3	13	2	PH1636	Ig H chain V-D-J r
44	20	23.3	14	2	A35105	hypothetical prote
45	20	23.3	15	2	A45103	7 alpha-hydroxy-4-

RESULT 1

S60294
tubulin 2 beta-3 chain - fruit fly (Drosophila melanogaster) (fragment)
C/Species: Drosophila melanogaster
C/Date: 19-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jun-2002
C/Accession: S60294
R/Chapel, S.; Sobrier, M.L.; Montpied, P.; Micard, D.; Brubet, A.; Couderc, J.L.; Dastu-
Insect Mol. Biol. 2, 39-48, 1993
A/Title: In Drosophila Kc cells 20-OHE induction of the 60C beta-3 tubulin gene express
A/Reference number: S60292; PMID:97242543; PMID:9087542
A/Accession: S60294
A/Molecule type: mRNA
A/Residues: 1-11 <CHA>
A/Cross-references: EMBL:X60393
C/Genetics:
A/Gen: FlyBase:beta-Tub60D
A/Cross-references: FlyBase:FBgn003888

Query Match 33.7%; Score 29; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 95;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 VVARSMGCK 9
DB 4 VTRSSGCK 11

RESULT 2

PH1769
T cell receptor alpha chain V region (clone 2V alpha 7.2-4) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1769
R/Portelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 176, 1-16, 1993
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A/Reference number: PH1754; PMID:93301585; PMID:8391057
A/Accession: PH1769
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-14 <FOR>

Query Match 29.1%; Score 25; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 66+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 SMGCKEDLIW 14
DB 4 SMDSNYQLIW 13

```
RESULT 3
A20190
Hypodermin B - early cattle grub (fragment)
C:Species: Hypoderma lineatum (early cattle grub)
C:Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
C:Accession: A20190
R:lecrotaey, A.; Tong, N.T.; Kell, B.
Eur. J. Biochem. 134, 261-267, 1983
A:Title: Hypodermin B, a trypsin-related enzyme from the insect Hypoderma lineatum.
A:Reference number: A20190; MUID:83261874; PMID:6307690
A:Accession: A20190
A:Molecule type: protein
A:Residues: 1-16 <LEC>
A:Cross-references: UNIPROT:P35588

Query Match      29.1%; Score 25; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 6.9e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      10 EDLWEL 16
      |||||
Db      10 EDFPMEV 16

RESULT 4
S47383
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47383
R:lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A:Reference number: S47355
A:Accession: S47383
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z55709; NID:9527513; PIDN:CAA84778.1; PID:9527514
C:Keywords: T-cell receptor

Query Match      27.9%; Score 24; DB 2; Length 13;
Best Local Similarity 83.3%; Pred. No. 8.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      3 ASMSG 8
      |||||
Db      2 ASMSG 7

RESULT 5
P00700
unidentified 6.3/40K protein [imported] - rice (fragment)
C:Species: Oryza sativa (rice)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: P00700
R:Komatsu, S.; Kajiwara, H.; Hirano, H.
Theor. Appl. Genet. 86, 935-942, 1993
A:Title: A rice protein library; a data-file of rice proteins separated by two-dimension
A:Reference number: P00696
A:Accession: P00700
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <KOM>
A:Cross-references: UNIPROT:Q7MLU1

Query Match      27.9%; Score 24; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 8.1e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      2 VARSGKEDLI 13
      |||||
Db      1 VAGATGALDIL 12
```

```
RESULT 6
I18031
Hypothetical MNI/TEL mutant fusion protein type II - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Apr-2000
C:Accession: I18031
R:Buijs, A.; Sherr, S.; van Baal, S.; van Bezouw, S.; van der Plas, D.; Van Kessel, A.G
Oncogene 10, 1511-1519, 1995
A:Title: Translocation (12;22) (p13;q11) in myeloproliferative disorders results in fusa
A:Reference number: I18031; MUID:95249265; PMID:7731705
A:Accession: I18031
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-15 <BUI>
A:Cross-references: EMBL:X85027; NID:9971465; PIDN:CA59400.1; PID:9971466
C:Comment: This sequence is the chimeric product of a translocation mutation.
C:Genetics:
A:Gene: MNI/ETV6; MNI/TEL
A:Map position: 22q11/12p13
C:Keywords: fusion protein

Query Match      27.9%; Score 24; DB 4; Length 15;
Best Local Similarity 57.1%; Pred. No. 9.5e+02;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      11 DLWVEL 17
      |||||
Db      9 DVLVELL 15

RESULT 7
S69123
proton-translocating transhydrogenase - Rhodospirillum rubrum (fragment)
C:Species: Rhodospirillum rubrum
C:Date: 10-Mar-1998 #sequence_revision 24-Apr-1998 #text_change 24-Apr-1998
C:Accession: S69123
R:Diggle, C.; Hutcheon, M.; Jones, G.R.; Thomas, C.M.; Jackson, J.B.
Eur. J. Biochem. 228, 719-726, 1995
A:Title: Properties of the soluble polypeptide of the proton-translocating transhydrogen
A:Reference number: S69123; MUID:95255277; PMID:7737169
A:Accession: S69123
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <DIG>

Query Match      26.7%; Score 23; DB 2; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.1e+03;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      11 DLWVEL 16
      |||||
Db      3 DVWVKV 8

RESULT 8
PH1183
T-cell receptor alpha chain V region (Cw3/A8) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1183
R:Caasanova, J.L.; Cerotini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A:Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A:Reference number: S26512; MUID:92364546; PMID:1380061
A:Accession: PH1183
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12 <CAS>

Query Match      26.7%; Score 23; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
```

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ARSMG 8
|
|
|
|

Db 2 ALSMG 7

RESULT 9

PH1626

19 H chain V-D-J region (clone B-less 118) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C/Accession: PH1626

R/Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A/Reference number: PH1580; MUID:93301609; PMID:8315387

A/Accession: PH1626

A/Molecule type: DNA

A/Residues: 1-14 <LEV>

A/Experimental source: bone marrow pre-B lymphocyte

C/Keywords: Immunoglobulin

Query Match 26.7%; Score 23; DB 2; Length 14;

Best Local Similarity 75.0%; Pred. No. 1.3e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 DLW 14
|
|
|
|

Db 10 DLW 13

RESULT 10

S26527

T-cell receptor alpha chain V region (clone Cw3/A8, A3/74.1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

A/Variety: clone Cw3/A8; A3/74.1

C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999

C/Accession: S26527; PH1442

R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wild

J. Exp. Med. 176, 439-447, 1992

A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor

A/Reference number: S26512; MUID:92364546; PMID:1380061

A/Accession: S26527

A/Molecule type: mRNA

A/Residues: 1-15 <CAS>

A/Cross-references: EMBL:X67978

A/Experimental source: cytolytic T-lymphocyte, clone Cw3/A8

R/Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannefier, C.; Regnault, A.; Kc

J. Exp. Med. 177, 811-820, 1993

A/Title: T cell receptor selection by and recognition of two class I major histocompatib

A/Reference number: PH1430; MUID:93171821; PMID:8436911

A/Accession: PH1442

A/Molecule type: mRNA

A/Residues: 1-15 <CA2>

A/Experimental source: cytolytic T-lymphocyte

C/Suprafamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match 26.7%; Score 23; DB 2; Length 15;

Best Local Similarity 83.3%; Pred. No. 1.4e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ARSMG 8
|
|
|
|

Db 2 ALSMG 7

RESULT 11

PH0782

T-cell receptor alpha chain (H3 V-alpha-10, TA57) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C/Accession: PH0782

R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A/Title: T cell receptor genes in a series of class I major histocompatibility complex-

allelic exclusion and antigen-specific repertoire.

A/Reference number: PH0746; MUID:9207846; PMID:1836010

A/Accession: PH0782

A/Molecule type: mRNA

A/Residues: 1-15 <CAS>

A/Cross-references: EMBL:X60883

A/Experimental source: T lymphocyte

A/Note: the authors translated the codon TTC for residue 6 as Leu

C/Keywords: T-cell receptor

Query Match 26.7%; Score 23; DB 2; Length 15;

Best Local Similarity 50.0%; Pred. No. 1.4e+03;

Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 GKGEDLIW 14
|
|
|
|

Db 7 GDNKSLIW 14

RESULT 12

B60560

formyltetrahydrofolate dehydrogenase (EC 1.5.1.6) / aldehyde dehydrogenase (NADP) (EC 1

C/Species: Homo sapiens (man)

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C/Accession: B60560

R/Johnlin, F.C.; Swain, B.; Smith, C.; Tephly, T.R.

Mol. Pharmacol. 35, 745-750, 1989

A/Title: Studies on the mechanism of methanol poisoning: purification and comparison of

A/Reference number: A60560; MUID:89281497; PMID:2733692

A/Accession: B60560

A/Molecule type: protein

A/Residues: 1-16 <JOH>

A/Cross-references: UNIPROT:Q8TBPE

C/Keywords: multifunctional enzyme; NADP; oxidoreductase

Query Match 26.7%; Score 23; DB 2; Length 16;

Best Local Similarity 40.0%; Pred. No. 1.5e+03;

Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 VVARSMGKE 10
|
|
|
|

Db 5 VIQGSLEFG 14

RESULT 13

B61334

trypsin (EC 3.4.21.4) 2 - starfish (Dermasterias imbricata) (fragment)

C/Species: Dermasterias imbricata

C/Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004

C/Accession: B61334

R/Betell, D.A.; Laskowski, Jr., M.

Biochemistry 19, 124-131, 1980

A/Title: Dermasterias imbricata trypsin 1: an enzyme which rapidly hydrolyzes the react

A/Reference number: A61334; MUID:80109692; PMID:7352972

A/Accession: B61334

A/Molecule type: protein

A/Residues: 1-17 <BST>

A/Cross-references: UNIPROT:Q7M432

C/Suprafamily: trypsin; trypsin homology

C/Keywords: hydrolase; protein digestion; serine proteinase

Query Match 26.7%; Score 23; DB 2; Length 17;

Best Local Similarity 80.0%; Pred. No. 1.6e+03;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 MGSGE 10
|
|
|
|

Db 2 VGSGE 6

Job time : 40 secs

RESULT 14

YFPG

thymic factor - pig

N:Alternate names: FTS (facteur thymique serieque)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004

C:Accession: A01523; A60983

R:Pleau, J.M.; Dardenne, M.; Blouguit, Y.; Bach, J.F.

J. Biol. Chem. 252, 8045-8047, 1977

A:Title: Structural study of circulating thymic factor: a peptide isolated from pig seru

A:Reference number: A01523; PMID:78026571; PMID:914862

A:Accession: A01523

A:Molecule type: protein

A:Residues: 1-9

A:Cross-references: UNIPROT:P01255

R:Bach, J.F.; Dardenne, M.; Pleau, J.M.; Rosa, J.

Nature 266, 55-57, 1977

A:Title: Biochemical characterisation of a serum thymic factor.

A:Reference number: A60983; PMID:77123829; PMID:300146

A:Accession: A60983

A:Molecule type: protein

A:Residues: 'Z', '2-4', 'Z', '6-9

C:Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral

in a variety of immunosays.

C:Comment: See PIR:A60957 (sheep) for discussion of another possible N-terminal modifica

C:Superfamily: thymic factor

C:Keyword: pyroglutamic acid

F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

Best Local Similarity 25.6%; Score 22; DB 1; Length 9;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ARSMG 8

DB 2 AKSOG 7

RESULT 15

A60957

thymocyte growth peptide - sheep

N:Contains: FTS (facteur thymique serieque)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C:Accession: A60957

R:Ernstroem, U.; Garvelin, G.; Rudja, J.M.

Bioesci. Rep. 10, 403-412, 1990

A:Title: Purification of thymocyte growth peptide (TGP) from sheep thymus. Relationship

A:Reference number: A60957; PMID:91064427; PMID:2249004

A:Accession: A60957

A:Molecule type: protein

A:Residues: 1-9

A:Cross-references: UNIPROT:Q7M3C5

C:Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral

in a variety of immunosays.

C:Comment: This peptide was isolated in two forms. One form contained the pyrrolidone ca

r form (thymocyte growth peptide) contains a large, non-peptide blocking group with a hi

C:Superfamily: thymic factor

C:Keywords: blocked amino end, pyroglutamic acid

F1/Modified site: pyrrolidone carboxylic acid (Glx) (in FTS) #status experimental

F1/Modified site: blocked amino end (Glx) (in thymocyte growth peptide) #status experim

Query Match

Best Local Similarity 25.6%; Score 22; DB 2; Length 9;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 ARSMG 8

DB 2 AKSOG 7

Search completed: November 1, 2005, 13:32:32

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:57:41 ; Search time 167 Seconds

(without alignments)
52.128 Million cell updates/sec

Title: US-10-612-162A-1

Sequence: 86
1 VVARSMGKEDLIWELL 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 8390

Minimum DB seq length: 0
Maximum DB seq length: 17

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	33.7	17	2	Q6LDL9
2	29	33.7	17	2	Q6LEA8
3	28	32.6	15	2	Q6SLP7
4	27	31.4	13	2	Q9UDE0
5	25	29.1	10	2	Q76ML6
6	24	27.9	12	1	UR2B_CYP6A
7	24	27.9	13	1	CRBL_VESXA
8	24	27.9	13	2	Q7MI1
9	24	27.9	15	1	RL11_STRAU
10	24	27.9	15	2	Q6QGR7
11	23	26.7	12	2	Q9H126
12	23	26.7	13	2	Q9UPES
13	23	26.7	14	1	UP07_ORYSA
14	23	26.7	16	2	Q8UUE1
15	23	26.7	16	2	Q8UUE2
16	23	26.7	16	2	Q8UUE3
17	23	26.7	16	2	Q8UUE4
18	23	26.7	16	2	Q8UUE5
19	23	26.7	16	2	Q8UUE6
20	23	26.7	16	2	Q8UUE7
21	23	26.7	16	2	Q8UUE8
22	23	26.7	16	2	Q8UUE9
23	23	26.7	16	2	Q8UUF0
24	23	26.7	16	2	Q8UUF2
25	23	26.7	16	2	Q8UUF3
26	23	26.7	16	2	Q8UUF4
27	23	26.7	16	2	Q8UUF5
28	23	26.7	16	2	Q8UUF6
29	23	26.7	16	2	Q8UUF7
30	23	26.7	16	2	Q8UUF8
31	23	26.7	17	2	Q7M432

32	23	26.7	17	2	Q9R4A5	Q9R4A5 oerakovia x
33	22	25.6	8	2	Q7R6C3	Q7R6C3 largemouth
34	22	25.6	9	1	MEF_HVIZ8	P12481 human immun
35	22	25.6	9	1	THYF_PIG	P01255 sus scrofa
36	22	25.6	9	2	Q7M3C5	Q7M3C5 ovis aries
37	22	25.6	11	2	Q9UEL0	Q9UEL0 homo sapien
38	22	25.6	12	2	Q8L1C3	Q8L1C3 trifolium r
39	22	25.6	12	2	Q41611	Q41611 human immun
40	22	25.6	12	2	Q75729	Q75729 human immun
41	22	25.6	13	1	CRBL_VESAN	P17233 vespa anall
42	22	25.6	13	2	Q9AMK2	Q9AMK2 xanthomonas
43	22	25.6	15	2	Q8R5G1	Q8R5G1 spermophilu
44	22	25.6	15	2	Q8UM88	Q8UM88 human immun
45	22	25.6	15	2	Q8USK4	Q8USK4 human immun

ALIGNMENTS

```

RESULT 1
ID Q6LDL9 PRELIMINARY; PRT; 17 AA.
AC Q6LDL9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN Name=NCAM-C;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=90287121; PubMed=1694009;
RA Chen A., Reyes A., Akesson R.A.;
RT "transcription initiation sites and structural organization of the
RL extreme 5' region of the rat neural cell adhesion molecule gene.";
RL Mol. Cell. Biol. 10:3314-3324 (1990).
DR EMBL; M32612; AAA41680.1; -.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2026 MW; AEA1BB5F252B84F5 CRC64;

Query Match 33.7%; Score 29; DB 2; Length 17;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 EDLIWEL 16
Db 5 KDLIWTLL 11

RESULT 2
ID Q6LEA8 PRELIMINARY; PRT; 17 AA.
AC Q6LEA8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Neural cell adhesion molecule (Fragment).
GN Name=NCAM;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OX Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnson A.D., Ovesnek N., Tonissen K.F., Krieg P.A.;
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; L26396; AAA49911.1; -.
FT NON_TER 17

```

SQ SEQUENCE 17 AA; 2005 MW; AEBD9B5855262107 CRC64;

Query Match 33.7%; Score 29; DB 2; Length 17;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 10 EDLWEL 16
:|||||
Db 5 KDLIWL 11

RESULT 3

Q6SLF7 PRELIMINARY; PRT; 15 AA.
ID Q6SLF7;
AC Q6SLF7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Ghrelin (Fragment).
OS Rangifer tarandus (Reindeer) (Caribou).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Odocoileinae; Rangifer.
NCBI_TaxId=9870;
RN [1]

RP SEQUENCE FROM N.A.
RA Dickin J.C., Thue T.D., Buchanan F.C.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB455989; AAS67354.1; -.

FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1763 MW; CBSEFF57F7D20AF8 CRC64;

Query Match 32.6%; Score 28; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 10 EDLWEL 15
:|||||
Db 1 QDLWEL 6

RESULT 4

Q9UDE0 PRELIMINARY; PRT; 13 AA.
ID Q9UDE0;
AC Q9UDE0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Aggrecaan core protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxId=9606;
RN [1]

RP SEQUENCE FROM N.A.
RA MEDLINE=9223526; PubMed=1569188;
RA Sandy J.D., Flannery C.R., Neame P.J., Lohmender L.S.;
RL J. Clin. Invest. 89:1512-1516(1992).

DR GO; GO:0030021; Extracellular matrix structural constituent. . .; ISS.
DR GO; GO:0005540; Extracellular matrix organization and bioge. . .; ISS.
DR GO; GO:0030196; Extracellular matrix organization and bioge. . .; ISS.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1407 MW; 3A1B032DD2751B18 CRC64;

Query Match 31.4%; Score 27; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 1.8e+03;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 6 MGKEDL 12
:|||||
Db 4 VGGEDI 10

RESULT 5

Q76ML6 PRELIMINARY; PRT; 10 AA.
ID Q76ML6;
AC Q76ML6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE NADH dehydrogenase subunit 4 (Fragment).
GN Name=ND4;
OS Eurypharynx pelicanoides (pelican eel).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes;
OC Eurypharyngidae; Eurypharynx.
NCBI_TaxId=55117;
RN [1]

RP SEQUENCE FROM N.A.
RA MEDLINE=22967687; PubMed=12949142; DOI=10.1093/molbev/msg206;
RA Inoue J.G., Miya M., Tsukamoto K., Nishida M.;
RT "Evolution of the deep-sea gulper eel mitochondrial genomes: large-scale gene rearrangements originated within the eels";
RL Mol. Biol. Evol. 20:1917-1924(2003).

RN [2]
RP SEQUENCE FROM N.A.
RA Inoue J., Inoue J., Miya M., Tsukamoto K., Nishida M.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB046482; BAB87149.1; -.
DR EMBL; AB046486; BAB87157.1; -.
DR EMBL; AB046490; BAB87165.1; -.
DR EMBL; AB046478; BAB87141.1; -.
DR GO; GO:0005739; Mitochondrion; IEA.

FT NON_TER 1 1
SQ SEQUENCE 10 AA; 1263 MW; 62D604786370572B CRC64;

Query Match 29.1%; Score 25; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 9 KEDLIW 14
:|||||
Db 1 KPELIW 6

RESULT 6

UR2B_CYPCA STANDARD; PRT; 12 AA.
ID UR2B_CYPCA;
AC P04561;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Urotensin II-beta (U-II-beta).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
NCBI_TaxId=7962;
RN [1]

RP SEQUENCE.
RA Munkata E., Ohtaki T., Ichikawa T., McMaster D., Lederis K.;
RL (in) Rich D.H., Gross E. (eds.);
RL Proceedings of the 7th American peptide symposium, pp.69-72, Pierce Chemical Co., Rockford IL. (1981)

CC -1- FUNCTION: Urotensin is found in the teleost caudal neurosecretory system. It has a suggested role in osmoregulation and as a corticotropin-releasing factor.
CC -1- SUBCELLULAR LOCATION: Secreted.

CC InterPro: IPR001483; Urotensin II.
DR Pfam: PF02083; Urotensin II; 1.
DR PROSITE: PS00984; UROTENSIN_II; 1.

KM Direct protein sequencing; Hormone.
 FT DISUFID 6 11 G->S
 FT VARIANT 2 2
 SQ SEQUENCE 12 AA; 1407 MW; 73960A9FB879CEBB CRC64;
 Query Match 27.9%; Score 24; DB 1; Length 12;
 Best Local Similarity 33.3%; Pred. No. 5.5e+03;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 GGEKDLWE 15
 DB 1 GGTECFWK 9

RESULT 7
 ID CRBL_VESXA STANDARD; PRT; 13 AA.
 AC P17234;
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Vespid chemotactic peptide X (VSCP-X).
 OS Vespa xanthoptera (Japanese hornet).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 NC NCB1_TaxID=7448;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Venom;
 RA Yasuhara T., Iokawa H., Suzuki N., Nakamura H., Nakajima T.;
 RL (in) Izumiya N. (eds.);
 RL Peptide chemistry 1984, pp.177-182, Protein Research Foundation, Osaka
 CC (1985).
 CC -1- FUNCTION: Mast cell degranulating peptide. Induces the chemotaxis
 of neutrophils.
 CC Amidation; Chemotaxis; Direct protein sequencing;
 KW Mast cell degranulation.
 FT MOD_RES 13 Leucine amide.
 SQ SEQUENCE 13 AA; 1368 MW; C85040365DF9233D CRC64;
 Query Match 27.9%; Score 24; DB 1; Length 13;
 Best Local Similarity 37.5%; Pred. No. 5.9e+03;
 Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVARSMCG 8
 DB 4 IIAKLGG 11

RESULT 8
 ID Q7M1U1 PRELIMINARY; PRT; 13 AA.
 AC Q7M1U1;
 DT 01-MAR-2004 (TRENBLREL. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last sequence update)
 DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
 DE Unidentified 6.3/40K protein (Fragment).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriocaridaceae; Oryzaceae; Oryza.
 NC NCB1_TaxID=4530;
 RN [1]
 RP SEQUENCE.
 RA Komatsu S., Kajiwara H., Hirano H.;
 RT "A rice protein library: a data-file of rice proteins separated by
 RT two-dimensional electrophoresis";
 RL Theor. Appl. Genet. 86:935-942(1993).
 DR PIR; P00700; P00700.
 DR Gramene; Q7M1U1; -;
 FT NON_TER 1 1
 FT NON_TER 13 13
 GN NON_TER 13 13

SQ SEQUENCE 13 AA; 1218 MW; 27EA7291E7D3D878 CRC64;
 Query Match 27.9%; Score 24; DB 2; Length 13;
 Best Local Similarity 41.7%; Pred. No. 5.9e+03;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 VVARSMCGDLI 13
 DB 1 VAGAYGAIDL 12

RESULT 9
 ID RL11_STRAU STANDARD; PRT; 15 AA.
 AC Q9X520;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 50S ribosomal protein L11 (Fragment).
 GN Name=rpL1;
 OS Streptomyces aureofaciens.
 OC Bacteria; Actinobacteria; Actinomycetales;
 OC Streptomycetales; Streptomycetaceae; Streptomyces.
 NC NCB1_TaxID=1894;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10762 / CCM 3239;
 RA Kormanec J., Novakova R., Klucar L., Homerova D., Sevcikova B.,
 RA Sprusansky O.;
 RT "Cloning of the rplA gene encoding ribosomal protein L1 from
 RT Streptomyces aureofaciens, and its transcriptional analysis in the
 RT course of differentiation";
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: This protein binds directly to 23S ribosomal RNA (by
 CC similarity).
 CC -1- PTM: One or more lysine residues are methylated (by similarity).
 CC -1- SIMILARITY: Belongs to the ribosomal protein L11P family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF120458; AAD24568.1; -;
 CC HAMAP; MF_00736; -; 1.
 DR InterPro; IPR000911; Ribosomal_L11.
 DR Pfam; PF00288; Ribosomal_L11; 1.
 DR PROSITE; PS00359; RIBOSOMAL_L11; PARTIAL.
 KW Methylation; Ribosomal protein; rRNA-binding.
 FT NON_TER 1 1
 SQ SEQUENCE 15 AA; 1476 MW; 80B147826B0701A8 CRC64;
 Query Match 27.9%; Score 24; DB 1; Length 15;
 Best Local Similarity 100.0%; Pred. No. 6.8e+03;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 ARSMG 7
 DB 6 ARSMG 10

RESULT 10
 ID Q6OQR7 PRELIMINARY; PRT; 15 AA.
 AC Q6OQR7;
 DT 05-JUL-2004 (TRENBLREL. 27, Created)
 DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=HP1080;

```

OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OK NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=92-28;
RA Terry C., Madigan K., McGinnis L., Cao P., Cover T., Liechti G.,
RL Peek R. Jr., Forsyth M.; to the EMBL/GenBank/DBJ databases.
DR EMBL; AF525680; AAS20947.1; -.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 15 AA; 1780 MW; 4F3C63D9DD7D6BED CRC64;

Query Match
Best Local Similarity 27.9%; Score 24; DB 2; Length 15;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 RSMGKED 11
DB 6 RFLGSKNE 13

RESULT 11
ID 09H1Z6 PRELIMINARY; PRT; 12 AA.
AC 09H1Z6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Estrogen receptor 1 (Fragment).
GN Name=ESRL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gonzalez-Gomez F., Vergara F., Pedrosa C., Ramirez J.P.,
RA Castellia J.A., Yoldi A., Ruiz A., Real L.M.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF326912; AAG42501.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
KW Receptor.
FT NON_TER
FT NON_TER
SQ SEQUENCE 12 AA; 1385 MW; 0916B8CB76C41404 CRC64;

Query Match
Best Local Similarity 26.7%; Score 23; DB 2; Length 12;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RSMGKKE 10
DB 6 RROGGRRE 12

RESULT 12
ID 09UPB5 PRELIMINARY; PRT; 13 AA.
AC 09UPB5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Inosine monophosphate 2 (Fragment).
GN Name=IMP2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OK NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RX MEDLINE=97463449; PubMed=9322233;
RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
RA Decker-Wadleigh S.D.;
RT "A novel human myo-inositol monophosphatase gene, IMP18p, maps to a
RT susceptibility region for bipolar disorder.";
RL Mol. Psychiatry 2:393-397(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20284187;
RA Yoshikawa T., Padigaru M., Karkera J.D., Sharma M., Berrettini W.H.,
RA Esterling L.E., Decker-Wadleigh S.D.;
RT "Genomic structure and novel variants of myo-inositol monophosphatase
RT 2.";
RL Mol. Psychiatry 5:165-171(2000).
DR EMBL; AF025886; AAD2138.1; -.
DR EMBL; AF025885; AAD22138.1; JOINED.
FT NON_TER
FT NON_TER
SQ SEQUENCE 13 AA; 1331 MW; 89C724C8E3457865 CRC64;

Query Match
Best Local Similarity 26.7%; Score 23; DB 2; Length 13;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 VVARSGKEDLI 13
DB 1 IVIDTSGGPLDLM 13

RESULT 13
ID 07ORYSA STANDARD; PRT; 14 AA.
AC P83648;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of leaf (OsL8) (Fragmente).
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriaristaceae; Oryzaeae; Oryza.
OK NCBI_TaxID=4530;
RN [1]
RP SEQUENCE.
RA STRAIN=cv. Indica / IR64; TISSUE=leaf;
RA Hosseini Salekdeh S.G., Bennett J.;
RT "Proteome analysis of rice leaf.";
RL Submitted (JUL-2003) to Swiss-Prot.
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC protein is: 6.2, its MW is: 28 kDa.
CC -1- CAUTION: The order of the peptides is uncertain.
KW Chloroplast; Direct protein sequencing.
FT NON_TER
FT UNSTRE
FT UNSTRE
FT NON_CONS
FT NON_TER
SQ SEQUENCE 14 AA; 1403 MW; CC78FB817B5C8FB2 CRC64;

Query Match
Best Local Similarity 26.7%; Score 23; DB 1; Length 14;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 VVARSGKEDLI 12
DB 1 VVANIGVTEEL 11

RESULT 14
ID 08UBE1 PRELIMINARY; PRT; 16 AA.
AC 08UBE1;
DT 01-MAR-2002 (TREMBlrel. 20, Created)

```

```

DT 01-MAR-2002 (T-EMBLrel. 20, last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, last annotation update)
DE Rhodopsin (Fragment).
GN Name=RDPI;
OS Megapodius tenimberensis (Tanimbar scrubfowl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Megapodidae; Megapodius.
OX NCBI_TaxID=177170;
RN [1]
RP SEQUENCE FROM N.A.
RA Birks S.M., Edwards S.V.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF394659; AAL36887.1; -.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1683 MM; CDC571884A940BF0 CRC64;

Query Match
Best Local Similarity 40.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 8 GKEDLIWBL 17
Db 2 GGEIALMSLV 11

```

RESULT 15

```

ID Q8UUE2 PRELIMINARY; PRT; 16 AA.
AC Q8UUE2;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, last sequence update)
DT 01-MAR-2002 (T-EMBLrel. 20, last annotation update)
DE Rhodopsin (Fragment).
GN Name=RDPI;
OS Megapodius pitcheardi (Polynesian scrubfowl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Megapodidae; Megapodius.
OX NCBI_TaxID=177169;
RN [1]
RP SEQUENCE FROM N.A.
RA Birks S.M., Edwards S.V.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF394658; AAL36886.1; -.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1683 MM; CDC571884A940BF0 CRC64;

Query Match
Best Local Similarity 40.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 8 GKEDLIWBL 17
Db 2 GGEIALMSLV 11

```

Search completed: November 1, 2005, 13:31:48
Job time : 169 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using bw model

Run on: November 1, 2005, 12:28:13; Search time 131.574 Seconds

(without alignments)
67,608 Million cell updates/sec

Title: US-10-612-162a-2

Sequence: 1 TTBDSIAKIMNGEADMSLDGCF 23

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

A_Geneseq_16Dec04:*
1: geneseq1980a:*
2: geneseq1990a:*
3: geneseq2000a:*
4: geneseq2001a:*
5: geneseq2002a:*
6: geneseq2003a:*
7: geneseq2003b:*
8: geneseq2004a:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	23	ADG46076	Adg46076 Human CDT
2	110	95.7	328	AA884371	Aab84371 Angiotens
3	110	95.7	539	AAU02980	Aau02980 Angiotens
4	110	95.7	575	ABR82321	Abt82321 Human met
5	110	95.7	609	ABM63782	Abm63782 Human dia
6	110	95.7	627	ABM63781	Abm63781 Human dia
7	110	95.7	628	ABM63779	Abm63779 Human dia
8	110	95.7	643	ABM63778	Abm63778 Human dia
9	110	95.7	645	ABM63783	Abm63783 Human dia
10	110	95.7	646	AAU02938	Aau02938 Angiotens
11	110	95.7	646	ABM63780	Abm63780 Human dia
12	110	95.7	665	AAU02937	Aau02937 Angiotens
13	110	95.7	679	ABP72820	Abp72820 Human tra
14	110	95.7	679	ADH89360	Adh89360 Human tra
15	110	95.7	679	ADK15869	Adk15869 Mature hu
16	110	95.7	679	ADL70732	Adl70732 Human tra
17	110	95.7	679	ADL24413	Adl24413 Human tra
18	110	95.7	698	AAK12499	Aak12499 Human tra
19	110	95.7	698	AAK66492	Aak66492 Human tra
20	110	95.7	698	AAK64354	Aak64354 Serotrans
21	110	95.7	698	AAK50717	Aak50717 Human ser
22	110	95.7	698	ABP72819	Abp72819 Human tra
23	110	95.7	698	ADD45282	Add45282 Human tra
24	110	95.7	698	ADP74796	Adp74796 Human NOV
25	110	95.7	698	ADP74800	Adp74800 Human NOV

ALIGNMENTS

RESULT 1	ADG46076	standard; peptide; 23 AA.
ID	ADG46076	
AC	ADG46076;	
XX		
DT	25-MAR-2004	(first entry)
XX		
DE	Human CDT peptide fragment #2.	
XX		
KM	antibody; carbohydrate-deficient transferrin; CDT;	
KW	non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.	
XX		
OS	Homo sapiens.	
XX		
PN	EP1378521-A1.	
XX		
PD	07-JAN-2004.	
XX		
PF	19-MAY-2003; 2003EP-00011334.	
XX		
PR	05-JUL-2002; 2002DE-01030550.	
XX		
PA	(DADE-) DADE BEHRING MARBURG GMBH.	
PI	Althaus H;	
XX		
DR	WPI; 2004-073743/08.	
XX		
PT	New antibody specific for carbohydrate-deficient transferrin, useful for	
PT	diagnosis of alcoholism, can bind its target in solution, eliminating	
PT	need for immobilization.	
XX		
PS	Claim 4; SEQ ID NO 2; 21pp; German.	
XX		
CC	This invention describes a novel antibody that, in aqueous solution,	
CC	binds selectively to carbohydrate-deficient transferrin (CDT) without	
CC	having to bind CDT to a solid phase. The invention also describes an	
CC	antibody that binds selectively to CDT at regions containing the	
CC	sequences VVARSMGKEDLWEL, TTBDSIAKIMNGEADMSLDGCF, SKLSGSLNISEPN and	
CC	YEKYLGEYKAV (ADG46075-ADG46078) and an immunoassay for detecting CDT	
CC	using the antibodies of the invention. The antibodies of the invention	
CC	are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The	
CC	antibodies are obtained by immunisation with non-glycosylated	
CC	transferrin, or a fragment, then generation of hybridomas by standard	
CC	fusion of spleen and myeloma cells. Hybridomas are then selected for	
CC	production of antibodies that specifically bind CDT from the aqueous	
CC	phase. The antibodies are useful for diagnosis of alcoholism, CDT, which	

26	110	95.7	698	8	ADH34559	Adh34559 Human tra
27	110	95.7	698	8	ADH89359	Adh89359 Human tra
28	110	95.7	698	8	ADK15868	Adk15868 Human tra
29	110	95.7	698	8	ADL70731	Adl70731 Human tra
30	110	95.7	698	8	ADL24412	Adl24412 Human tra
31	110	95.7	698	8	ADP21259	Adp21259 Human tra
32	110	95.7	1074	2	AAW07621	Aaw07621 LDR/TF C
33	110	95.7	1410	2	AAW07622	Aaw07622 LDR/TF C
34	110	95.7	1410	6	ABU04139	Abu04139 Human exp
35	110	95.7	1418	4	AAU32831	Aau32831 Novel hum
36	110	95.7	1418	6	ABU04138	Abu04138 Human exp
37	101	87.8	676	8	ADL70764	Adl70764 Rabbit tr
38	101	87.8	676	8	ADL24458	Adl24458 Rabbit tr
39	96	83.5	688	8	ADL70767	Adl70767 Horse tra
40	96	83.5	688	8	ADL24461	Adl24461 Horse tra
41	93.5	81.3	696	1	AAK70384	Aak70384 Sequence
42	92	80.0	677	8	ADL70766	Adl70766 Mouse tra
43	92	80.0	677	8	ADL24460	Adl24460 Murine tr
44	92	80.0	685	2	AAK11664	Aak11664 Partial p
45	92	80.0	685	2	AAK11663	Aak11663 Partial p

CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcohols. The antibodies allow direct detection of CPT in solution,
CC eliminating the need for immobilising it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CPT peptide
CC fragments used in the method of the invention.

XX Sequence 23 AA;

Query Match 100.0%; Score 115; DB 8; Length 23;
Best Local Similarity 100.0%; Pred. No. 4e-11; 0; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADAMSIDGCF 23
Db 1 TTEDSIKIMNGEADAMSIDGCF 23

RESULT 2
AAB84371
ID AAB84371 standard; protein; 328 AA.

XX AAB84371;

XX 22-AUG-2001 (first entry)

XX Amino acid sequence of a human transferrin.

DE Humen; transferrin; autoimmune disease; rheumatoid arthritis;
XX hyperproliferative disorder; neoplasm; cardiovascular disorder;
KW cardiac arrest; cerebrovascular disorder; cerebral ischemia;
KW angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KW ocular disorder; corneal infection; wound healing;
KW epithelial cell proliferation; aging; organ transplant.

XX Homo sapiens.

XX WO200146254-A1.

XX 28-JUN-2001.

XX 21-DEC-2000; 2000WO-US034769.

XX 23-DEC-1999; 99US-0171595P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Shi Y, Choi GH;

XX WPI; 2001-381910/40.

XX N-PSDB; AAB25190.

XX Isolated nucleic acid molecule encoding a human transferrin protein is
XX used in preventing, treating or ameliorating a medical condition.

XX Claim 11; Page 286-287; 290pp; English.

XX The present sequence represents human transferrin polypeptide.

CC Transferrin polypeptides and polynucleotides are used to prevent, treat
CC or ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
CC horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or
CC treated include autoimmune diseases e.g. Rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
CC ocular disorders e.g. corneal infection. The polypeptides can also be
CC used to aid wound healing and epithelial cell proliferation, to prevent
CC skin aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities

XX Sequence 328 AA;

Query Match 95.7%; Score 110; DB 4; Length 328;
Best Local Similarity 95.7%; Pred. No. 5.6e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADAMSIDGCF 23
Db 56 TTEDSIKIMNGEADAMSIDGCF 78

RESULT 3
AAU02980
ID AAU02980 standard; protein; 539 AA.

XX AAU02980;

XX 12-SEP-2001 (first entry)

XX Angiotensin converting enzyme (ACEV) splice variant protein #80.

DE Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
XX granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KW vasodilative intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW nonarctoidotic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; asbestosis.

XX Homo sapiens.

XX WO200136632-A2.

XX 25-MAY-2001.

XX 17-NOV-2000; 2000WO-IL000766.

XX 17-NOV-1999; 99IL-00132978.

XX 10-DEC-1999; 99IL-00133455.

XX (COMP-) COMPUGEN LTD.

XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;

XX WPI; 2001-336004/35.

XX N-PSDB; AAS06080.

XX Novel alternative splicing variants e.g. variant of angiotensin
XX converting enzyme (ACEV), useful in identifying candidate compounds
XX capable of binding to the variant and to detect anti-variant antibodies.

XX Claim 4; Fig 80; 519pp; English.

CC The sequence represents an angiotensin converting enzyme splice variant
CC (ACEV) polypeptide. The polypeptides of the invention include variants of
CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
CC inhibitor 1C, cellular tumour antigen P53, and vasodilative intestinal
CC polypeptide receptor 2. The polypeptides and their associated nucleic
CC acids are useful for identification of variant sequences and detection of
CC candidate compounds capable of binding the molecules. The sequences of
CC the invention can be used in the treatment and diagnosis of various
CC disorders including cardiovascular diseases such as arteriosclerosis,
CC myocardial infarction and coronary arterial thrombosis, renal diseases
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
CC immune disorders such as immune complex nephritis, multiple sclerosis,
CC cancer, sarcoidosis, nonarctoidotic pulmonary granulomatous diseases such
CC as asbestosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis

XX Sequence 539 AA;

CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX SQ Sequence 609 AA;

Query Match 95.7%; Score 110; DB 8; Length 609;
Best Local Similarity 95.7%; Pred. No. 1.2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIATKIMGADAMSJDGF 23
DB 321 TTEDCIATKIMGADAMSJDGF 343

RESULT 6

ABM83781
ID ABM83781 standard; protein; 627 AA.

AC ABM83781;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic protein SEQ ID NO:4030.

KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

OS Homo sapiens.

PN WO2004023973-A2.

PD 25-MAR-2004.

PF 12-SEP-2003; 2003WO-US028227.

PR 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

PA (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Hartschorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;

PI Patury S, Shi X, Suarez CJ;

DR WPI; 2004-329368/30.

DR N-PSDB; ACN42433.

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

PS Claim 27; Page: 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly

CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX SQ Sequence 627 AA;

Query Match 95.7%; Score 110; DB 8; Length 627;
Best Local Similarity 95.7%; Pred. No. 1.2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIATKIMGADAMSJDGF 23
DB 321 TTEDCIATKIMGADAMSJDGF 343

RESULT 7

ABM83779
ID ABM83779 standard; protein; 628 AA.

AC ABM83779;

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic protein SEQ ID NO:4028.

KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

OS Homo sapiens.

PN WO2004023973-A2.

PD 25-MAR-2004.

PF 12-SEP-2003; 2003WO-US028227.

PR 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

PA (INCY-) INCYTE CORP.

PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Hartschorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;

PI Patury S, Shi X, Suarez CJ;

DR WPI; 2004-329368/30.

DR N-PSDB; ACN42431.

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

PS Claim 27; Page: 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly

CC From WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 628 AA;

SQ Sequence 628 AA;

```
Query Match      95.7%  Score 110, DB 8; length 628;
Best Local Similarly 95.7%  Pred No. 1.2e-08;
Matches 22, Conservative 0; Mismatches 1; Indels 0; Gaps 0
```

OY	1	TTEDSI	AKIMNGE	ADAMS	LDGGF	23
Db	340	TTEDCI	AKIMNGE	ADAMS	LDGGF	362

RESULT 8
ABM83778
ID ABM83778 standard; protein; 643 AA

AC ABM83778;

DT 18-NOV-2004 (first entry)

Human diagnostic and therapeutic protein SEQ ID NO:4027.

gene therapy; human diagnostic and therapeutic polynucleotide; dithp

OS Homo sapiens

PN WO2004023973-A2.

PD 25-MAR-2004.

PF 12-SEP-2003; 2003WO-US028227.

PR 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

PA (INCY-) INCYTE CORP.

PI Schmidt P, Wright RJ, Bruns CM, Martinovic MM, Shen F, Hartshorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV, Mooney EM, Delegane AM, Panssar IS, Banville SC, Reddy TP, Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH, Peralta CA, Anderson SB, Rioux P, Shen EJ, Wu MC, Seuve LL, Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitron ES, Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D, Patry S, Shi X, Suarez CJ,

DR WPI; 2004-329368/30.

DR N-PSDB; ACN42430.

DR N-PSDB; ACN42430

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human PT molecule, e.g. autoimmune or inflammatory disorders, in gene therapy or PT in gene mapping.

PS Claim 27; page; 190pp; English.

The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dthp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dthp protein of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from www.wipo.int/pct/en/sequences/listing.htm

XX	Sequence 643 AA;
SQ	

Query Match	95.7%	Score	110;	DB	8;	Length	643;
Best Local Similarity	95.7%	Pred.	No.1.2e-08;				
Matches	22;	Conservative	1;	Indels	0;	Gaps	0

Oy		1	T	T	E	D	S	I	A	K	I	M	N	G	E	A	D	A	M	S	L	D	G	G	F	23
Db		355	T	T	E	D	C	I	A	K	I	M	N	G	E	A	D	A	M	S	L	D	G	G	F	377

RESULT 9
ABM83783
ID ABM83783 standard; protein; 645 AA

AC ABM83783

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4032.

KW gene therapy; human diagnostic and therapeutic polynucleotide; dithp

OS Homo sapiens.

PN WO2004023973-A2

PD 25-MAR-2004

PF 12-SEP-2003; 2003WO-US028227.

PR 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

PA (INCY-) INCYTE CORP.

PI Schmidt P, Wright RJ, Bruns CM, Marjanovic MM, Shen F, Hartschorne TA, Suchorolski MR, Albus CM, Pitte SJ, Elder LV, Pi Mooney EM, Deleagane AM, Panssar IS, Banville SC, Reddy TP, Pi Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH, Pi Peralta CH, Anderson SB, Rioux P, Shen EC, Wu MC, Stuve LL, Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kiron ES, Pi Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D, Pi Y, Shi X, Suarez CJ;

DR WPI; 2004-329368/30.

DR N-PSDB; ACN42435.

DR N-PSDB; ACN42435

PT New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human PT molecule, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.

PS Claim 27; Page: 190pp; English

CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dthnp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dthnp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dthnp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from www.wipo.int/pct/en/sequences/lilecting.htm

Query Match 95.7%; Score 110; DB 8; Length 646;
Best Local Similarity 95.7%; Pred. No. 1.2e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADAMSJDGF 23
Db 340 TTEDCIKIMNGEADAMSJDGF 362

RESULT 12

AAU02937
ID AAU02937 standard; protein; 665 AA.

XX AAU02937;

DT 12-SEP-2001 (first entry)

DE Angiotensin converting enzyme (ACEV) splice variant protein #17.

KM Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KM granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KM platelet-derived endothelial cell growth factor; cardiovascular disease;
KM cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1c;
KM vasoreactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KM myocardial infarction; coronary arterial thrombosis; renal disease;
KM diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KM multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KM noncardiotoxic pulmonary granulomatous disease; endothelial abnormality;
KM vascular disorder; asbestosis.

XX Homo sapiens.

OS WO200136632-A2.

PN 25-MAY-2001.

XX 17-NOV-2000; 2000MO-IL000766.

XX 17-NOV-1999; 99IL-00132978.

PR 10-DEC-1999; 99IL-00133455.

XX (COMP-) COMPUGEN LTD.

PA Levine Z, David A, Azar I, Khosravi R, Bernstejn J;

PI WPI; 2001-336004/35.

XX N-PSDB; AAS06037.

PT Novel alternative splicing variants e.g. variant of angiotensin
converting enzyme (ACEV), useful in identifying candidate compounds
capable of binding to the variant and to detect anti-variant antibodies.

XX Claim 4; Fig 37; 519p; English.

CC The sequence represents an angiotensin converting enzyme splice variant
(ACEV) polypeptide. The polypeptides of the invention include variants of
granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
platelet-derived endothelial cell growth factor, cyclin-dependent kinase
inhibitor 1c, cellular tumour antigen P53, and vasoreactive intestinal
polypeptide receptor 2. The polypeptides and their associated nucleic
acid are useful for identification of variant sequences and detection of
candidate compounds capable of binding the molecules. The sequences of
the invention can be used in the treatment and diagnosis of various
disorders including cardiovascular diseases such as arteriosclerosis,
myocardial infarction and coronary arterial thrombosis, renal diseases
such as diabetic nephropathy, muscular diseases such as hypertrophy,
immune disorders such as immune complex nephritis, multiple sclerosis,
cancer, sarcoidosis, noncardiotoxic pulmonary granulomatous diseases such
as asbestosis and vascular pathologies involving an endothelial
abnormality such as deep vein thrombosis

CC Sequence 665 AA;

Query Match 95.7%; Score 110; DB 4; Length 665;
Best Local Similarity 95.7%; Pred. No. 1.3e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADAMSJDGF 23
Db 392 TTEDCIKIMNGEADAMSJDGF 414

RESULT 13

ABP72820
ID ABP72820 standard; protein; 679 AA.

XX ABP72820;

DT 11-AUG-2003 (first entry)

DE Human transferrin (mature polypeptide).

KM Human; transferrin; neuroprotective; cerebroprotective; vasotropic;
KM antiparkinsonian; nootropic; anti-HIV; antiallergic; antiallergic;
KM cytotactic; immunosuppressive; antithrombotic; cardiac;
KM gynaecological; immunostimulant; antinaemic; haemostatic;
KM antiinflammatory; dermatological; antibacterial; virucide; antiparasitic;
KM fungicide; hepatotropic; antipneumatic; antirheumatic; antipruritic;
KM tranquilizer; vulnary; antidiabetic; nephrotropic; antipyretic;
KM gastrointestinal; gene therapy; transgenic animal.

XX Homo sapiens.

OS Location/Qualifiers

XX Key Binding-site 63 /note= "Iron binding site"

XX Region 94..96 /note= "Hinge region"

XX Binding-site 95 /note= "Iron binding site"

XX Binding-site 120 /note= "Carbonate ion binding site"

XX Binding-site 124 /note= "Carbonate ion binding site"

XX Binding-site 126 /note= "Carbonate ion binding site"

XX Binding-site 127 /note= "Carbonate ion binding site"

XX Binding-site 188 /note= "Carbonate ion binding site"

XX Binding-site 245..247 /note= "Iron binding site"

XX Region 249 /note= "Hinge region"

XX Binding-site 316..318 /note= "Iron binding site"

XX Region 392 /note= "Hinge region"

XX Binding-site 413 /note= "Iron binding site"

XX Modified-site 425..427 /note= "N-glycosylated"

XX Region 426 /note= "Hinge region"

XX Binding-site 452 /note= "Iron binding site"

XX Binding-site 456 /note= "Carbonate ion binding site"

XX Binding-site 458 /note= "Carbonate ion binding site"

XX Binding-site 459 /note= "Carbonate ion binding site"

XX Binding-site 514 /note= "Carbonate ion binding site"

XX Binding-site 517 /note= "Iron binding site"

FT	/note= "Iron binding site"
FT	581..582
FT	/note= "Hinge region"
FT	Binding-site
FT	585
FT	/note= "Iron binding site"
FT	Modified-site
FT	611
FT	/note= "N-glycosylated"
FT	Region
FT	652..658
FT	/note= "Hinge region"
XX	
PN	WO2003020746-A1.
PD	
PD	13-MAR-2003.
XX	
XX	30-AUG-2002; 2002WO-US027637.
PF	
PR	30-AUG-2001; 2001US-0315745P.
PR	30-NOV-2001; 2001US-0334059P.
XX	
PA	(BIOR-) BIOREXIS PHARM CORP.
PI	
P1	Prior CP;
XX	
DR	WPI; 2003-332916/31.
XX	
PT	New fusion protein, useful in the diagnosis and treatment of diseases or disorders relating to the respiratory, cardiovascular and digestive systems, comprises a transferrin protein fused to a therapeutic protein.
PT	
PS	Disclosure; Page 280-281; 298pp; English.
XX	
CC	The present sequence is the protein sequence of human transferrin (Tf), minus the signal peptide. The invention relates to modified Tf fusion proteins comprising at least one therapeutic protein, polypeptide or peptide, in which the Tf portion is engineered to extend the serum half-life or bioavailability of the molecule. The modified Tf fusion protein preferably comprises a human Tf moiety that has been modified to reduce or prevent glycosylation, iron binding and/or transferrin receptor binding, having at least one amino acid substitution, deletion or addition in the hinge region, or at residues Asp-63, Gly-65, Tyr-95, Tyr-188, Lys-206, His-207, Asn-249, Asp-392, Tyr-426, Tyr-514, Tyr-517, His-585, Thr-120, Arg-124, Ala-126, Gly-127, Thr-452, Arg-456, Ala-458 and Gly-459, or a mutation which prevents glycosylation at Asn-413 or Asn-611 (all claimed). Nucleic acids encoding such fusion proteins, vectors, host cells and transgenic animals which produce the fusion protein in their serum or milk are also claimed. The modified fusion protein is useful for treating a disease or disease symptom, or for delivering a therapeutic agent complexed to the ferric iron of transferrin to the inside of a cell or across the blood-brain barrier. The modified fusion protein, or a nucleic acid encoding it, can be used in the diagnosis, prognosis, prevention and/or treatment of diseases and/or disorders of the endocrine, nervous, immune, respiratory, cardiovascular, reproductive and digestive systems, diseases and/or disorders relating to the blood or to cell proliferation, inflammatory conditions, and to treat viral, fungal, bacterial or parasitic infection
SQ	Sequence 679 AA;
XX	
QY	Query Match 95.7%; Score 110; DB 6; Length 679;
Dd	Best Local Similarity 95.7%; Pred. No. 1.3e-08;
XX	Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0
XX	1 TTEDSIAKIMNGEADMSLDGSE 23
XX	
XX	TTEDCIAKIMNGEADMSLDGSE 395
XX	
XX	RESULT 14
ID	ADH89360
XX	ADH89360 standard; protein; 679 AA.
XX	ADH89360;
XX	

DT	15-APR-2004	(first entry)
XX		
DE	Human transferrin protein mature amino acid sequence.	
XX		
KW	fusion protein; transferrin protein; glycosylation;	
KV	antibody variable region; cytostatic; antibacterial; virucide;	
KM	antiparasitic; immunosuppressive; antiarthritic; gene therapy;	
KX	septic shock; endotoxic shock; cachexia syndrome; bacterial infection;	
KY	vital infection; parasitic infection; neoplasm; autoimmune disease;	
KZ	arthritis; graft rejection; human.	
OS	Homo sapiens.	
XX		
PV	US20032615-A1.	
XX		
PD	04-DEC-2003.	
XX		
PF	10-MAR-2003; 2003US-00384060.	
XX		
PR	30-AUG-2001; 2001US-0315745P.	
PR	30-NOV-2001; 2001US-0334059P.	
PR	30-AUG-2002; 2002US-00231494.	
PR	30-AUG-2002; 2002US-0406977P.	
XX		
PA	(BIOR-) BIOREXIS PHARM CORP.	
XX		
PI	Sadeghi H, Prior CP, Turner A;	
XX		
DR	WPI; 2004-0223093/02.	
DR	N-PSTDB; ADH89358.	
XX		
PT	New fusion protein comprising a transferrin protein exhibiting reduced	
PT	glycosylation fused to at least one antibody variable region, useful for	
PT	preparing a composition for treating e.g., septic shock, neoplasm or	
PT	autoimmune disease.	
XX		
PS	Disclosure; SEQ ID NO 3; 82pp; English.	
XX		
CC	This invention relates to a novel fusion protein which comprises a	
CC	transferrin protein exhibiting reduced glycosylation fused to at least	
CC	one antibody variable region. The invention may be useful for the	
CC	development of compounds with cytostatic, antibacterial, virucide,	
CC	antiparasitic, immunosuppressive or antiarthritic activity. In addition,	
CC	the sequences disclosed may be useful for gene therapy. The fusion	
CC	protein is useful for preparing a composition for treating a disease or	
CC	disease symptom in a patient for example septic shock, endotoxic shock,	
CC	cachexia syndromes associated with bacterial, viral or parasitic	
CC	infections, neoplasm, autoimmune disease, arthritis or adverse effects	
CC	associated with treatment for preventing graft rejection. The present	
CC	sequence is that of the mature human transferrin protein which is related	
CC	to the invention.	
XX		
XX		
SQ	Sequence 679 AA;	
Query Match	95.7%; Score 110; DB 8; Length 679;	
Best Local Similarity	95.7%; Pred. No.1.3e-08;	
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0		
Oy	1 TTEDSIKINMGADAMSLDGGF 23 Db 373 TTEDCIKINMGADAMSLDGGF 395	
RESULT 15		
ID	ADK15869 standard; protein; 679 AA.	
XX	ADK15869;	
XX	ADK15869;	
XX	AC	
XX	06-MAY-2004 (first entry)	
DT		
XX	Mature human transferrin (TF) protein.	
XX		

KM fusion protein; transferrin; Tf; beta-interferon; beta-IFN;
 KM glucagon-like peptide; GLP-1; erythropoietin mimetic peptide; EMP1;
 KM T-20; soluble toxin receptor; epitope tagging; human.

OS Homo sapiens.

PN US2003221201-A1.

PD 27-NOV-2003.

PF 04-MAR-2003; 2003US-00378094.

PR 30-AUG-2001; 2001US-0315745P.

PR 30-NOV-2001; 2001US-0334059P.

PR 30-AUG-2002; 2002US-00231494.

PR 30-AUG-2002; 2002US-0406977P.

PA (BIOR-) BIOREXIS PHARM CORP.

PI Prior CP, Lai C, Sadeghi H, Turner A;

DR WPI; 2004-010899/01.

PT New fusion protein comprising a modified transferrin (Tf) protein fused
 to a therapeutic protein or peptide, useful for epitope tagging.

PS Example 5; SEQ ID NO 3; 70pp; English.

CC The invention comprises a fusion protein that contains a modified
 CC transferrin (Tf) protein fused to a therapeutic protein/peptide (e.g.
 CC beta-interferon - IFN, glucagon-like peptide - GLP-1, erythropoietin
 CC mimetic peptide - EMP1, T-20 and soluble toxin receptor). The fusion
 CC protein of the invention is useful for epitope tagging. The present amino
 CC acid sequence represents the mature human Tf protein.

XX SQ Sequence 679 AA;

Query Match 95.7%; Score 110; DB 8; Length 679;

Best Local Similarity 95.7%; Pred. No. 1,3e-08; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTEDSIKINNGEADAMSLDGGF 23

DB 373 TTEDCIKINNGEADAMSLDGGF 395

Search completed: November 1, 2005, 12:48:52
 Job time : 132.574 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:37:09 ; Search time 33.8235 Seconds
(without alignments)
50.761 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115
Sequence: 1 TTEDSIAKIMNGEADAMSJDGR 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfile1.pep:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	110	95.7	698	2	US-08-175-158A-2
2	110	95.7	698	4	US-09-439-740-2
3	110	95.7	1074	2	US-08-470-058-2
4	110	95.7	1074	3	US-09-037-188-2
5	110	95.7	1074	3	US-09-285-310-2
6	110	95.7	1410	2	US-08-470-058-4
7	110	95.7	1410	3	US-09-037-188-4
8	110	95.7	1410	3	US-09-285-310-4
9	93.5	81.3	696	6	5262177-4
10	93.5	81.3	696	6	5262177-4
11	92	80.0	697	3	US-09-724-864-54
12	92	80.0	703	1	US-08-145-681-6
13	92	80.0	703	1	US-08-453-703-6
14	92	80.0	703	2	US-08-456-106-6
15	92	80.0	703	3	US-08-456-108-6
16	92	80.0	703	3	US-09-265-577-6
17	92	80.0	703	4	US-09-633-739-6
18	92	80.0	703	4	US-08-724-586-2
19	90	78.3	694	3	US-09-421-632-2
20	90	78.3	694	4	US-09-332-190-2
21	90	78.3	705	2	US-08-655-640-2
22	90	78.3	705	2	US-08-655-640-4
23	90	78.3	709	1	US-08-154-019-2
24	90	78.3	709	1	US-08-461-333-2
25	90	78.3	709	3	US-08-464-167-2
26	90	78.3	709	3	US-09-158-313-2
27	90	78.3	709	3	US-08-476-798-2

28	90	78.3	711	1	US-08-145-681-2	Sequence 2, App11
29	90	78.3	711	1	US-08-250-308-2	Sequence 2, App11
30	90	78.3	711	1	US-08-154-019-4	Sequence 4, App11
31	90	78.3	711	1	US-08-461-333-4	Sequence 4, App11
32	90	78.3	711	1	US-08-453-703-2	Sequence 2, App11
33	90	78.3	711	2	US-08-456-106-2	Sequence 2, App11
34	90	78.3	711	3	US-08-464-167-4	Sequence 4, App11
35	90	78.3	711	3	US-09-158-313-4	Sequence 4, App11
36	90	78.3	711	3	US-08-456-108-2	Sequence 2, App11
37	90	78.3	711	3	US-08-476-798-2	Sequence 2, App11
38	90	78.3	711	3	US-09-265-577-2	Sequence 2, App11
39	90	78.3	711	4	US-09-633-739-2	Sequence 2, App11
40	90	78.3	711	5	PCT-US93-03614-2	Sequence 2, App11
41	77	67.0	708	1	US-08-145-681-4	Sequence 4, App11
42	77	67.0	708	1	US-08-453-703-4	Sequence 4, App11
43	77	67.0	708	2	US-08-456-106-4	Sequence 4, App11
44	77	67.0	708	3	US-08-456-108-4	Sequence 4, App11
45	77	67.0	708	3	US-09-265-577-4	Sequence 4, App11

ALIGNMENTS

RESULT 1
US-08-175-158A-2

; Sequence 2, Application US/08175158A

; Patent No. 5986067

; GENERAL INFORMATION:

; APPLICANT: FUNK, Walter D.

; APPLICANT: MASON, Anne B.

; APPLICANT: WOODMORTH, Robert C.

; TITLE OF INVENTION: RECOMBINANT TRANSFERRIN, TRANSFERRIN HALF-

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/175,158A

; FILING DATE: 28-DEC-1993

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/832,029

; FILING DATE: 06-FEB-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: DeConti, Giulio A.

; REGISTRATION NUMBER: 31,503

; REFERENCE/DOCKET NUMBER: UVI-005CP2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 698 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-175-158A-2

Query Match 95.7%; Score 110; DB 2; Length 698;
Best Local Similarity 95.7%; Prod. No. 1e-09; 1; Indels 0; Gaps 0;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-2

Query Match 95.7%; Score 110; DB 3; Length 1074;
Best Local Similarity 95.7%; Pred. No. 1.7e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSJDGF 23
DB 768 TTEDCIKIMNGEADAMSJDGF 790

RESULT 5
US-09-285-310-2
Sequence 2, Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-2

Query Match 95.7%; Score 110; DB 3; Length 1074;
Best Local Similarity 95.7%; Pred. No. 1.7e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSJDGF 23
DB 768 TTEDCIKIMNGEADAMSJDGF 790

RESULT 6
US-08-470-058-4
Sequence 4, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
OF A Selected Substance Into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-4

Query Match 95.7%; Score 110; DB 2; Length 1410;
Best Local Similarity 95.7%; Pred. No. 2.4e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSJDGF 23
DB 1104 TTEDCIKIMNGEADAMSJDGF 1126

RESULT 7
US-09-037-188-4
Sequence 4, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

```

; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/037,188
; FILING DATE: 02-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 07236/009002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1410 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
US-09-037-188-4

Query Match          95.7%; Score 110; DB 3; Length 1410;
Best Local Similarity 95.7%; Pred. No. 2,4e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSLDGGF 23
DB 1104 TTEDCIKIMNGEADAMSLDGGF 1126

RESULT 8
US-09-285-310-4
; Sequence 4, Application US/09285310
; Patent No. 6262026
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemontt, Jeffrey F.
; APPLICANT: Concino, Michael F.
; TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
; TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/285,310
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/037,188
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Ph.D., J.D., Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 07236/009002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1410 amino acids
```

```

; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
;
US-09-285-310-4

Query Match          95.7%; Score 110; DB 3; Length 1410;
Best Local Similarity 95.7%; Pred. No. 2,4e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSLDGGF 23
DB 1104 TTEDCIKIMNGEADAMSLDGGF 1126

RESULT 9
5262177-4
; Patent No. 5262177
; APPLICANT: BROWN, J. JOSEPH P.; ESTIN, CHARLES D.; FLOWMAN, GREGORY
; D.; HELLSROM, KARL E.; ROSE, TIMOTHY M.; HELLSROM, INGEGERD;
; PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 827,313
; FILING DATE: 07-FEB-1986
; SEQ ID NO: 4:
; LENGTH: 696
;
5262177-4

Query Match          81.3%; Score 93.5; DB 6; Length 696;
Best Local Similarity 91.3%; Pred. No. 5,4e-07;
Matches 21; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 TTEDSIKIMNGEADAMSLDGGF 23
DB 392 TTEDCIKIMN-EDAMSLDGGF 413

RESULT 10
5262177-4
; Patent No. 5262177
; APPLICANT: BROWN, J. JOSEPH P.; ESTIN, CHARLES D.; FLOWMAN, GREGORY
; D.; HELLSROM, KARL E.; ROSE, TIMOTHY M.; HELLSROM, INGEGERD;
; PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 827,313
; FILING DATE: 07-FEB-1986
; SEQ ID NO: 4:
; LENGTH: 696
;
5262177-4

Query Match          81.3%; Score 93.5; DB 6; Length 696;
Best Local Similarity 91.3%; Pred. No. 5,4e-07;
Matches 21; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 TTEDSIKIMNGEADAMSLDGGF 23
DB 392 TTEDCIKIMN-EDAMSLDGGF 413

RESULT 11
US-09-724-864-54
; Sequence 54, Application US/09724864
```

```
Patent No. 6380362
GENERAL INFORMATION:
APPLICANT: Watson, James D
APPLICANT: Morrison, James G.
TITLE OF INVENTION: Polynucleotides, polypeptides expressed
TITLE OF INVENTION: by the polynucleotides and methods for their use.
FILE REFERENCE: 11000.105001
CURRENT APPLICATION NUMBER: US/09/724,864
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 54
LENGTH: 697
TYPE: PRT
ORGANISM: Mouse
US-09-724-864-54

Query Match      80.0%; Score 92; DB 3; Length 697;
Best Local Similarity 81.8%; Pred. No. 9.6e-07;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTEDSIKINGEADAMSIDG 22
DB 391 TTEDCIKIVNGEADAMTLDG 412

RESULT 12
US-08-145-681-6
Sequence 6, Application US/08145681
Patent No. 5571691
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Baker & Botts, L.L.P.
STREET: 910 Louisiana St
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/145,681
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McGregor, Martin L.
REGISTRATION NUMBER: 29,329
REFERENCE/DOCKET NUMBER: 19928-0125
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713/229/1874
TELEFAX: 713/229/1522
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
SEQUENCE: NO
```

```
ORGANISM: Sus scrofa
US-08-145-681-6

Query Match      80.0%; Score 92; DB 1; Length 703;
Best Local Similarity 73.9%; Pred. No. 9.7e-07;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKINGEADAMSIDG 23
DB 390 TTEDCIKIVNGEADAMSLDGF 412

RESULT 13
US-08-453-703-6
Sequence 6, Application US/08453703
Patent No. 5766939
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,703
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sus scrofa
US-08-453-703-6

Query Match      80.0%; Score 92; DB 1; Length 703;
Best Local Similarity 73.9%; Pred. No. 9.7e-07;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKINGEADAMSIDG 23
DB 390 TTEDCIKIVNGEADAMSLDGF 412

RESULT 14
```

US-08-456-106-6
Sequence 6, Application US/08456106
Patent No. 5849881
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Heaton, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,106
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sus scrofa
US-08-456-106-6

Query Match 80.0%; Score 92; DB 2; Length 703;
Best Local Similarity 73.9%; Pred. No. 9.7e-07;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKIMGEADAMSLDGGF 23
||||| : : : : :
Db 390 TTEDCIVVLKGEADAMSLDGGF 412

RESULT 15
US-08-456-108-6
Sequence 6, Application US/08456108
Patent No. 6100054
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Heaton, Denis R.
APPLICANT: O'Malley, Bert W.
APPLICANT: May, Gregory S.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,108
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sus scrofa
US-08-456-108-6

Query Match 80.0%; Score 92; DB 3; Length 703;
Best Local Similarity 73.9%; Pred. No. 9.7e-07;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKIMGEADAMSLDGGF 23
||||| : : : : :
Db 390 TTEDCIVVLKGEADAMSLDGGF 412

Search completed: November 1, 2005, 12:57:30
Job time : 34.8235 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:54:52 ; Search time 116.353 Seconds
(without alignments)
82.636 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115
Sequence: 1 TTEDSIKIMNGEADAMSJDGGR 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 1865214

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/ptodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubppa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubppa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubppa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubppa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubppa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubppa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/1/pubppa/US10E_PUBCOMB.pep:*
18: /cgn2_6/ptodata/1/pubppa/US11A_PUBCOMB.pep:*
19: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep:*
20: /cgn2_6/ptodata/1/pubppa/US11_NEW_PUB.pep:*
21: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*
22: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115	100.0	23	US-10-612-162-2	Sequence 2, Appl1
2	110	95.7	328	US-09-891-126-5	Sequence 5, Appl1
3	110	95.7	328	US-10-266-745-5	Sequence 3, Appl1
4	110	95.7	679	US-10-378-094-3	Sequence 3, Appl1
5	110	95.7	679	US-10-384-060-3	Sequence 3, Appl1
6	110	95.7	679	US-10-231-494-3	Sequence 3, Appl1
7	110	95.7	679	US-10-429-482-4	Sequence 4, Appl1
8	110	95.7	679	US-10-429-497-4	Sequence 4, Appl1
9	110	95.7	679	US-10-429-515-4	Sequence 4, Appl1
10	110	95.7	679	US-10-429-598-4	Sequence 4, Appl1
11	110	95.7	679	US-10-429-635-4	Sequence 4, Appl1

12	110	95.7	679	US-10-429-653-4	Sequence 4, Appl1
13	110	95.7	679	US-10-429-659-4	Sequence 4, Appl1
14	110	95.7	679	US-10-429-661-4	Sequence 4, Appl1
15	110	95.7	679	US-10-429-660-4	Sequence 4, Appl1
16	110	95.7	679	US-10-429-662-4	Sequence 4, Appl1
17	110	95.7	679	US-10-429-665-4	Sequence 4, Appl1
18	110	95.7	679	US-10-429-654-4	Sequence 4, Appl1
19	110	95.7	698	US-09-935-642-6	Sequence 6, Appl1
20	110	95.7	698	US-10-378-094-2	Sequence 2, Appl1
21	110	95.7	698	US-10-384-060-2	Sequence 2, Appl1
22	110	95.7	698	US-10-231-494-2	Sequence 2, Appl1
23	110	95.7	698	US-10-383-201-10	Sequence 10, Appl1
24	110	95.7	698	US-10-383-201-14	Sequence 14, Appl1
25	110	95.7	698	US-10-887-711-2	Sequence 2, Appl1
26	110	95.7	698	US-10-513-523-3	Sequence 3, Appl1
27	110	95.7	1074	US-09-753-385-2	Sequence 2, Appl1
28	110	95.7	1410	US-09-753-385-4	Sequence 4, Appl1
29	110	95.7	1410	US-10-473-127-805	Sequence 805, App
30	110	95.7	1418	US-10-473-127-804	Sequence 804, App
31	92	80.0	703	US-10-620-256-6	Sequence 6, Appl1
32	92	80.0	704	US-10-513-523-4	Sequence 4, Appl1
33	90	78.3	359	US-10-169-297-49	Sequence 49, Appl1
34	90	78.3	690	US-10-076-816-4	Sequence 4, Appl1
35	90	78.3	690	US-10-077-381-4	Sequence 4, Appl1
36	90	78.3	690	US-10-639-835-4	Sequence 4, Appl1
37	90	78.3	694	US-10-023-095-2	Sequence 2, Appl1
38	90	78.3	695	US-10-316-253-273	Sequence 273, App
39	90	78.3	698	US-10-316-253-275	Sequence 275, App
40	90	78.3	698	US-10-205-331-55	Sequence 55, Appl1
41	90	78.3	709	US-10-170-221-2	Sequence 2, Appl1
42	90	78.3	709	US-10-987-587-9	Sequence 9, Appl1
43	90	78.3	711	US-10-169-297-2	Sequence 2, Appl1
44	90	78.3	711	US-10-170-221-4	Sequence 4, Appl1
45	90	78.3	711	US-10-341-434-202	Sequence 202, App

ALIGNMENTS

RESULT 1
US-10-612-162-2
; Sequence 2, Appl1
; Publication No. US2004001415A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
; FILE REFERENCE: 2002/B001
; CURRENT APPLICATION NUMBER: US/10/612,162
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; PRIOR FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-162-2

Query Match 100.0%; Score 115; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADAMSJDGGR 23
Db 1 TTEDSIKIMNGEADAMSJDGGR 23

RESULT 2
US-09-891-126-5

```

: Sequence 5, Application US/09891126
: Patent No. US20020072596A1
: GENERAL INFORMATION:
: APPLICANT: Ruben et al.
: TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
: FILE REFERENCE: PR035P1
: CURRENT APPLICATION NUMBER: US/09/891,126
: PRIORITY FILING DATE: 2001-06-26
: PRIOR APPLICATION NUMBER: PCT/US00/34769
: PRIOR FILING DATE: 2000-12-21
: PRIOR APPLICATION NUMBER: 60/171,595
: PRIOR FILING DATE: 1999-12-23
: NUMBER OF SEQ ID NOS: 7
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 5
: LENGTH: 328
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-891-126-5

```

Query Match	95.7%	Score 110;	DB 9;	Length 328;
Best Local Similarity	95.7%	Pred. No. 7.6e-09;		
Matches 22; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

QY	1	TTEDSI	AKIMNG	EADAM	SLDGF	23
Db	56	TTEDCI <td>AKIMNG <th>EADAM</th> <th>SLDGF</th> <th>78</th> </td>	AKIMNG <th>EADAM</th> <th>SLDGF</th> <th>78</th>	EADAM	SLDGF	78

```

RESULT 3
US-10-266-745-5
Sequence 5, Application US/10266745
Publication No. US20030149236A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: P035P1
CURRENT FILING DATE: 2002-10-09
PRIORITY FILING DATE: 2002-10-09
PRIORITY FILING DATE: 2001-06-26
PRIORITY APPLICATION NUMBER: PCT/US00/34769
PRIORITY FILING DATE: 2000-12-21
PRIORITY APPLICATION NUMBER: 60/171,595
PRIORITY FILING DATE: 1999-12-23
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 328
TYPE: PRT
ORGANISM: Homo sapiens
US-10-266-745-5

```

Query Match	95.7%	Score 110;	DB 14;	Length 328;
Best Local Similarity	95.7%;	Pred. No. 7.6e-09;		
Matches 22; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

QY	1	TTEDSI	AKIMNG	EADAM	SLDGF	23
Db	56	TTEDCI	AKIMNG <td>EADAM <td>SLDGF <td>78</td> </td></td>	EADAM <td>SLDGF <td>78</td> </td>	SLDGF <td>78</td>	78

RESULT 4
 US-10-378-094-3
 ; Sequence 3, Application US/10378094
 ; Publication No. US20030221201A1
 ; GENERAL INFORMATION:
 ; APPLICANT: PRIOR, Christopher P.
 ; APPLICANT: LAI, Char-Huei
 ; APPLICANT: SADEGH, Homayoun
 ; APPLICANT: TUNMER, Andrew
 ; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
 ; FILE REFERENCE: 54710-5001-01-US

```

1 CURRENT APPLICATION NUMBER: US/10/378,094
2
3 CURRENT FILING DATE: 2003-03-04
4
5 PRIOR APPLICATION NUMBER: US 10/231,494
6
7 PRIOR FILING DATE: 2002-08-30
8
9 PRIOR APPLICATION NUMBER: US 60/334,059
10
11 PRIOR FILING DATE: 2001-11-30
12
13 PRIOR APPLICATION NUMBER: US 60/315,745
14
15 PRIOR FILING DATE: 2001-08-30
16
17 NUMBER OF SEQ ID NOS: 66
18
19 SOFTWARE: PatentIn version 3.2
20
21 SEQ ID NO 3
22
23 LENGTH: 679
24
25 TYPE: prt
26
27 ORGANISM: Homo sapiens
28
29 FEATURE:
30 NAME/KEY: MISC_FEATURE
31
32 OTHER INFORMATION: Mature Transferrin Protein
33
34 US-10-378-094-3

```

Query Match	95.7%	Score 110;	DB 15;	Length 679;
Best Local Similarity	95.7%	Pred. No. 1.8e-08;		
Matches 22;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0

Qy 1 TTEDSIKIMNGEADAMSLDGGF 23
 |||||
Dd 373 TTEDCIKIMNGEADAMSLDGGF 395

```

RESULT 5
US-10-384-060-3
; Sequence 3, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGH, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384, 060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; OTHER INFORMATION: Mature Transferrin Protein
US-10-384-060-3

```

Query Match	95.7%	Score 110;	DB 15;	Length 679;
Best Local Similarity	95.7%;	Pred. No. 1.8e-08;		
Matches	22;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0

QY 1 TTEDSI AKIMNGEADAMS LDGGF 23
 |||||
Db 373 TTEDCI AKIMNGEADAMS LDGGF 395

RESULT 6
US-10-231-494-3
; Sequence 3, Application US/10231494
; Publication No. US20040023334A1
; GENERAL INFORMATION:

```

; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Mature transferrin protein
US-10-231-494-3
```

```

Query Match          95.7%; Score 110; DB 16; Length 679;
Best Local Similarity 95.7%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 TTEDSIKIMNGEADAMSIDGCF 23
DB 373 TTEDCIKIMNGEADAMSIDGCF 395
```

```

RESULT 7
US-10-429-482-4
; Sequence 4, Application US/10429482
; Publication No. US20040219097A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For The Diagnosis, Imaging and Treatment Of Tu
; FILE REFERENCE: 2537,000001
; CURRENT APPLICATION NUMBER: US/10/429,482
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-482-4
```

```

Query Match          95.7%; Score 110; DB 16; Length 679;
Best Local Similarity 95.7%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 TTEDSIKIMNGEADAMSIDGCF 23
DB 373 TTEDCIKIMNGEADAMSIDGCF 395
```

```

RESULT 8
US-10-429-497-4
; Sequence 4, Application US/10429497
; Publication No. US20040219098A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For The Treatment Of Tumors
; FILE REFERENCE: 2537,000006
; CURRENT APPLICATION NUMBER: US/10/429,497
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-497-4
```

```

Query Match          95.7%; Score 110; DB 16; Length 679;
Best Local Similarity 95.7%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 TTEDSIKIMNGEADAMSIDGCF 23
DB 373 TTEDCIKIMNGEADAMSIDGCF 395
```

```

RESULT 9
US-10-429-515-4
; Sequence 4, Application US/10429515
; Publication No. US20040219099A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For The Treatment Of Tumors
; FILE REFERENCE: 2537,000005
; CURRENT APPLICATION NUMBER: US/10/429,515
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-515-4
```

```

Query Match          95.7%; Score 110; DB 16; Length 679;
Best Local Similarity 95.7%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 TTEDSIKIMNGEADAMSIDGCF 23
DB 373 TTEDCIKIMNGEADAMSIDGCF 395
```

```

RESULT 10
US-10-429-598-4
; Sequence 4, Application US/10429598
; Publication No. US20040219100A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For The Treatment Of Tumors
; FILE REFERENCE: 2537,000003
; CURRENT APPLICATION NUMBER: US/10/429,598
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-598-4
```

```

Query Match          95.7%; Score 110; DB 16; Length 679;
Best Local Similarity 95.7%; Pred. No. 1.8e-08;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 TTEDSIKIMNGEADAMSIDGCF 23
DB 373 TTEDCIKIMNGEADAMSIDGCF 395
```

```

RESULT 11
US-10-429-635-4
; Sequence 4, Application US/10429635
; Publication No. US20040219101A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For Treatment Of Tumors
; FILE REFERENCE: 2537,000007
; CURRENT APPLICATION NUMBER: US/10/429,635
; CURRENT FILING DATE: 2003-05-02
```

```

; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-635-4

```

Query Match	95.7%	Score 110;	DB 16;	Length 679;
Best Local Similarity	95.7%;	Pred. No. 1.8e-08;		
Matches 22;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0

Qy 1 TTEDSIKIMNGEADAMSLDGGF 23
Db 373 TTEDCIKIMNGEADAMSLDGGF 395

```

RESULT 12
US-10-429-653-4
; Sequence 4, Application US/10429653
; Publication No. US20040219102A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jaabir
; TITLE OF INVENTION: Compositions For Drug Delivery
; FILE REFERENCE: 2537.000009
; CURRENT APPLICATION NUMBER: US/10-429,653
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-429-653-4

```

Query Match	95.7%	Score 110;	DB 16;	Length 679;
Best Local Similarity	95.7%	Pred. No. 1.8e-08;		
Matches 22; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

OY 1 TTEDSI AKIMNGEADAMSLDGGF 23
 |||||
Db 373 TTEDCI AKIMNGEADAMSLDGGF 395

```

RESULT 13
US-10-429-659-4
; Sequence 4, Application US/10429659
; Publication No. US20040219103A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods Useful For The Diagnosis, Imaging and Treatment Of Tumors
; FILE REFERENCE: 2537.000004
; CURRENT APPLICATION NUMBER: US/10/429,659
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-429-659-4

```

Query Match	95.7%	Score 110;	DB 16;	Length 679;
Best Local Similarity	95.7%	Pred. No. 1.8e-08;		
Matches	22;	Conservative	0;	Mismatches 1;
			Indels	0;
			Gaps	0

QY	1	TTEDSI	AKIMNGEAD	AMSLDGGF	23
Db	373	TTEDCI	AKIMNGEAD	AMSLDGGF	395

RESULT 14
US-10-429-661-4

```

Sequence 4, Application US/10429661
Publication No. US200400219104A1
GENERAL INFORMATION:
APPLICANT: Sandhu, Jasbir
TITLE OF INVENTION: Methods For Treatment Of Tumors
FILE REFERENCE: 2537, 000008
CURRENT APPLICATION NUMBER: US/10/429,661
CURRENT FILING DATE: 2003-05-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 679
TYPE: PRT
ORGANISM: Homo sapiens
US-10-429-661-4

```

Query Match	95.7%	Score 110;	DB 16;	Length 679;
Best Local Similarity	95.7%	Pred. No. 1.8e-08;		
Matches 22; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0

OY		1	TTEDSI AKIMNGEADAMS LDGGF	23
Db		373	TTEDCI AKIMNGEADAMSLDGGF	395

```

RESULT 15
US-10-429-660-4
? Sequence 4, Application US/10429660
? Publication No. US20040220084A1
? GENERAL INFORMATION:
? APPLICANT: Sandhu, Jasbir
? TITLE OF INVENTION: Methods For Nucleic Acid Delivery
? FILE REFERENCE: 2537.000012
? CURRENT APPLICATION NUMBER: US/10/429,660
? NUMBER OF SEQ ID NOS: 12
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 4
? LENGTH: 679
? TYPE: PRT
? ORGANISM: Homo sapiens
? US-10-429-660-4

```

Query Match	95.7%	Score 110;	DB 16;	Length 679;
Best Local Similarity	95.7%	Pred. No. 1.8e-08;		
Matches 22;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0

QY	1	TTEDSI	AKIMNGEAD	PAMSLDGGF	23
Db	373	TTEDCI	AKIMNGEAD	PAMSLDGGF	395

Search completed: November 1, 2005, 13:26:06
Job time : 116.353 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: November 1, 2005, 12:35:39 ; Search time 23.3382 Seconds
(without alignments)
94.822 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115
Sequence: 1 TTEDSLAKIMNGEADMSLDGR 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110	95.7	698	1 TFHUP	transferrin precur
2	101	87.8	694	1 TFRBP	transferrin precur
3	96	83.5	706	2 S33761	transferrin precur
4	92	80.0	311	2 A28446	transferrin - mous
5	92	80.0	696	1 S01384	transferrin - pig
6	92	80.0	703	2 A45543	transferrin precur
7	90	78.3	695	2 S49163	transferrin precur
8	90	78.3	711	1 TFRUL	transferrin precur
9	88	76.5	707	1 A28438	transferrin precur
10	86	74.8	704	2 I47228	carbonic anhydrase
11	84	73.0	708	2 JC2323	lactoferrin - goat
12	77	67.0	705	1 TFCHE	ovotransferrin pre
13	77	67.0	708	1 TFRBL	lactotransferrin p
14	71	61.7	717	2 S12100	transferrin precur
15	66	57.4	690	2 T11749	transferrin - Atla
16	50	43.5	280	1 G70126	phosphatase ABC tran
17	48	41.7	609	2 E86780	hypothetical prote
18	47	40.9	466	2 D72733	probable membrane-
19	46	40.0	47	2 S13486	transferrin - bovi
20	46	40.0	737	2 AE0819	probable membrane
21	46	40.0	1238	1 A40185	virulence sensor p
22	46	40.0	1238	1 S17944	virulence sensor p
23	46	40.0	1238	1 S17946	virulence sensor p
24	45.5	39.6	483	2 D87752	protein C18B3.6 [i
25	45.5	39.6	483	2 T15180	hypothetical prote
26	45	39.1	110	2 E83571	conserved hypotet
27	45	39.1	288	2 F69973	transcription regu
28	45	39.1	491	2 A86824	sensor protein kin
29	45	39.1	505	1 P5XR44	outer capsid prote

30	45	39.1	852	2 D72230	conserved hypotet
31	44	38.3	339	2 G69253	hypothetical prote
32	44	38.3	371	2 A69379	conserved hypotet
33	44	38.3	461	2 D84971	phosphotransferase
34	44	38.3	747	2 E91049	probable cytochrom
35	44	38.3	747	2 A85894	probable cytochrom
36	44	38.3	747	2 F65026	hypothetical prote
37	44	38.3	1012	2 T13503	probable N-methyl-
38	43.5	37.8	187	2 D82794	limbittin AF0339
39	43.5	37.8	738	1 TFRUM	melanotransferrin
40	43	37.4	246	2 A64326	hypothetical prote
41	43	37.4	298	2 B71317	hypothetical prote
42	43	37.4	320	2 JC7929	ATP-dependent gluc
43	43	37.4	352	2 AC0299	probable membrane
44	43	37.4	358	2 A82206	protein-glucamate
45	43	37.4	376	2 F72514	probable glucokina

ALIGNMENTS

RESULT 1
TFHUP
transferrin precursor [validated] - human
N:Alternate names: siderophilin
C:Species: Homo sapiens (man)
C>Date: 15-Oct-1982 #sequence, revision 30-Sep-1993 #text, change 09-Jul-2004
C/Accession: A20981; A92417; A94044; A23090; A23739; I51959; I61133; I54011; I68160; A0
R:Yang, F.; Lum, J.B.; McGill, J.R.; Moore, C.M.; Naylor, S.L.; Van Bragt, P.H.; Baldwi
Proc. Natl. Acad. Sci. U.S.A. 81, 2752-2756, 1984
A>Title: Human transferrin: cDNA characterization and chromosomal localization.
A/Reference number: A20981; PMID:84194084; PMID:6585826
A/Contents: variant C
A/Accession: A20981
A/Molecule type: mRNA
A/Residues: 1-698 <YAN>
A/Cross-references: UNIPROT:P02787; EMBL:M12530; NID:G339452; PIDD:AAA61140.1; PID:G339
A/Note: the authors translated the codon CAA for residue 203 as Glu
R:MacGillivray, R.T.A.; Mendes, E.; Shewale, J.G.; Sinha, S.K.; Lineback-zins, J.; Brew
J. Biol. Chem. 258, 3543-3553, 1983
A>Title: The primary structure of human serum transferrin. The structures of seven cyan
A/Reference number: A92417; PMID:83160878; PMID:6833213
A/Accession: A92417
A/Molecule type: protein
A/Residues: 20-263, 'E', 265-328, 'N', 330-379, 'SD', 382-435, 'D', 437-557, 'T', 559-560, 'P', 562
A/Note: the sequence shown is the predominant electrophoretic genetic variant (C or TFC
R:Park, I.; Schaeffer, E.; Stoll, A.; Baralle, F.E.; Cohen, G.N.; Zakin, M.M.
Proc. Natl. Acad. Sci. U.S.A. 82, 3149-3153, 1985
A>Title: Organization of the human transferrin gene: direct evidence that it originated
A/Reference number: A94044; PMID:85216459; PMID:3858812
A/Accession: A94044
A/Molecule type: DNA
A/Residues: 73-263, 'E', 265-328, 'N', 330-562 <PAR>
A/Cross-references: EMBL:M1361
R:Adrian, G.S.; Korinek, B.W.; Bowman, B.H.; Yang, F.
Gene 49, 167-175, 1986
A>Title: The human transferrin gene: 5' region contains conserved sequences which match
A/Reference number: A29090; PMID:87192006; PMID:3106157
A/Accession: A29090
A/Molecule type: DNA
A/Residues: 1-72; 291-300 <ADR>
A/Cross-references: EMBL:M5673
R:Uzan, G.; Frain, M.; Park, I.; Besmond, C.; Maessen, G.; Trepac, J.S.; Zakin, M.M.; K
Biochem. Biophys. Res. Commun. 119, 273-281, 1984
A>Title: Molecular cloning and sequence analysis of cDNA for human transferrin.
A/Reference number: A37339; PMID:84153910; PMID:6322780
A/Accession: A37339
A/Molecule type: mRNA
A/Residues: 422-690, 'G', 692-698 <UZA>
A/Cross-references: EMBL:M2525; NID:G339468; PIDD:AAA61142.1; PID:G339469
R:MacGillivray, R.T.A.; Mendes, E.; Sinha, S.K.; Sutton, M.R.; Lineback-zins, J.; Brew,
Proc. Natl. Acad. Sci. U.S.A. 79, 2504-2508, 1982

A>Title: The complete amino acid sequence of human serum transferrin.
A:Reference number: A93911; MUID:82222166; PMID:6553407
A:Contents: annotation; disulfide bonds
R:Herberberger, C.L.; Larson, J.L.; Arnold, B.; Roelcke, P.R.
Ann. N. Y. Acad. Sci. 646, 140-154, 1991
A>Title: A cloned gene for human transferrin.
A:Reference number: I51959; MUID:92231399; PMID:1809186
A:Accession: I51959
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-698 <RES>
A:Cross-references: GB:SP5936; NID:G248647; PIDN:AA61233.1; PID:G248648
R:Duguid, J.R.; Bohmont, C.W.; Liu, N.G.; Tourtellotte, W.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 7260-7264, 1989
A>Title: Changes in brain gene expression shared by scrapie and Alzheimer disease.
A:Reference number: I48174; MUID:89386721; PMID:2780570
A:Accession: I63133
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 636-696 <RE2>
A:Cross-references: GB:M26641; NID:G339988; PIDN:AA61233.1; PID:G339989
R:Scheffner, E.; Lucero, M.A.; Jeltch, J.M.; Py, M.C.; Levin, M.J.; Chandon, P.; Cohen, Gene 56, 109-116, 1987
A>Title: Complete structure of the human transferrin gene. Comparison with analogous chi
A:Reference number: I54011; MUID:88056305; PMID:3678832
A:Accession: I54011
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-72 <RE3>
A:Cross-references: GB:M17611; NID:G339480; PIDN:AA61147.1; PID:G339485
A:Accession: I68160
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 564-698 <RE4>
A:Cross-references: GB:M17614; NID:G339483; PIDN:AA61148.1; PID:G339486
C:Comment: Each of the two repetitive domains binds a ferric ion and a bicarbonate anion
C:Genetics:
A:Gene: GDB:TF
A:Cross-references: GDB:120432; OMIM:190000
A:Map position: 3q21-3q21
A:Intron: 15/1; 72/3; 119/1; 166/1; 212/2; 231/1; 290/3; 350/1; 401/3; 433/1; 444/1; 49
C:Function:
A:Description: binds iron for delivery into cells
A:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-698/Product: transferrin #status experimental <MAT>
F:20-350/Domain: transferrin repeat homology <TRH1>
F:356-686/Domain: transferrin repeat homology <TRH2>
F:28-67,38-58,137-213,156-350,177-193,180-196,190-198,246-260,358-615,364-396,374-387,42
F:432,630/Binding site: carbohydrate (Aan) (covalent) #status experimental
Query Match 95.7%; Score 110; DB 1; Length 698;
Best Local Similarity 95.7%; Pred. No. 2,5e-09;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSJDGF 23
DB 392 TTEDCIKIMNGEADAMSJDGF 414

RESULT 2
TFRBP
transferrin precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
C:Accession: S16246; A61239; C61573; S00335; S02654; A26504; S14853
R:Banfield, D.K.; Chow, B.K.C.; Funk, W.D.; Robertson, K.A.; Umels, T.M.; Woodworth, R.
Biochim. Biophys. Acta 1089, 262-265, 1991
A>Title: The nucleotide sequence of rabbit liver transferrin cDNA.
A:Reference number: S16246; MUID:91274362; PMID:2054387
A:Accession: S16246
A:Molecule type: mRNA

A:Residues: 1-694 <BAN>
A:Cross-references: EMBL:X58533; NID:G1750; PIDN:CAA41424.1; PID:G1751
R:Pierpaoli, W.; Dall'Ara, A.; Yi, C.; Neri, P.; Santucci, A.; Choay, J.
Cell. Immunol. 134, 225-234, 1991
A>Title: Iron carrier proteins facilitate engraftment of allogeneic bone marrow and en
A:Reference number: A61239; MUID:91191584; PMID:2013104
A:Accession: A61239
A:Molecule type: protein
A:Residues: 19-36 <PIE>
R:Chung, M.C.M.; Chan, S.L.; Shimizu, S.
Int. J. Biochem. 23, 609-616, 1991
A>Title: Purification of transferrins and lactoferrin using DEAE Affi-Gel Blue.
A:Reference number: A61573; MUID:91293379; PMID:2065820
A:Accession: C61573
A:Molecule type: protein
A:Residues: 19-26, 'X', 28-36, 'X', 38-53 <CHU>
R:Godovac-Zimmermann, J.
Biol. Chem. Hoppe-Seyler 369, 93-96, 1988
A>Title: Isolation, characterization and N-terminal amino-acid sequence of rabbit transf
A:Reference number: S00335; MUID:88209278; PMID:3365331
A:Accession: S00335
A:Molecule type: protein
A:Residues: 19-45, 'S', 47-48, 'Y', 50 <GOD>
R:Evans, R.W.; Aitken, A.; Patel, K.J.
FEBS Lett. 238, 39-42, 1988
A>Title: Evidence for a single glycan moiety in rabbit serum transferrin and location of
A:Reference number: S02694; MUID:89005676; PMID:3169252
A:Accession: S02694
A:Molecule type: protein
A:Residues: 482-515, 'V', 517-544 <EVA>
A:Note: 516-11e was also found
R:Heaphy, S.; Williams, J.
Biochem. J. 205, 611-617, 1982
A>Title: The preparation and partial characterization of N-terminal and C-terminal iron-
A:Reference number: A26504; MUID:83074540; PMID:6816218
A:Accession: A26504
A:Molecule type: protein
A:Residues: 19-24, 'N', 26, 'X', 28-29, 'S' <HEA>
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-694/Product: transferrin #status experimental <MAT>
F:19-349/Domain: transferrin repeat homology <TRH1>
F:355-682/Domain: transferrin repeat homology <TRH2>
F:27-66,37-57,136-212,155-345,176-192,179-195,189-197,245-259,357-611,363-395,373-386,42
F:508/Binding site: carbohydrate (Aan) (covalent) #status experimental
Query Match 87.8%; Score 101; DB 1; Length 694;
Best Local Similarity 87.0%; Pred. No. 6,8e-08;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSJDGF 23
DB 391 TTEDCIKIMNGEADAMSJDGF 413

RESULT 3
S33761
transferrin precursor - horse
N:Alternate names: growth-promoting factor
C:Species: Equus caballus (domestic horse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S33761; S02145
R:Carpenier, M.A.; Broad, T.B.
Biochim. Biophys. Acta 1173, 230-237, 1993
A>Title: The cDNA sequence of horse transferrin.
A:Reference number: S33761; MUID:93277958; PMID:8504171
A:Accession: S33761
A:Molecule type: mRNA
A:Residues: 1-706 <CAR>
A:Cross-references: UNIPROT:P27425; EMBL:M69020; NID:G1644242; PIDN:AAA30958.1; PID:G1642
A:Experimental source: liver; developmental stage adult
R:Yoshinari, K.; Yuasa, F.; Mimura, A.

```

Biochim. Biophys. Acta 1010, 28-34, 1989
A>Title: A growth-promoting factor for human myeloid leukemia cells from horse serum ide
A/Reference number: S02145; MUID:80076897; PMID:2909248
A/Accession: S02145
A/Molecule type: protein
A/Residues: 20-35,'X',37,'X',39-40,'X',43-44 <YOS>
C/Complex: monomer
C/Superfamily: transferrin; transferrin repeat homology
C/Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-706/Product: transferrin #status experimental <MAT>
F/358-694/Domain: transferrin repeat homology <TRH2>
F/26-64,36-55,134-215,174-190,177-198,187-200,248-262,360-623,366-398,376-389,423-701,44

Query Match      83.5%; Score 96; DB 2; Length 706;
Best Local Similarity 82.6%; Pred. No. 4,4e-07;
Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTEDSIKINMGADAMSLDGGF 23
      :|||||:|||||:|||||:
Db      394 STEDCIATKIVGADAMSLDGGF 416

RESULT 4
A28446
transferrin - mouse (fragments)
C/Species: Mus musculus (house mouse)
C/Date: 30-Jun-1989 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: A28446; A34482; B28438
R/Chen, L.H.; Biesecl, M.J.
J. Biol. Chem. 262, 17247-17250, 1987
A>Title: Transferrin mRNA level in the mouse mammary gland is regulated by pregnancy and
A/Reference number: A28446; MUID:8086992; PMID:3653348
A/Accession: A28446
A/Molecule type: mRNA
A/Residues: 15-80/81-141,217-251,252-301 <CHE>
A/Cross-references: UNIPROT:Q92111
A/Note: the authors translated the codon ACC for residue 61 as Tyr, TCC for residue 62 as
Mol. Cell. Biol. 9, 5154-5162, 1989
A>Title: Expression from the transferrin gene promoter in transgenic mice.
A/Reference number: A34482; MUID:90097932; PMID:2601714
A/Accession: A34482
A/Molecule type: DNA
A/Residues: 114,302-311 <IDZ>
A/Cross-references: GB:M30819; GB:M30820
R/Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A>Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret
A/Reference number: A92596; MUID:87280033; PMID:3611056
A/Accession: B28438
A/Molecule type: mRNA
A/Residues: 86-216 <PEN>
A/Cross-references: GB:J02373; GB:J02377; NID:G198847; PIDN:AAA39438.1; PID:G198848
C/Superfamily: transferrin; transferrin repeat homology
C/Keywords: duplication

Query Match      80.0%; Score 92; DB 2; Length 311;
Best Local Similarity 81.8%; Pred. No. 7,4e-07;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      1 TTEDSIKINMGADAMSLDGG 22
      :|||||:|||||:|||||:
Db      195 TTEDCIATKIVGADAMSLDGG 216

RESULT 5
S01384
transferrin - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: S01384; A60520; A61573
R/Baldwin, G.S.; Weinstock, J.

```

```

Nucleic Acids Res. 16, 8720, 1988
A>Title: Nucleotide sequence of porcine liver transferrin.
A/Reference number: S01384; MUID:88335629; PMID:341934
A/Accession: S01384
A/Status: translation not shown
A/Molecule type: mRNA
A/Residues: 1-696 <BAL>
A/Cross-references: UNIPROT:P09571; EMBL:X12386; NID:92126; PIDN:CAA30943.1; PID:G83380
A/Note: 308-Arg was also found
R/Baldwin, G.S.; Bacic, T.; Chandler, R.; Grego, B.; Pedersen, J.; Simpson, R.J.; Toh,
Comp. Biochem. Physiol. B 95, 261-268, 1990
A>Title: Isolation of transferrin from porcine gastric mucosa: comparison with porcine
A/Reference number: A60520; MUID:90227903; PMID:2328566
A/Accession: A60520
A/Molecule type: protein
A/Residues: 1-8,'X',10-11,'X',13-15 <BA2>
A/Experimental source: gastric mucosa
A/Note: the authors suggest transferrin from gastric mucosa may act in dietary iron upt
R/Chung, M.C.M.; Chan, S.L.; Shimizu, S.
Int. J. Biochem. 23, 609-616, 1991
A>Title: Purification of transferrin and lactoferrin using DEAE Affi-gel Blue.
A/Reference number: A61573; MUID:91293379; PMID:2065820
A/Accession: A61573
A/Molecule type: protein
A/Residues: 1-8,'X',10-18,'XE' <CHU>
C/Superfamily: transferrin; transferrin repeat homology
C/Keywords: duplication; glycoprotein; iron transport; plasma
F/1-696/Product: transferrin #status predicted <MAT>
F/1-335/Domain: transferrin repeat homology <TRH1>

Query Match      80.0%; Score 92; DB 1; Length 696;
Best Local Similarity 81.8%; Pred. No. 1,9e-06;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 TEDSIKINMGADAMSLDGGF 23
      :|||||:|||||:|||||:
Db      378 TEDCIATKIVGADAMSLDGGY 399

RESULT 6
A45543
lactoferrin precursor - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C/Accession: A45543; S24173
R/Alexander, L.J.; Levine, W.B.; Teng, C.T.; Beattie, C.W.
Ann. Genet. 23, 251-256, 1992
A>Title: Cloning and sequencing of the porcine lactoferrin cDNA.
A/Reference number: A45543; MUID:92367939; PMID:1503259
A/Accession: A45543
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-703 <ALE>
A/Cross-references: UNIPROT:P14632
A/Note: sequence extracted from NCBI backbone (NCBI:111151, NCBI:111153)
R/Lydon, J.P.; O'Malley, B.R.; Sancedo, O.; Lee, T.; Heaton, D.R.; Connely, O.M.
Biochim. Biophys. Acta 1133, 97-99, 1992
A>Title: Nucleotide and primary amino acid sequence of porcine lactoferrin.
A/Reference number: S24173; MUID:92379101; PMID:1511016
A/Accession: S24173
A/Molecule type: mRNA
A/Residues: 111,'W',13-50,'I',52-84,'G',86-120,'U',121-130,'I',132-282,'S',284-571,'Q'
A/Cross-references: EMBL:M92089; NID:G164613; PIDN:AAA31102.1; PID:G164614
A/Experimental source: mammary gland
C/Superfamily: transferrin; transferrin repeat homology
C/Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-703/Product: lactoferrin #status predicted <MAT>
F/20-350/Domain: transferrin repeat homology <TRH1>
F/36-48/Region: antimicrobial
F/354-691/Domain: transferrin repeat homology <TRH2>
F/28-62,38-53,129-212,171-187,184-195,245-259,362-394,372-385,419-698,439-661,471-546,4

```

F:77,107,206,267/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
 F:135/Binding site: carbonate (Arg) #status predicted
 F:409,447,540,609/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
 F:477/Binding site: carbonate (Arg) #status predicted
 F:490/Binding site: carbonate (Asp) (covalent) #status predicted

Query Match 80.0%; Score 92; DB 2; Length 703;
 Best Local Similarity 73.9%; Pred. No. 1,9e-06;
 Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIATKMGADAMSIDGCF 23
 ||||| :||:|||||||
 Db 390 TTEDCIVQLKGEADAMSIDGCF 412

RESULT 7

S49163 transferrin precursor - rat

N:Alternate names: lung-derived growth factor; siderophilin

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Feb-1995 #sequence revision 12-May-1995 #text change 09-Jul-2004

C:Accession: S49163; S54980; A30014; A14679; A53289; A30512; I52203

R:Reactiva: H.; Pierce, A.; Coddeville, B.; Gonzalez, F.; Benalissa, M.; Leger, D.; Wierus

submitted to the EMBL Data Library, January 1994

A:Description: Rat mammary gland transferrin: glycan structure, nucleotide sequence and

A:Reference number: S49163

A:Accession: S49163

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-695 <ES>

A:Cross-references: UNIPROT:P12346; UNIPROT:Q63602; EMBL:X77158; NID:G510195; PIDN:CAA54

R:Reactiva: H.; Pierce, A.; Coddeville, B.; Gonzalez, F.; Benalissa, M.; Leger, D.; Wierus

Biochem. J. 307, 47-55, 1995

A:Title: Rat mammary-gland transferrin: nucleotide sequence, phylogenetic analysis and

A:Reference number: S54980; NID:95234054; PMID:7717992

A:Accession: S54980

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-695 <ES>

A:Cross-references: EMBL:X77158; NID:G510195; PIDN:CAA54403.1; PID:G510196

R:Hugenvik, J.T.; Idzerda, R.L.; Haywood, L.; Lee, D.C.; McKnight, G.S.; Griswold, M.D.

Endocrinology 120, 332-340, 1987

A:Title: Transferrin messenger ribonucleic acid: molecular cloning and hormonal regulati

A:Reference number: A30014; NID:87053639; PMID:3023031

A:Accession: A30014

A:Status: preliminary

A:Molecule type: protein

A:Residues: 20-47 <SCH>

R:Cavanaugh, P.G.; Nicolson, G.L.

J. Cell. Biochem. 47, 261-271, 1991

A:Title: Lung-derived growth factor that stimulates the growth of lung-metastasizing tum

A:Reference number: A53289; NID:92165927; PMID:1791188

A:Accession: A53289

A:Status: preliminary

A:Molecule type: protein

A:Residues: 89,'Y',91,'A',93-99,'V',101-102,'N',213,'AN',236-243;401-406,'N',408 <CAV>

A:Experimental source: lung

A:Note: sequence modified after extraction from NCBI backbone

A:Note: sequence extracted from NCBI backbone (NCBIP:86115, NCBIP:86116, NCBIP:86114)

R:Purves, L.R.; Purves, M.; Linton, N.; Brandt, W.; Johnson, G.; Jacobs, P.

Biochem. Biophys. Acta 966, 318-327, 1998

A:Title: Properties of the transferrin associated with rat intestinal mucosa.

A:Reference number: A30512; NID:88327006; PMID:3046665

A:Accession: A30512

A:Molecule type: protein

A:Residues: 20-30;639-643,'KD',646,'LKACD' <PDR>

R:Aldred, A.R.; Howlett, G.T.; Schreiber, G.

Biochem. Biophys. Res. Commun. 122, 960-965, 1984

A:Title: Synthesis of rat transferrin in *Escherichia coli* containing a recombinant bacter

A:Reference number: I52203; NID:84307580; PMID:6236811

A:Accession: I52203

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 7-25,'X',27-56,'A',58-64,267-295 <RES>

A:Cross-references: GB:M26113; NID:G207437; PIDN:AAA42266.1; PID:G207438

C:Genetics: TF

C:Superfamily: transferrin; transferrin repeat homology

C:Keywords: duplication

F:20-348/Domain: transferrin repeat homology <TRH1>

Query Match 78.3%; Score 90; DB 2; Length 695;
 Best Local Similarity 81.8%; Pred. No. 3.9e-06;
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTEDSIATKMGADAMSIDGCF 22
 :||| :||:|||||||
 Db 388 STEDCIDTKVNGEADAMSIDGCF 409

RESULT 8
 TFHUL
 lactotransferrin precursor [validated] - human

N:Alternate names: lactoferrin

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000

C:Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74

R:Cho, Y.

submitted to the EMBL Data Library, March 1994

A:Reference number: G06820

A:Accession: G01394

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-711 <CHO>

A:Cross-references: EMBL:U07643; NID:G467236; PIDN:AAB60324.1; PID:G467237

R:Rey, M.W.; Moloshuk, S.L.; deBoer, H.A.; Pieper, F.R.

Nucleic Acids Res. 18, 5288, 1990

A:Title: Complete nucleotide sequence of human mammary gland lactoferrin.

A:Reference number: S11228; NID:90384839; PMID:2402455

A:Accession: S11228

A:Molecule type: mRNA

A:Residues: 1-148,'T',150-422,'C',424-711 <REV>

A:Cross-references: EMBL:X53961; NID:G34415; PIDN:CAA37914.1; PID:G34416

R:Reng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.

Mol. Endocrinol. 6, 1969-1981, 1992

A:Title: Differential molecular mechanism of the estrogen action that regulates lactofer

A:Reference number: A45401; NID:93125571; PMID:1480183

A:Accession: A45401

A:Molecule type: DNA

A:Residues: 1-15 <TEN>

A:Cross-references: GB:S52659; NID:9263311; PIDN:AAB24877.1; PID:9263312

A:Experimental source: placenta

A:Note: sequence extracted from NCBI backbone (NCBIP:122202)

R:Powell, M.J.; Ogden, J.B.

Nucleic Acids Res. 18, 4013, 1990

A:Title: Nucleotide sequence of human lactoferrin cDNA.

A:Reference number: S10324; NID:90326549; PMID:2374734

A:Accession: S10324

A:Molecule type: mRNA

A:Residues: 3-711 <POW>

A:Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A:Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A:Reference number: S15853; NID:91264786; PMID:2049066

A:Accession: S15853

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 20-31 <STI>

A:Accession: 520841
 A:Molecule type: protein
 A:Residues: 20-28,'X',30-31 <ST2>
 R:Radio, T.A.; Wei, X.; Benz Jr., E.J.
 Blood 70, 989-993, 1987
 A:Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA
 A:Reference number: 507160; PMID:8001031; PMID:3477300
 A:Accession: 507160
 A:Molecule type: mRNA
 A:Residues: 436-487,'A',489-711 <RAD>
 A:Cross-references: EMBL:M8642; NID:9186815; PIDN:AAA86665.1; PID:9386855
 R:Panel1a, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
 Cancer Res. 51, 3037-3043, 1991
 A:Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes
 A:Reference number: A61169; PMID:91235214; PMID:1674448
 A:Accession: A61169
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 3-701,'SMKPVN' <PAN>
 A:Experimental source: normal breast tissue
 R:Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.; Eur. J. Biochem. 145, 659-666, 1994
 A:Title: Human lactotransferrin: amino acid sequence and structural comparisons with och
 A:Reference number: A31000; PMID:85076667; PMID:6510420
 A:Accession: A31000
 A:Molecule type: protein
 A:Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
 A:Note: this is the final paper in a series
 R:Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norakov, L.
 Eur. J. Biochem. 241, 303-308, 1996
 A:Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affini
 A:Reference number: S74119; PMID:97054624; PMID:8898921
 A:Accession: S74119
 A:Molecule type: protein
 A:Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
 A:Experimental source: neutrophil granulocytes
 C:Genetics:
 A:Gene: GDB:LTF
 A:Cross-references: GDB:119368; OMIM:150210
 A:Map position: 3q21-3q23
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein; iron binding; milk
 F:1-19/Domain: signal sequence #status predicted <Sig>
 F:20-71/Product: lactotransferrin #status experimental <MAT>
 F:21-356/Domain: transferrin repeat homology <TRH1>
 F:360-699/Domain: transferrin repeat homology <TRH2>
 F:29-65,39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e
 F:157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat

Query Match 78.3%; Score 90; DB 1; Length 711;
 Best Local Similarity 73.9%; Pred. No. 4e-06;
 Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIATKTMGEADMSLDGCF 23
 DB 396 TTEDCIATLVKGBADMSLDGCF 418

RESULT 9
 A28438
 lactoferrin precursor - mouse
 N:Alternate names: lactotransferrin
 C:Species: Mus musculus (house mouse)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A28438; A41205
 R:Penecocot, B.T.; Teng, C.T.
 J. Biol. Chem. 262, 10134-10139, 1987
 A:Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secr
 A:Reference number: A92596; PMID:87280033; PMID:3611056
 A:Accession: A28438
 A:Molecule type: mRNA
 A:Residues: 3-707 <PEN>

A:Cross-references: EMBL:J03298
 R:Liu, Y.; Teng, C.T.
 J. Biol. Chem. 266, 21880-21885, 1991
 A:Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
 A:Reference number: A41205; PMID:92042099; PMID:1939212
 A:Accession: A41205
 A:Molecule type: DNA
 A:Residues: 115 <LIU>
 A:Cross-references: GB:M74778
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:1-19/Domain: signal sequence #status predicted <Sig>
 F:20-707/Product: lactotransferrin #status predicted <MAT>
 F:358-695/Domain: transferrin repeat homology <TRH2>
 F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 76.5%; Score 88; DB 1; Length 707;
 Best Local Similarity 73.9%; Pred. No. 8.3e-06;
 Matches 17; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTEDSIATKTMGEADMSLDGCF 23
 DB 394 TTEDCIATLVKGBADMSLDGCF 416

RESULT 10
 147228
 carbonic anhydrase II inhibitor (transferrin homology) precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C>Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
 C:Accession: 147228
 R:Roush, E.D.; Fierke, C.A.
 Biochemistry 31, 12536-12542, 1992
 A:Title: Purification and characterization of a carbonic anhydrase II inhibitor from po
 A:Reference number: 147228; PMID:93099129; PMID:1463741
 A:Accession: 147228
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-704 <ROU>
 A:Cross-references: UNIPROT:Q29545; EMBL:U36916; NID:G1016329; PIDN:AAB58956.1; PID:G10
 C:Genetics:
 A:Gene: PICA
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication
 F:20-350/Domain: transferrin repeat homology <TRH1>

Query Match 74.8%; Score 86; DB 2; Length 704;
 Best Local Similarity 78.3%; Pred. No. 1.7e-05;
 Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TTEDSIATKTMGEADMSLDGCF 23
 DB 388 TTEDCIATLVKGBADMSLDGCF 410

RESULT 11
 JC2323
 lactoferrin - goat
 C:Species: Capra aegagrus hircus (domestic goat)
 C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
 C:Accession: JC2323
 R:Le Provost, F.; Nocard, M.; Guerin, G.; Martin, P.
 Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
 A:Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locu
 A:Reference number: JC2323; PMID:9438047; PMID:8093048
 A:Accession: JC2323
 A:Molecule type: mRNA
 A:Residues: 1-708 <LEP>
 C:Superfamily: transferrin; transferrin repeat homology
 C:Keywords: duplication; glycoprotein
 F:359-696/Domain: transferrin repeat homology <TRH2>
 F:252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	73.0%	Score 84	DB 2	Length 708
Best Local Similarity	65.2%	Pred. No.	3.6e-05	
Matches	15	Conservative	5	Matches 3
				Indels 0
				Gaps 0
QY	1	TTEDSIKINNGEADAMSIDGAF	23	
		:::		
Db	395	TTDDCIALVLKGEADALSIDGAY	417	

RESULT 12

ovotransferrin precursor - chicken
N/Alternate names: conalbumin; transferrin
C/Species: Gallus gallus (chicken)
C/Date: 24-Apr-1994 #sequence revision 30-Sep-1993 #text change 09-Jul-2004
C/Accession: A26845; A91115; A92229; A91116; A40674; B61573; A90282; S02476; A03662
R/Jeltsch, J.M.; Hen, R.; Maroix, L.; Garnier, J.M.; Chambon, P.
Nucleic Acids Res. 15, 7643-7645, 1987
A/Title: Sequence of the chicken ovotransferrin gene.
A/Reference number: A26845; MUID:88015626; PMID:3658709
A/Accession: A26845
A/Molecule type: DNA
A/Residues: 1-705 <TE5>
A/Cross-references: UNIPROT:P02789; GB:X00407; NID:G63131; PIDN:CAA68468.1; PID:G295721
R/Jeltsch, J.M.; Chambon, P.
Eur. J. Biochem. 122, 291-295, 1982
A/Title: The complete nucleotide sequence of the chicken ovotransferrin mRNA.
A/Reference number: A91115; MUID:82138851; PMID:7060577
A/Accession: A91115
A/Molecule type: mRNA
A/Residues: 1-82, 'V', 84-99, 'I', 101-153, 'W', 155-238, 'LN', 241-685, 'N', 687-705 <TE2>
A/Cross-references: EMBL:X02009
A/Note: the codons given for residues 132 (AAC) and 317 (UUC) are inconsistent with the
R/Thibodeau, S.N.; Lee, D.C.; Palmiter, R.D.
J. Biol. Chem. 253, 3771-3774, 1978
A/Title: Identical precursors for serum transferrin and egg white conalbumin.
A/Reference number: A92229; MUID:78171533; PMID:649604
A/Accession: A92229
A/Molecule type: Protein
A/Residues: 1-23 <TH3>
R/Williams, J.; Eillemann, T.C.; Kingston, I.B.; Wilkins, A.G.; Kuhn, K.A.
Eur. J. Biochem. 122, 297-303, 1982
A/Title: The primary structure of hen ovotransferrin.
A/Reference number: A91116; MUID:82138852; PMID:6895872
A/Accession: A91116
A/Molecule type: Protein
A/Residues: 1-50; 54-82, 'V', 84-92; 102-146; 162-168; 170-228; 241-283; 289-333; 338-344; 350-351
R/Gentili, C.; Bianco, P.; Neri, M.; Malpeli, M.; Campanile, G.; Castagnola, P.; Cancedda
J. Cell Biol. 122, 703-712, 1993
A/Title: Cell proliferation, extracellular matrix mineralization, and ovotransferrin tre
A/Reference number: A40674; MUID:93328771; PMID:8393014
A/Accession: A40674
A/Molecule type: Protein
A/Residues: 20-28, 'X', 30-38, 'X', 40-44 <GEN>
R/Chung, M.C.M.; Chan, S.L.; Shimizu, S.
Int. J. Biochem. 23, 609-616, 1991
A/Title: Purification of transferrins and lactoferrin using DEAE Affi-Gel Blue.
A/Reference number: A61573; MUID:91293379; PMID:2065820
A/Accession: B61573
A/Molecule type: Protein
A/Residues: 20-28, 'X', 30-38, 'X', 40-43, 'S' <CHU>
R/Kingston, I.B.; Williams, J.
Biochem. J. 147, 463-472, 1975
A/Title: The amino acid sequence of a carbohydrate-containing fragment of hen ovotransferrin
A/Reference number: A90282; MUID:76039467; PMID:1172663
A/Accession: A90282
A/Molecule type: Protein
A/Residues: 480-582 <KIN>
R/Eillemann, T.C.; Williams, J.
Biochem. J. 116, 515-532, 1970
A/Title: The amino acid sequences of cysteine-containing peptides from performic acid

A;Contents: annotation, disulfide bonds
R;Williams, J.; Moreton, K.
Biochem. J. 251, 849-855, 1988
A;Title: The dimerization of half-molecule fragments of transferrin.
A;Reference number: S02476; MUID:88336225; PMID:3415649
A;Accession: S02476

A:Reidites: 20:33,295-302;336-366;674-679.'T',681,'F',683-685,'N',687-705.<M2>
C:Comment: Ovatransferrin (conalbumin) and transferrin have identical protein components
with is synthesized in the liver.
C:Comment: Ovatransferrin has a bacteriostatic function. Its concentration in avian egg
C:Comment: Plasma apotransferrin promotes the oxidation of ferrous ions, which would otherwise
C:Comment: in electrophoretic and genetic studies, transferrin shows strong polymorphism
C:Genetics:
A:introns: 15/1; 69/3; 106/1; 170/1; 215/2; 234/1; 290/3; 353/1; 404/3; 436/1; 448/1; 50
C:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; egg white; glycoprotein; iron binding; plasma
F.1-19/Domains: signal sequence #status experimental <SIG>
F.21-705/Product: transferrin #status experimental <MAT>
F.21-355/Domains: transferrin repeat homology <TRH1>
F.355-692/Domains: transferrin repeat homology <TRH2>
F.129-64,134-216,179-193,190-201,447-261,367-399,424-699,440-662,473-549,497-690/Diulfid
F.3-55,377-390,589-603/Diulfid bonds: #status predicted
F.492/Binding site: carbonyldate (Asn) (covalent) (partial) #status experimental
F.507-521,518-532/Diulfid Bonds: (or 507-518, 521-532) #status predicted

Query Match	67.0%	Score 77;	DB 1;	Length 705;
Best Local Similarity	71.4%;	Pred. No. 0.00047;		
Matches 15; Conservative	3;	Mismatches 3;	Indels 0;	Gaps 0

QY	2	TEDSI	AKI	MNGE	ADAM	SLDG	22
		:					
		:					
Db	396	TKDCI	IKIM	KGAD	AVAL	DGG	416

RESULT 13

1. laccase
 2. lactotransferrin precursor - bovine
 N/Alternate names: lactoferrin
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 09-Jul-2004
 A/Ccession: I45910; S14674; S14110; S18517; J70595; S13097; S18518; S13881; P10148; S211
 R/Tsang, T.C.; Burns, D.K.; Wang, F.; Pan, Y.
 P/ASB J. 6, 233, 1991
 A/TITLE: Cloning of a 80-kD advanced glycosylation end product (AGE) binding protein from
 A/Reference number: I45919
 A/Ccession: I45919
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-708 <TSA>
 A/Cross-references: UNIPROT:P24627; GB:L08604; NID:G163269; P1DN:AAA50609.1; PID:G163270
 R/Pierce, A.
 submitted to the EMBL Data Library, November 1990
 A/Reference number: S14674
 A/Ccession: S14674
 A/Molecule type: mRNA
 A/Residues: 1-144, 'V', 146-163, 'PP', 166-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <PI1>
 A/Cross-references: EMBL:X57084; NID:G505; P1DN:CAA40366.L; PID:9506
 R/Pierce, A.; Colavizza, D.; Benlises, M.; Maes, P.; Tartar, A.; Montreuil, J.; Spik, G
 Eur. J. Biochem. 196, 177-184, 1991
 A/TITLE: Molecular cloning and sequence analysis of bovine lactotransferrin.
 A/Reference number: S14110; NUID:91160550; PMID:2001696
 A/Ccession: S14110
 A/Molecule type: mRNA
 A/Residues: 3-144, 'V', 146-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <PI2>
 A/Cross-references: EMBL:X57084
 A/Ccession: S18517
 A/Molecule type: protein
 A/Residues: 20-35,82-114,148-163, 'PP', 166-178, 'V', 'P', 183-190;205-212;230-239;304-339;59
 R/Goodman, R.E.; Schanbacher, F.L.
 Biochem. Biophys. Res. Commun. 180, 75-84, 1991
 A/TITLE: Bovine lactoferrin mRNA: sequence, analysis, and expression in the mammary gland
 A/Reference number: J70595; NUID:92028986; PMID:1718281

```

A/Accession: J10595
A/Molecule type: mRNA
A/Residues: 1-65, 'PC', 68-296, 'S', 298-339, 'A', 341-708 <GOO>
A/Cross-references: GB:M63502
A/Note: the authors translated the codon CCG for residue 66 as Arg and TCT for residue 2
R/Mead, P.E.; Tweedle, J.W.
Nucleic Acids Res. 18, 7167, 1990
A/Title: cDNA and protein sequence of bovine lactoferrin.
A/Reference number: S13097; MUID:91088328; PMID:2263492
A/Accession: S13097
A/Molecule type: mRNA
A/Residues: 28-33, 'DS', 36-38, 'P', 40-708 <MEA>
A/Cross-references: EMBL:X54801
A/Accession: S18518
A/Molecule type: protein
A/Residues: 20-47, 59-66, 132-139, 256-277, 278, 305-332, 343-351, 361-363, 586, 587-589, 598-619
R/Mead, P.E.
Submitted to the EMBL Data Library, October 1990
A/Reference number: S13881
A/Accession: S13881
A/Molecule type: mRNA
A/Residues: 28-38, 'P', 40-86, 'C', 88-708 <ME3>
A/Cross-references: EMBL:X54801
R/Rejman, J.J.; Hegarty, H.M.; Hurley, W.L.
Comp. Biochem. Physiol. B 93, 929-934, 1989
A/Title: Purification and characterization of bovine lactoferrin from secretions of the
A/Reference number: P10148; MUID:90031466; PMID:2805645
A/Accession: P10148
A/Molecule type: protein
A/Residues: 20-27, 'X', 29-37, 'X', 39-54, 'X', 56-59 <REJ>
R/Beallmy, W.; Tkasek, M.; Yamuchi, K.; Wakabayashi, H.; Kawase, K.; Tomita, M.
Biochim. Biophys. Acta 1121, 130-136, 1992
A/Title: Identification of the bactericidal domain of lactoferrin.
A/Reference number: S21756; MUID:92287941; PMID:1599934
A/Accession: S21756
A/Molecule type: protein
A/Residues: 36-60 <BBL>
R/Shimazaki, K.; Tanaka, T.; Kon, H.; Oota, K.; Kawaguchi, A.; Maki, Y.; Sato, T.
J. Dairy Sci. 76, 946-955, 1993
A/Title: Separation and characterization of the C-terminal half molecule of bovine lacto
A/Reference number: A56659; MUID:93253156; PMID:846845
A/Accession: A56659
A/Molecule type: protein
A/Residues: 20-25, 302-308, 359-366, 'X', 368-376, 'X', 378 <SHI>
C/Superfamily: transferrin; transferrin repeat homology
C/Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-708/Product: lactotransferrin #status experimental <MAT>
F:20-355/Domain: transferrin repeat homology <TRH1>
F:36-60/Region: antimicrobial
F:359-696/Domain: transferrin repeat homology <TRH2>
F:28-64, 134-217, 176-192, 179-200, 189-202, 250-264, 367-399, 377-390, 424-703, 444-666, 476-551,
F:38-55/Diulfide bonds: #status predicted
F:79, 111, 211, 272/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
F:140/Binding site: carbonate (Arg) #status experimental
F:252, 300, 387, 495, 564/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:414, 452, 545, 614/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
F:482/Binding site: carbonate (Arg) #status experimental

Query Match 67.0%; Score 77; DB 1; Length 708;
Best Local Similarity 56.5%; Pred. No. 0.00047;
Matches 13; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSIDGCF 23
DB 395 TTDDCIYLVKGEADALNDGGY 417

RESULT 14
612100
transferrin precursor - African clawed frog
C/Species: Xenopus laevis (African clawed frog)
C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

```

```

C/Accession: S12100
R/Moskaitis, J.E.; Pastori, R.L.; Schoenberg, D.R.
Nucleic Acids Res. 18, 6135, 1990
A/Title: The nucleotide sequence of Xenopus laevis transferrin mRNA.
A/Reference number: S12100; MUID:91045087; PMID:2235503
A/Accession: S12100
A/Molecule type: mRNA
A/Residues: 1-717 <MOS>
A/Cross-references: UNIPROT:P20233; EMBL:X54530; NID:965158; PIND:CAA38396.1; PID:96515
C/Superfamily: transferrin; transferrin repeat homology
F:346-689/Domain: transferrin repeat homology <TRH2>

Query Match 61.7%; Score 71; DB 2; Length 717;
Best Local Similarity 52.2%; Pred. No. 0.0043;
Matches 12; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSIDGCF 23
DB 385 TAECIVQLKGEADAVTLDDGY 407

RESULT 15
111749
transferrin - Atlantic salmon
C/Species: Salmo salar (Atlantic salmon)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C/Accession: T11749
R/Kvingedal, A.M.; Rorvik, K.A.; Alestrom, P.
Mol. Marine Biol. Biotechnol. 2, 233-238, 1993
A/Title: Cloning and characterization of Atlantic salmon (Salmo salar) serum transferrin
A/Reference number: Z17332; MUID:94122797; PMID:8293074
A/Accession: T11749
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-690 <KVI>
A/Cross-references: UNIPROT:P60426; EMBL:L20313; NID:9431609; PIND:AA18838.1; PID:9431
A/Experimental source: liver
C/Superfamily: transferrin; transferrin repeat homology
C/Keywords: iron binding

Query Match 57.4%; Score 66; DB 2; Length 690;
Best Local Similarity 59.1%; Pred. No. 0.026;
Matches 13; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADAMSIDGCF 22
DB 375 TVECIKIMRKEADAIADVG 396

Search completed: November 1, 2005, 12:55:47
Job time : 25.3382 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:34:09 / Search time 112.632 Seconds
(without alignments)
104.569 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115

Sequence: 1 TTEDSIKIMNGEADMSLDGCF 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	110	95.7	698	1 TRFE_HUMAN	P02787 homo sapien
2	103	89.6	694	2 Q7TSX6	Q7TSX6 marmota mon
3	101	87.8	695	1 TRFE_RABIT	P19134 oryctolegus
4	96	83.5	706	1 TRFE_HORSE	P27425 equus cabal
5	92	80.0	696	1 TRFE_PIG	P09571 sus scrofa
6	92	80.0	697	1 TRFE_MOUSE	Q29111 mus musculu
7	92	80.0	704	1 TRFE_BOVIN	Q29443 bos taurus
8	92	80.0	704	1 TRFL_PIG	P14632 sus scrofa
9	92	80.0	704	2 Q8MNA8	Q8MNA8 sus scrofa
10	92	80.0	704	2 Q6Y7J9	Q6Y7J9 sus scrofa
11	92	80.0	704	2 Q7YS20	Q7YS20 sus scrofa
12	90	78.3	698	1 TRFE_RAT	P12346 rattus norv
13	90	78.3	698	2 Q7TNX0	Q7TNX0 rattus norv
14	90	78.3	711	1 TRFL_HUMAN	P02788 homo sapien
15	90	78.3	979	2 Q7TMC7	Q7TMC7 rattus norv
16	90	78.3	980	2 Q7TP24	Q7TP24 rattus norv
17	88	76.5	705	2 Q6A169	Q6A169 chrysemys s
18	88	76.5	707	1 TRFL_MOUSE	P08071 mus musculu
19	88	76.5	707	2 Q8CBA0	Q8CBA0 mus musculu
20	87	75.7	700	2 Q8VC96	Q8VC96 mus musculu
21	87	75.7	700	2 Q9DBD0	Q9DBD0 mus musculu
22	87	75.7	708	1 TRFL_CANDR	Q9TUN0 camelus dro
23	86	73.0	704	1 ICA_PIG	Q29545 sus scrofa
24	84	73.0	421	2 Q7TP03	Q7TP03 rattus norv
25	84	73.0	708	1 TRFL_BUBBU	Q77688 bubalus bub
26	84	73.0	708	1 TRFL_CAPHI	Q29477 capra hircu
27	83	72.2	695	1 TRFL_HORSE	Q77811 equus cabal
28	83	72.2	711	2 Q9XT72	Q9XT72 trichosurus
29	82	71.3	701	2 Q6A168	Q6A168 struthio ca
30	80	69.6	462	2 Q6Q147	Q6Q147 rattus norv
31	77	67.0	355	2 Q8MI10	Q8MI10 bos taurus

ALIGNMENTS

RESULT 1	TRFE_HUMAN	STANDARD;	PRT;	698 AA.
AC	P02787; O43890; Q9NQB8; Q9UHV0;			
DT	21-OCT-1986 (Rel. 01, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Serotransferrin precursor (Transferrin) (siderophilin) (Beta-1-metal			
DE	binding globulin) (PRO1400).			
GN	Name=TF;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND VARIANTS TF*B2; TF*CHI AND TF*DI.			
RX	MDL:LINE=64194084; PubMed=6585826;			
RA	Yang F., Lum J.B., McGill J.R., Moore C.M., Naylor S.L.,			
RA	van Bragt P.H., Baldwin W.D., Bowman B.H.,			
RT	"Human transferrin: cDNA characterization and chromosomal			
RT	localization.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 81:2752-2756(1984).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MDL:LINE=88056305; PubMed=3678832; DOI=10.1016/0378-1119(87)90163-6;			
RA	Schaeffer E., Lucero M.A., Jeltsch J.-M., Py M.-C., Levin M.J.,			
RA	Chambon P., Cohen G.N., Zakin M.W.,			
RT	"Complete structure of the human transferrin gene. Comparison with			
RT	analogous chicken gene and human pseudogene.";			
RL	Gene 56:109-116(1987).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RX	MDL:LINE=92221399; PubMed=1809186;			
RA	Hershenberger C.L., Larson J.L., Arnold B., Roestek P.R. Jr.,			
RA	Williams P., Dehoff B., Dunn P., O'Neal K.L., Rlemen M.W., Tice P.A.;			
RT	"A cloned gene for human transferrin.";			
RL	Ann. N.Y. Acad. Sci. 646:140-154(1991).			
RN	[4]			
RP	SEQUENCE FROM N.A., AND VARIANT ATRANSFERRINEMIA PRO-477.			
RX	MDL:LINE=20563920; PubMed=11110675;			
RA	Beutler E., Gelbart T., Lee P.L., Trevino R., Fernandez M.A.,			
RA	Fairbanks V.F.;			
RT	"Molecular characterization of a case of atransferrinemia.";			
RL	Blood 96:4071-4074(2000).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Rieder M.J., Carrington D.P., da Ponce S.H., Haerlings N.C.,			
RA	Ahearn M.O., Koldanek S.A., Rajkumar N., Toth E.J., Yi Q.,			
RA	Nickerson D.A.;			
RT	"SeattleSNP: NHU81 HU66682 program for genomic applications, UW-			
RT	PHRCR, Seattle, WA (URL: http://pga.gs.washington.edu).";			
RL	Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.			
RN	[6]			

32	77	67.0	681	2 Q6LAN7	Q6LAN7 bos taurus
33	77	67.0	705	1 TRFE_CHICK	P02789 gallus gall
34	77	67.0	708	1 TRFL_BOVIN	P24627 bos taurus
35	77	67.0	708	2 Q6LEC7	Q6LEC7 bos taurus
36	76	66.1	686	1 TRFE_ANAPL	P56410 anas platyr
37	71	61.7	532	2 Q7SYA2	Q7SYA2 xenopus lae
38	71	61.7	701	1 TRFE_XENLA	P20233 xenopus lae
39	71	61.7	701	2 Q6PCT3	Q6PCT3 xenopus lae
40	71	61.7	720	2 Q7ZTQ7	Q7ZTQ7 xenopus lae
41	70	60.9	615	2 Q6TXX2	Q6TXX2 ctenopharyn
42	70	60.9	685	1 TRFE_PAROL	Q93429 paraliichth
43	70	60.9	686	2 Q9IA82	Q9IA82 paraliichth
44	70	60.9	686	2 Q9IA83	Q9IA83 paraliichth
45	70	60.9	691	2 Q6UPC0	Q6UPC0 acanthopagr

RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22286257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.J., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[7]
RP SEQUENCE OF 99-698 FROM N.A.
RC TISSUE=Fetal liver;
RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
RA He F.;
RT "Functional prediction of the coding sequences of 33 new genes deduced
by analysis of cDNA clones from human fetal liver.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
[8]
RP SEQUENCE OF 422-698 FROM N.A.
RX MEDLINE=84153910; PubMed=6322780;
RA Uzan G., Frain M., Park I., Besmond C., Maessen G., Trepac J.S.,
RA Zakin M.M., Kahn A.;
RT "Molecular cloning and sequence analysis of cDNA for human
transferrin.";
RL Biochem. Biophys. Res. Commun. 119:273-281(1984).
[9]
RP SEQUENCE OF 20-698
RX MEDLINE=83160878; PubMed=6833213;
RA McGillyray R.T.A., Mendez E., Shewale J.G., Sinha S.K.,
RA Lineback-Zins J., Brew K.;
RT "The primary structure of human serum transferrin. The structures of
seven cyanogen bromide fragments and the assembly of the complete
structure.";
RL J. Biol. Chem. 258:3543-3553(1983).
[10]
RP SEQUENCE OF 73-698 FROM N.A.
RX MEDLINE=85216459; PubMed=3858812;
RA Park I., Schaeffer E., Sidoli A., Baralle F.E., Cohen G.N.,
RA Zakin M.M.;
RT "Organization of the human transferrin gene: direct evidence that it
originated by gene duplication.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3149-3153(1985).
[11]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=87066744; PubMed=3786138;
RA Lucero M.A., Schaeffer E., Cohen G.N., Zakin M.M.;
RT "The 5' region of the human transferrin gene: structure and potential
regulatory sites.";
RL Nucleic Acids Res. 14:8692-8692(1986).
[12]
RP SEQUENCE OF 1-72 AND 291-300 FROM N.A.
RX MEDLINE=87192006; PubMed=3106157; DOI=10.1016/0378-1119(86)90277-5;
RA Adrian G.S., Korinek B.W., Bowman B.H., Yang F.;
RT "The human transferrin gene: 5' region contains conserved sequences
that match the control elements regulated by heavy metals,
glucocorticoids and acute phase reaction.";
RL Gene 49:167-175(1986).
[13]
RP SEQUENCE OF 45-72 FROM N.A.

RX MEDLINE=20392111; PubMed=10931525;
RX DOI=10.1002/1097-4547(20000815)61:4<388::AID-JNRS>3.0.CO;2-O;
RA de Arriba Zepa G.A., Saleh M.C., Fernandez P.M., Guillou F.,
RA Espinosa de los Monteros A., de Vellis J., Zakin M.M., Baron B.;
RT "Alternative splicing prevents transferrin secretion during
differentiation of a human oligodendrocyte cell line.";
RL J. Neurosci. Res. 61:388-395(2000).
[14]
RP SEQUENCE OF 564-624 FROM N.A., AND VARIANT TP+C2.
RC TISSUE=Brain;
RX MEDLINE=97418135; PubMed=9272172;
RA Namekata K., Oyama F., Imagawa M., Ihara Y.;
RT "Human transferrin (Tf): a single mutation at codon 570 determines Tf
C1 or Tf C2 variant.";
RL Hum. Genet. 100:457-458(1997).
[15]
RP SEQUENCE OF 564-624 FROM N.A.
RA Tsuchida S., Ikemoto S., Kajii E.;
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
[16]
RP SEQUENCE OF 636-696 FROM N.A.
RX MEDLINE=89386721; PubMed=2780570;
RA Duguid J.R., Bolmont C.W., Liu N.G., Tourtellotte W.W.;
RT "Changes in brain gene expression shared by scrapie and Alzheimer
disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:7260-7264(1989).
[17]
RP SEQUENCE OF 263-266; 454-458; 531-538 AND 589-595.
RC TISSUE=Heart;
RX MEDLINE=96007936; PubMed=7998159;
RA Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,
RA Ershova E.S., Egorov T.A., Musalyanov A.K.;
RT "The major protein expression profile and two-dimensional protein
database of human heart.";
RL Electrophoresis 16:1160-1169(1995).
[18]
RP DISULFIDE BONDS.
RX MEDLINE=8222166; PubMed=6953407;
RA McGillyray R.T.A., Mendez E., Sinha S.K., Sutton M.R.,
RA Lineback-Zins J., Brew K.;
RT "The complete amino acid sequence of human serum transferrin.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2504-2508(1982).
[19]
RP MUTAGENESIS.
RX MEDLINE=92031536; PubMed=1932003;
RA Woodworth R.C., Mason A.B., Funk W.D., McGillyray R.T.A.;
RT "Expression and initial characterization of five site-directed mutants
of the N-terminal half-molecule of human transferrin.";
RL Biochemistry 30:10824-10829(1991).
[20]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 22-350.
RX MEDLINE=98272665; PubMed=9609685; DOI=10.1021/bi980355j;
RA McGillyray R.T.A., Moore S.A., Chen J., Anderson B.F., Baker H.,
RA Luo Y., Bewley M.C., Smith C.A., Murphy M.E.P., Wang Y., Mason A.B.,
RA Woodworth R.C., Brayer G.D., Baker E.N.;
RT "Two high-resolution crystal structures of the recombinant N-lobe of
human transferrin reveal a structural change implicated in iron
release.";
RL Biochemistry 37:7919-7928(1998).
[21]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-350.
RX MEDLINE=98434369; PubMed=9760232; DOI=10.1021/bi9812064;
RA Jeffrey P.D., Bewley M.C., McGillyray R.T.A., Mason A.B.,
RA Woodworth R.C., Baker E.N.;
RT "Ligand-induced conformational change in transferrins: crystal
structure of the open form of the N-terminal half-molecule of human
transferrin.";
RL Biochemistry 37:13978-13986(1998).
[22]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 23-352.
RX MEDLINE=99155227; PubMed=10029548; DOI=10.1021/bi992454j;
RA Bewley M.C., Tam B.M., Grewal J., He S., Shewty S., Murphy M.E.P.,
RA Mason A.B., Woodworth R.C., Baker E.N., McGillyray R.T.A.;

RT "X-ray crystallography and mass spectroscopy reveal that the N-lobe of human transferrin expressed in *Pichia pastoris* is folded correctly but

Query Match 95.74; Score 110; DB 1; Length 698;

Best Local Similarity 95.74; Pred. No. 3.3e-08; Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTEDSTAKINGEADAMSLDGF 23
 DB 392 STEDCIKAKINGEADAMSLDGF 414

RESULT 2

O7TSX8 PRELIMINARY; PRT; 694 AA.

AC O7TSX8; 01-OCT-2003 (TREMBLrel. 25, Created)

DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)

DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

OS Marmota monax (Woodchuck).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;

OC Marmota.

NCBI_TaxID=9995;

SEQUENCE FROM N.A.

TISSUE=Liver;

Rinaldo J.A.S., Gerin J.L.;

Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Transferrin are iron binding proteins which

bind ferric iron in association with the binding of an anion,

usually bicarbonate (by similarity).

-1- DOMAIN: Composed of two homologous domains (by similarity).

EMBL; AY288100; AAP37129.1; -.

HSSP; P19134; UNF.

GO: GO:0005576; Cytoplasm; IEA.

GO: GO:0008199; F: ferric iron binding; IEA.

GO: GO:0006879; P: iron ion homeostasis; IEA.

GO: GO:0006826; P: iron ion transport; IEA.

GO: GO:0006810; P: iron transport; IEA.

InterPro: IPR001156; Peptidase_S60.

Pfam: PF00405; Transferrin; 2.

SMART; SM00094; TR_FER; 2.

PROSITE; PS00205; TRANSFERRIN_1; 2.

PROSITE; PS00206; TRANSFERRIN_2; 2.

PROSITE; PS00207; TRANSFERRIN_3; 2.

Iron transport; Metal-binding; Transport.

SEQUENCE 694 AA; 76466 MW; 400537DCICFCAB7 CRC64;

Query Match 89.64; Score 103; DB 2; Length 694;

Best Local Similarity 87.04; Pred. No. 4e-07; Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 TTEDSTAKINGEADAMSLDGF 23
 DB 392 STEDCIKAKINGEADAMSLDGF 414

RESULT 3

TRFE_RABIT STANDARD; PRT; 695 AA.

AC P19134; 046514; 01-NOV-1990 (Rel. 16, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal

binding globulin).

GN Name=TF;

Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

SEQUENCE FROM N.A.

TISSUE=Liver;

MDL:MDL=91274362; PubMed=2054387; DOI=10.1016/0167-4781(91)90021-D;

RA Banfield D.K., Chow B.K.-C., Funk W.D., Robertson K.A., Umelaas T.M.,

RA Woodworth R.C., Macgillivray R.T.A.;

RT "The nucleotide sequence of rabbit liver transferrin cDNA.";

RL Biochim. Biophys. Acta 1089:262-265(1991).

SEQUENCE FROM N.A.

STRAIN=New Zealand white;

RA Chareb B.A.A., Thepot D., Puisant C., Cajero-Juarez M.,

RA Houdebine L.M.;

RT "Cloning and structural organisation of the rabbit transferrin encoding

gene.";

RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

SEQUENCE OF 20-51.

MDL:MDL=88209278; PubMed=3365331;

RA Godoyac-Zimmermann J.;

RT "Isolation, characterization and N-terminal amino-acid sequence of

rabbit transferrin.";

RL Biol. Chem. Hoppe-Seyler 369:93-96(1988).

SEQUENCE OF 483-545.

MDL:MDL=89005676; PubMed=3169252; DOI=10.1016/0014-5793(88)80221-7;

RA Evans R.W., Aitken A., Patel K.J.;

RT "Evidence for a single glycan moiety in rabbit serum transferrin and

location of the glycan within the polypeptide chain.";

RL FEBS Lett. 238:39-42(1988).

MDL:MDL=89026775; PubMed=3179277;

RA Bailey S., Evans R.W., Garratt R.C., Gorinsky B., Hasnain S.,

RA Horsburgh C., Jhoti H., Lindley P.F., Mydin A., Sarras R., Watson J.L.;

RT "Molecular structure of serum transferrin at 3.3-A resolution.";

RL Biochemistry 27:5804-5812(1988).

X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).

Sarra R., Garratt R.C., Gorinsky B., Jhoti H., Lindley P.F.;

RT "High-resolution X-ray studies on rabbit serum transferrin:

preliminary structure analysis of the N-terminal half-molecule at 2.3-

A resolution.";

Acta Crystallogr. B 46:763-771(1990).

-1- FUNCTION: Transferrins are iron binding transport proteins which

can bind two atoms of ferric iron in association with the binding

of an anion, usually bicarbonate. It is responsible for the

transport of iron from sites of absorption and heme degradation to

those of storage and utilization. Serum transferrin may also have

a further role in stimulating cell proliferation.

-1- SUBUNIT: Monomer.

-1- SUBCELLULAR LOCATION: Secreted.

-1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.

-1- DOMAIN: Composed of two homologous domains.

-1- SIMILARITY: Belongs to the transferrin family.

This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to license@isb-sib.ch).

EMBL; X58533; CAA1424.1; -.

EMBL; AF031625; AAB94136.1; -.

EMBL; AF031611; AAB94136.1; JOINED.

EMBL; AF031612; AAB94136.1; JOINED.

EMBL; AF031613; AAB94136.1; JOINED.

EMBL; AF031614; AAB94136.1; JOINED.

EMBL; AF031615; AAB94136.1; JOINED.

```

DR EMBL; AF031616; AAB94136.1; JOINED.
DR EMBL; AF031617; AAB94136.1; JOINED.
DR EMBL; AF031618; AAB94136.1; JOINED.
DR EMBL; AF031619; AAB94136.1; JOINED.
DR EMBL; AF031620; AAB94136.1; JOINED.
DR EMBL; AF031621; AAB94136.1; JOINED.
DR EMBL; AF031622; AAB94136.1; JOINED.
DR EMBL; AF031623; AAB94136.1; JOINED.
DR EMBL; AF031624; AAB94136.1; JOINED.
DR PDB; 1JNP; X-ray; A=20-695.
DR PDB; 1TFD; X-ray; @=20-323.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW 3D-structure; Direct protein sequencing; Glycoprotein; Iron transport;
KW Metal-binding; Repeat; Signal; Transport.
FT SIGNAL 1 19
FT CHAIN 20 695
FT REPEAT 20 355
FT REPEAT 356 695
FT DISULFID 28 67
FT DISULFID 38 58
FT DISULFID 137 213
FT DISULFID 156 350
FT DISULFID 177 193
FT DISULFID 180 196
FT DISULFID 180 198
FT DISULFID 246 260
FT DISULFID 358 612
FT DISULFID 364 396
FT DISULFID 374 387
FT DISULFID 421 690
FT DISULFID 436 653
FT DISULFID 468 539
FT DISULFID 492 681
FT DISULFID 502 516
FT DISULFID 513 522
FT DISULFID 579 593
FT DISULFID 631 636
FT CARBOHYD 509 509
FT METAL 82 82
FT METAL 114 114
FT METAL 207 207
FT METAL 268 268
FT METAL 411 411
FT METAL 444 444
FT METAL 533 533
FT METAL 601 601
FT BINDING 139 139
FT BINDING 143 143
FT BINDING 145 145
FT BINDING 146 146
FT BINDING 470 470
FT BINDING 474 474
FT BINDING 476 476
FT BINDING 477 477
FT VARIANT 517 517
FT CONFLICT 7 7
FT CONFLICT 47 47
FT CONFLICT 50 50
FT STRAND 24 30
FT HELIX 31 48
FT TURN 51 52
FT STRAND 55 61
FT HELIX 64 72
FT TURN 73 74
FT STRAND 78 81
FT HELIX 83 90
FT TURN 92 94

```

```

FT STRAND 96 104
FT STRAND 111 111
FT STRAND 113 121
FT TURN 122 123
FT TURN 128 130
FT TURN 132 133
FT STRAND 136 138
FT TURN 141 142
FT TURN 144 147
FT HELIX 148 154
FT HELIX 155 157
FT HELIX 165 172
FT STRAND 176 177
FT TURN 179 180
FT TURN 183 185
FT TURN 187 190
FT HELIX 191 192
FT TURN 194 195
FT TURN 200 201
FT TURN 203 204
FT HELIX 206 215
FT TURN 216 217
FT STRAND 221 225
FT TURN 226 227
FT HELIX 228 232
FT HELIX 236 239
FT TURN 240 241
FT STRAND 242 245
FT TURN 247 248
FT STRAND 251 253
FT HELIX 254 256
FT TURN 257 258
FT STRAND 263 266
FT STRAND 269 273
FT HELIX 279 293
FT TURN 303 304
FT TURN 307 308
FT TURN 316 317
FT STRAND 320 323
FT TURN 326 327
FT HELIX 330 334
FT HELIX 336 346
FT TURN 347 348

Query Match 87.8%; Score 101; DB 1; Length 695;
Best Local Similarity 87.0%; Pred. No. 8.2e-07;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADMSLDGGE 23
Db 392 TPEDCIKIMNGEADMSLDGGE 414

RESULT 4
ID TRPE HORSE STANDARD; PRT; 706 AA.
AC P27425;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serotransferrin precursor (Transferrin) (Siderophilin) (beta-1-metal
DE binding globulin).
DE Name=TF;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OC NCB1_taxid=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93277958; PubMed=8504171; DOI=10.1016/0167-4781(93)90186-H;
RA "The cDNA sequence of horse transferrin.";
RT Biochim. Biophys. Acta 1173:230-232(1993).
RL

```

```

RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic tissue;
RA McDowell K.J., Adams M.H., Baker C.B.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrin are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate. It is responsible for the
CC transport of iron from sites of absorption and heme degradation to
CC those of storage and utilization. Serum transferrin may also have
CC a further role in stimulating cell proliferation.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M69020: AAA30958.1; -.
DR EMBL: U21127: AAA63684.1; -.
DR PIR: S33761; S33761.
DR HSSP: P02787; 1A8E.
DR InterPro: IPR001156; Peptidase_S60.
DR Pfam: PF00405; Transferrin_2.
DR PRINTS: PR00422; TRANSFERRIN.
DR SMART: SM00094; TR_PER_2.
DR PROSITE: PS00205; TRANSFERRIN_1; 2.
DR PROSITE: PS00206; TRANSFERRIN_2; 2.
DR PROSITE: PS00207; TRANSFERRIN_3; 2.
DR GlycoProtein: Iron transport; Metal-binding; Repeat; Signal;
KW Transport.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 706 Serotransferrin.
FT REPEAT 20 357 1.
FT REPEAT 358 706 2.
FT DISULFID 26 64 By similarity.
FT DISULFID 36 55 By similarity.
FT DISULFID 134 215 By similarity.
FT DISULFID 174 190 By similarity.
FT DISULFID 177 198 By similarity.
FT DISULFID 187 200 By similarity.
FT DISULFID 248 262 By similarity.
FT DISULFID 360 623 By similarity.
FT DISULFID 366 398 By similarity.
FT DISULFID 376 389 By similarity.
FT DISULFID 423 701 By similarity.
FT DISULFID 441 664 By similarity.
FT DISULFID 474 550 By similarity.
FT DISULFID 498 692 By similarity.
FT DISULFID 508 522 By similarity.
FT DISULFID 519 533 By similarity.
FT DISULFID 590 604 By similarity.
FT DISULFID 642 647 By similarity.
FT METAL 79 79 Iron 1 (By similarity).
FT METAL 111 111 Iron 1 (By similarity).
FT METAL 209 209 Iron 1 (By similarity).
FT METAL 270 270 Iron 1 (By similarity).
FT METAL 413 413 Iron 2 (By similarity).
FT METAL 449 449 Iron 2 (By similarity).
FT METAL 544 544 Iron 2 (By similarity).
FT METAL 612 612 Iron 2 (By similarity).
FT BINDING 136 136 Carbonate 1 (By similarity).
FT BINDING 140 140 Carbonate 1 (By similarity).
FT BINDING 142 142 Carbonate 1 (By similarity).
FT BINDING 143 143 Carbonate 1 (via amide nitrogen) (By

```

```

FT BINDING 476 476 similarity).
FT BINDING 480 480 Carbonate 2 (By similarity).
FT BINDING 482 482 Carbonate 2 (By similarity).
FT BINDING 483 483 Carbonate 2 (via amide nitrogen) (By
FT BINDING 483 483 similarity).
FT CARBOHYD 515 515 Carbonate 2 (via amide nitrogen) (By
FT SEQUENCE 706 AA, 78094 MW, 1A0FAS6C0409DBA CRC64;
SQ
Query Match 83.5%; Score 96; DB 1; Length 706;
Best Local Similarity 82.6%; Pred. No. 5e-06;
Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 TTEDSIATKIMGADAMSIDGCF 23
Db 394 STEDCIATKIVGADAMSIDGCF 416
:|||||:|||||:
RESULT 5
ID TRFE_PIG STANDARD; PRT; 696 AA.
AC P09571;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serotransferrin (Transferrin) (Siderophilin) (Beta-1-metal binding
DE globulin).
GN Name=TF;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sui.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=8835629; Pubmed=3419934;
RA Baldwin G.S., Weinstein J.;
RL Nucleic Acids Res. 16:8720-8720(1988).
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate. It is responsible for the
CC transport of iron from sites of absorption and heme degradation to
CC those of storage and utilization. Serum transferrin may also have
CC a further role in stimulating cell proliferation.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X12386: CAA30943.1; -.
DR PIR: S01384; S01384.
DR PDB: 1H76; X-ray; A=1-696.
DR InterPro: IPR001156; Peptidase_S60.
DR Pfam: PF00405; Transferrin_2.
DR PRINTS: PR00422; TRANSFERRIN.
DR SMART: SM00094; TR_PER_2.
DR PROSITE: PS00205; TRANSFERRIN_1; 2.
DR PROSITE: PS00206; TRANSFERRIN_2.
DR PROSITE: PS00207; TRANSFERRIN_3; 2.
KW 3D-structure; Glycoprotein; Iron transport; Metal-binding; Repeat;
KW Transport.
FT REPEAT 1 340 1.

```

FT	REPEAT	341	696	2.
FT	DISULFID	9	47	By similarity.
FT	DISULFID	19	38	By similarity.
FT	DISULFID	117	198	By similarity.
FT	DISULFID	157	173	By similarity.
FT	DISULFID	160	181	By similarity.
FT	DISULFID	170	183	By similarity.
FT	DISULFID	231	245	By similarity.
FT	DISULFID	343	605	By similarity.
FT	DISULFID	349	381	By similarity.
FT	DISULFID	359	372	By similarity.
FT	DISULFID	406	682	By similarity.
FT	DISULFID	423	646	By similarity.
FT	DISULFID	456	532	By similarity.
FT	DISULFID	480	673	By similarity.
FT	DISULFID	490	504	By similarity.
FT	DISULFID	501	515	By similarity.
FT	DISULFID	572	586	By similarity.
FT	DISULFID	624	629	By similarity.
FT	METAL	62	62	Iron 1 (By similarity).
FT	METAL	94	94	Iron 1 (By similarity).
FT	METAL	192	192	Iron 1 (By similarity).
FT	METAL	253	253	Iron 1 (By similarity).
FT	METAL	396	336	Iron 2 (By similarity).
FT	METAL	431	431	Iron 2 (By similarity).
FT	METAL	526	526	Iron 2 (By similarity).
FT	METAL	594	594	Iron 2 (By similarity).
FT	BINDING	119	119	Carbonate 1 (By similarity).
FT	BINDING	123	123	Carbonate 1 (By similarity).
FT	BINDING	125	125	Carbonate 1 (via amide nitrogen) (By similarity).
FT	BINDING	126	126	Carbonate 1 (via amide nitrogen) (By similarity).
FT	BINDING	458	458	Carbonate 2 (By similarity).
FT	BINDING	462	462	Carbonate 2 (By similarity).
FT	BINDING	464	464	Carbonate 2 (via amide nitrogen) (By similarity).
FT	BINDING	465	465	Carbonate 2 (via amide nitrogen) (By similarity).
FT	CARBOHYD	25	25	N-linked (GlcNAc. . .) (Potential).
FT	CARBOHYD	497	497	N-linked (GlcNAc. . .) (Potential).
FT	VARIANT	308	308	K -> R.
FT	STRAND	5	10	
FT	HELIX	13	29	
FT	STRAND	35	40	
FT	HELIX	44	52	
FT	TURN	53	54	
FT	STRAND	58	61	
FT	HELIX	63	69	
FT	TURN	70	70	
FT	TURN	72	74	
FT	STRAND	76	84	
FT	TURN	87	88	
FT	STRAND	91	91	
FT	STRAND	93	101	
FT	TURN	102	103	
FT	HELIX	108	110	
FT	TURN	112	113	
FT	STRAND	115	118	
FT	TURN	121	122	
FT	TURN	124	127	
FT	HELIX	128	134	
FT	HELIX	135	137	
FT	HELIX	145	152	
FT	STRAND	155	157	
FT	TURN	159	160	
FT	TURN	163	165	
FT	HELIX	167	170	
FT	TURN	171	172	
FT	HELIX	177	179	
FT	TURN	180	181	
FT	TURN	185	186	
FT	TURN	188	189	

FT	HELIX	191	200	
FT	TURN	201	202	
FT	STRAND	206	210	
FT	TURN	211	212	
FT	HELIX	213	217	
FT	STRAND	224	226	
FT	TURN	227	230	
FT	STRAND	232	233	
FT	STRAND	236	238	
FT	HELIX	239	244	
FT	STRAND	248	251	
FT	STRAND	254	258	
FT	HELIX	264	278	
FT	TURN	280	281	
FT	TURN	288	289	
FT	TURN	292	293	
FT	TURN	301	302	
FT	STRAND	305	308	
FT	TURN	311	312	
FT	HELIX	315	319	
FT	STRAND	321	331	
FT	HELIX	346	351	
FT	HELIX	352	365	
FT	TURN	366	368	
FT	STRAND	370	375	
FT	HELIX	378	387	
FT	TURN	388	388	
FT	STRAND	392	395	
FT	HELIX	397	405	
FT	TURN	406	407	
FT	STRAND	409	415	
FT	TURN	421	422	
FT	HELIX	423	425	
FT	STRAND	431	438	
FT	TURN	439	440	
FT	TURN	443	444	
FT	HELIX	447	449	
FT	TURN	451	452	
FT	STRAND	455	457	
FT	TURN	460	461	
FT	TURN	463	466	
FT	HELIX	467	477	
FT	HELIX	482	485	
FT	STRAND	490	490	
FT	TURN	492	493	
FT	TURN	496	497	
FT	HELIX	499	501	
FT	TURN	502	503	
FT	TURN	511	512	
FT	TURN	514	515	
FT	TURN	519	520	
FT	TURN	522	523	
FT	HELIX	525	535	
FT	TURN	536	536	
FT	STRAND	539	543	
FT	TURN	544	545	
FT	HELIX	546	549	
FT	TURN	550	550	
FT	TURN	552	553	
FT	TURN	558	562	
FT	HELIX	565	567	
FT	STRAND	568	571	
FT	TURN	573	574	
FT	STRAND	577	579	
FT	HELIX	580	585	
FT	STRAND	589	591	
FT	STRAND	595	598	
FT	HELIX	600	602	
FT	HELIX	603	617	
FT	TURN	619	620	
FT	STRAND	624	624	
FT	TURN	625	626	
FT	STRAND	627	627	

FT TURN 630 631
FT TURN 642 643

Query Match 80.0%; Score 92; DB 1; Length 696;
Best Local Similarity 81.8%; Pred. No. 2.1e-05;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

2 TEDSIKINGEDAMSLDGGF 23
378 TEDCIATKIVGADAMSLDGGY 399

RESULT 6
TREF_MOUSE STANDARD; PRT; 697 AA.
ID TREF_MOUSE
AC Q92111; Q35421; Q61803; Q62358; Q62359; Q63915; Q64515; Q8VIT5;
AC Q92200;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Sero transferrin precursor (transferrin) (Siderophilin) (Beta-1-metal
binding globulin).
GN Name=Trf; Synonyms=Trf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NBI Taxid=10090;
NCBI [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RA Lai D.-Z.;
RT "Construction of a robust CHO cell-line for biopharmaceutical
production."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Mammary gland;
RX MEDLINE=22354683; PubMed=1246685; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nakado I., Osato N., Saito R., Suzuki H., Yamana H., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gotohori T.,
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirral L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brucic V., Chochia C., Corradi L.E., Cousins S.,
RA Dalia E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimsmond S., Guellinich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedziercki R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglocz D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wyntshaw-Boris A., Yanagisawa M., Yang L., Yang L.,
RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirocane-Chikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki J., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=22386257; PubMed=12477933; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenman C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loguellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., McKernan K.J., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman A., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smalins D.E.,
RA Scherch A., Schein U.E., Jones S.U.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
RP SEQUENCE OF 1-11 FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=98284323; PubMed=9621303;
RX DOI=10.1002/(SICI)1098-2795(199807)50:3<273::AID-MRD3>3.3.CO;2-C;
RA Chaudhary J., Skinner M.K.;
RT "Comparative sequence analysis of the mouse and human transferrin
RT promoters: hormonal regulation of the transferrin promoter in Sertoli
RT cells."
RL Mol. Reprod. Dev. 50:273-283(1998).
RN [5]
RP SEQUENCE OF 277-337; 462-496 AND 526-575 FROM N.A.
RX MEDLINE=8086992; PubMed=3693348;
RA Chen L.-H., Bissell M.J.;
RT "Transferrin mRNA level in the mouse mammary gland is regulated by
RT pregnancy and extracellular matrix."
RL J. Biol. Chem. 262:17247-17250(1987).
RN [6]
RP SEQUENCE OF 268-307 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94068311; PubMed=8248032;
RA Kasik J.W., Rice E.J.;
RT "Transferrin gene expression in maternal liver, fetal liver and
RT placenta during pregnancy in the mouse."
RL Placenta 14:365-371(1993).
RN [7]
RP SEQUENCE OF 282-412 FROM N.A.
RX MEDLINE=87280033; PubMed=611056;
RA Panteos B.T., Teng C.T.;
RT "Transferrin is the major estrogen inducible protein of mouse
RT uterine secretions."
RL J. Biol. Chem. 262:10134-10139(1987).
CC - FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate. It is responsible for the
CC transport of iron from sites of absorption and heme degradation to
CC those of storage and utilization. Serum transferrin may also have
CC a further role in stimulating cell proliferation.
CC - SUBUNIT: Monomer.
CC - SUBCELLULAR LOCATION: Secreted.
CC - TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC - DOMAIN: Composed of two homologous domains.
CC - SIMILARITY: Belongs to the transferrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF440692; AA134533.1; -
DR EMBL; AK085754; BAC39532.1; -
DR EMBL; BC012313; AA112313.1; -

```

DR EMBL, BC022986; AAH22986.1; -.
DR EMBL, BC008559; AAH08559.1; -.
DR EMBL, AF027336; AAB84034.1; -.
DR EMBL, M23014; AAA40489.1; -.
DR EMBL, M23015; AAA40490.1; -.
DR EMBL, M23016; AAA40491.1; -.
DR EMBL, S67217; AAB28966.2; -.
DR EMBL, J03299; AAA39438.1; -.
DR PIR, A28446; A28446.
DR MGD; MGI:96821; Tf.
DR GO; GO:0030139; C:cytochrome vesicle; IDA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Glycoprotein; Iron transport; Metal-binding; Repeat; signal;
transport.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 697 Serotransferrin.
FT REPEAT 20 355 1.
FT REPEAT 356 697 2.
FT DISULFID 28 67 By similarity.
FT DISULFID 38 58 By similarity.
FT DISULFID 137 213 By similarity.
FT DISULFID 156 350 By similarity.
FT DISULFID 177 193 By similarity.
FT DISULFID 180 196 By similarity.
FT DISULFID 190 198 By similarity.
FT DISULFID 246 260 By similarity.
FT DISULFID 363 395 By similarity.
FT DISULFID 373 386 By similarity.
FT DISULFID 420 692 By similarity.
FT DISULFID 435 655 By similarity.
FT DISULFID 472 543 By similarity.
FT DISULFID 496 683 By similarity.
FT DISULFID 506 520 By similarity.
FT DISULFID 517 526 By similarity.
FT DISULFID 583 597 By similarity.
FT DISULFID 633 638 By similarity.
FT METAL 82 82 Iron 1 (By similarity).
FT METAL 114 114 Iron 1 (By similarity).
FT METAL 207 207 Iron 1 (By similarity).
FT METAL 268 268 Iron 1 (By similarity).
FT METAL 410 410 Iron 2 (By similarity).
FT METAL 448 448 Iron 2 (By similarity).
FT METAL 537 537 Iron 2 (By similarity).
FT METAL 605 605 Iron 2 (By similarity).
FT BINDING 139 139 Carbonate 1 (By similarity).
FT BINDING 143 143 Carbonate 1 (via amide nitrogen) (By similarity).
FT BINDING 145 145 Carbonate 1 (via amide nitrogen) (By similarity).
FT BINDING 146 146 Carbonate 1 (via amide nitrogen) (By similarity).
FT BINDING 474 474 Carbonate 2 (By similarity).
FT BINDING 478 478 Carbonate 2 (By similarity).
FT BINDING 480 480 Carbonate 2 (via amide nitrogen) (By similarity).
FT BINDING 481 481 Carbonate 2 (via amide nitrogen) (By similarity).
FT BINDING 481 481 Carbonate 2 (via amide nitrogen) (By similarity).
FT CARBOHYD 513 513 N-linked (GlcNAc...) (Potential).
FT CONFLICT 3 4 LT -> FA (in Ref. 1).
FT CONFLICT 71 74 ISAS -> HASG (in Ref. 3; AAH08559).
FT CONFLICT 283 283 W -> L (in Ref. 6).
FT CONFLICT 307 307 P -> L (in Ref. 6).
FT CONFLICT 350 351 CP -> SA (in Ref. 7).
FT CONFLICT 487 487 G -> C (in Ref. 5).
Query Match 80.0%; Score 92; DB 1; Length 697;
Best Local Similarity 81.8%; Pred. No. 2; e-05;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

Oy 1 TTEDSIKINGEADAMSLDGG 22
Db 391 TTEDCIEKIVNGEADAMTLDDGG 412

RESULT 7
TFE BOVIN STANDARD; PRT; 704 AA.
ID TRFE BOVIN
AC 029443;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Serotransferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal
binding globulin).
GN Name:TF;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
OX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=96132861; PubMed=8557646; DOI=10.1074/jbc.271.2.1166;
RA Retzer M.D., Kabani A., Button L.J., Yu R.H., Schryvers A.B.;
RT "Production and characterization of chimeric transferrins for the
determination of the binding domains for bacterial transferrin
receptors.";
RL J. Biol. Chem. 271:1166-1173 (1996).
CC -!- FUNCTION: Transferrins are iron binding transport proteins which
can bind two atoms of ferric iron in association with the binding
of an anion, usually bicarbonate. It is responsible for the
transport of iron from sites of absorption and heme degradation to
those of storage and utilization. Serum transferrin may also have
a further role in stimulating cell proliferation.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -!- DOMAIN: Composed of two homologous domains.
CC -!- SIMILARITY: Belongs to the transferrin family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
DR EMBL, U02564; AAA96735.1; -.
DR HSSP; P09571; 1H76.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KW Glycoprotein; Iron transport; Metal-binding; Repeat; Signal;
transport.
FT SIGNAL 1 19 By similarity.
FT CHAIN 20 704 Serotransferrin.
FT REPEAT 20 359 1.
FT REPEAT 360 704 2.
FT DISULFID 28 66 By similarity.
FT DISULFID 38 57 By similarity.
FT DISULFID 136 217 By similarity.
FT DISULFID 176 192 By similarity.
FT DISULFID 179 200 By similarity.
FT DISULFID 189 202 By similarity.
FT DISULFID 250 264 By similarity.
FT DISULFID 362 622 By similarity.
FT DISULFID 367 399 By similarity.

```

```

FT DISULFID 377 390 By similarity.
FT DISULFID 424 699 By similarity.
FT DISULFID 441 663 By similarity.
FT DISULFID 473 549 By similarity.
FT DISULFID 497 690 By similarity.
FT DISULFID 507 521 By similarity.
FT DISULFID 518 532 By similarity.
FT DISULFID 589 603 By similarity.
FT DISULFID 641 646 By similarity.
FT METAL 81 81 Iron 1 (By similarity).
FT METAL 113 113 Iron 1 (By similarity).
FT METAL 211 211 Iron 1 (By similarity).
FT METAL 272 272 Iron 1 (By similarity).
FT METAL 414 414 Iron 2 (By similarity).
FT METAL 449 449 Iron 2 (By similarity).
FT METAL 543 543 Iron 2 (By similarity).
FT METAL 611 611 Iron 2 (By similarity).
FT BINDING 138 138 Carbonate 1 (By similarity).
FT BINDING 142 142 Carbonate 1 (By similarity).
FT BINDING 144 144 Carbonate 1 (via amide nitrogen) (By similarity).
FT BINDING 145 145 Carbonate 1 (via amide nitrogen) (By similarity).
FT BINDING 475 475 Carbonate 2 (By similarity).
FT BINDING 479 479 Carbonate 2 (By similarity).
FT BINDING 481 481 Carbonate 2 (via amide nitrogen) (By similarity).
FT BINDING 482 482 Carbonate 2 (via amide nitrogen) (By similarity).
FT CARBOHYD 514 514 N-linked (GlcNAc...) (Potential).
FT SEQUENCE 704 AA; 77753 MW; D87BB2AF6C708D CRC64;

```

```

Query Match 80.0%; Score 92; DB 1; Length 704;
Best Local Similarity 81.8%; Pred. No. 2; Le-05;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Db 2 TEDSIKINGEADAMSIDGCF 23
396 TEECIKINGEADAMSIDGCF 417

```

```

RESULT 8
TRFL_PIG STANDARD; PRT; 704 AA.
AC P14632; 029557;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lactoferrin precursor (Lactoferrin).
GN Name-LTF.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OC NCBI_TaxID=9823;
RX MEDLINE=92379101; PubMed=1511016; DOI=10.1016/0167-4781(92)90061-4;
RA Conneely O.M.;
RL "Nucleotide and primary amino acid sequence of porcine lactoferrin.";
RL Biochim. Biophys. Acta 1132:97-99(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92367939; PubMed=1503259;
RA Alexander L.J.; Levine W.B.; Teng C.T.; Beattie C.W.;
RT "Cloning and sequencing of the porcine lactoferrin cDNA.";
RL Anim. Genet. 23:251-256(1992).
RN [3]
RP SEQUENCE OF 20-49.
RX MEDLINE=90105538; PubMed=2605266;
RA Hutcheon T.W.; Magnuson J.S.; Yip T.-T.;
RT "Rapid purification of porcine colostrum whey lactoferrin by affinity
chromatography on single-stranded DNA-agarose. Characterization, amino

```

```

RT acid composition and N-terminal amino acid sequence.";
RL Biochim. Biophys. Acta 999:323-329(1989).
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding
CC of an anion, usually bicarbonate.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M92089; AAA31102.1; -;
DR EMBL; M91327; AAA31059.1; -;
DR PIR; A45543; A45543.
DR HSSP; Q9TUM0; 1DTZ.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin_2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER_2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KM Direct protein sequencing; Glycoprotein; Iron transport;
KM Metal-binding; Repeat; Signal; Transport.
FT STGNAL 1 19
FT CHAIN 20 704
FT REPEAT 20 359
FT REPEAT 360 704
FT DISULFID 28 62 By similarity.
FT DISULFID 38 53 By similarity.
FT DISULFID 130 213 By similarity.
FT DISULFID 172 188 By similarity.
FT DISULFID 185 196 By similarity.
FT DISULFID 246 260 By similarity.
FT DISULFID 363 395 By similarity.
FT DISULFID 373 386 By similarity.
FT DISULFID 420 699 By similarity.
FT DISULFID 472 547 By similarity.
FT DISULFID 496 690 By similarity.
FT DISULFID 506 520 By similarity.
FT DISULFID 517 530 By similarity.
FT DISULFID 588 602 By similarity.
FT DISULFID 640 645 By similarity.
FT METAL 77 77 Iron 1 (By similarity).
FT METAL 107 107 Iron 1 (By similarity).
FT METAL 207 207 Iron 1 (By similarity).
FT METAL 268 268 Iron 1 (By similarity).
FT METAL 410 410 Iron 2 (By similarity).
FT METAL 448 448 Iron 2 (By similarity).
FT METAL 541 541 Iron 2 (By similarity).
FT METAL 610 610 Iron 2 (By similarity).
FT BINDING 132 132 Carbonate 1 (By similarity).
FT BINDING 136 136 Carbonate 1 (By similarity).
FT BINDING 138 138 Carbonate 1 (via amide nitrogen) (By similarity).
FT BINDING 139 139 Carbonate 1 (via amide nitrogen) (By similarity).
FT BINDING 474 474 Carbonate 2 (By similarity).
FT BINDING 478 478 Carbonate 2 (By similarity).
FT BINDING 480 480 Carbonate 2 (via amide nitrogen) (By similarity).
FT BINDING 481 481 Carbonate 2 (via amide nitrogen) (By similarity).
FT CARBOHYD 385 385 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 491 491 N-linked (GlcNAc...) (Potential).
FT CONFLICT 12 12 G -> W (in Ref. 1).

```

```

FT CONFLICT 46 48 RRT -> TTR (in Ref. 3).
FT CONFLICT 51 51 M -> I (in Ref. 1).
FT CONFLICT 85 85 D -> G (in Ref. 1).
FT CONFLICT 121 121 Missing (in Ref. 2).
FT CONFLICT 132 132 T -> I (in Ref. 1).
FT CONFLICT 284 284 E -> S (in Ref. 1).
FT CONFLICT 573 573 E -> Q (in Ref. 1).
FT CONFLICT 590 590 D -> N (in Ref. 1).
FT CONFLICT 625 625 V -> M (in Ref. 1).
FT CONFLICT 662 662 V -> C (in Ref. 1).
FT CONFLICT 704 704 NUKCSVSPLEKCAFMWR -> T (in Ref. 1).
SQ SEQUENCE 704 AA; 77625 MW; 93261EPD608AD358 CRC64;

Query Match
Best Local Similarity 73.9%; Score 92; DB 1; Length 704;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKIMGEADAMSJDGF 23
DB 391 TTEDCIVQVLKGEADAMSJDGF 413

RESULT 9
Q8WMN8 PRELIMINARY; PRT; 704 AA.
AC Q8WMN8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lactoferrin (Fragment).
GN Name=LTF;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Wang S.-R., Lin T.-Y., Weng C.-N.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL; L77887; AAL40161.1; -.
DR HSSP; P24627; INKX.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
DR Iron transport; Metal-binding; Transport.
KW NON_TER
FT CONFLICT 686 704
SQ SEQUENCE 704 AA; 77681 MW; 64EB769F7503CC32 CRC64;

Query Match
Best Local Similarity 80.0%; Score 92; DB 2; Length 704;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKIMGEADAMSJDGF 23
DB 391 TTEDCIVQVLKGEADAMSJDGF 413

RESULT 10
Q6Y739 PRELIMINARY; PRT; 704 AA.
AC Q6Y739;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Lactotransferrin.
GN Name=LTF;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RN SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL; AP06185; BAD08651.1; -.
DR HSSP; Q29477; LUTL.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
DR Iron transport; Metal-binding; Transport.
KW
SQ SEQUENCE 704 AA; 77611 MW; 10DFEA3C136D5DA CRC64;

Query Match
Best Local Similarity 80.0%; Score 92; DB 2; Length 704;
Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTEDSIKIMGEADAMSJDGF 23
DB 391 TTEDCIVQVLKGEADAMSJDGF 413

RESULT 11
Q7YS20 PRELIMINARY; PRT; 704 AA.
AC Q7YS20;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Lactoferrin.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Pecorini C., Fogher C., Baldi A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL; AY306198; AAP70487.1; -.
DR HSSP; P24627; INKX.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.

```

DR GO: GO:0006826; P:iron ion transport; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR Interpro: IPR001156; Peptidase_S60.
 DR Pfam: PF00405; transferrin; 2.
 DR SMART: SM00094; TR_FER; 2.
 DR PROSITE: PS00205; TRANSFERRIN_1; 2.
 DR PROSITE: PS00206; TRANSFERRIN_2; 1.
 DR PROSITE: PS00207; TRANSFERRIN_3; 1.
 DR Itron transport; Metal-binding; transport.
 KW SEQUENCE 704 AA; 77522 MW; AAC8B1767E56BFEA CRC64;
 SQ
 Query Match 80.0%; Score 92; DB 2; Length 704;
 Best Local Similarity 73.9%; Pred. No. 2; 1e-05;
 Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 TTEDSIKINNGEADAMSLDGGF 23
 Db 391 TTEDCIYQVLKGEADAMSLDGGF 413
 RESULT 12
 TRFE_RAT STANDARD; PRF; 698 AA.
 AC P12346; Q63602; Q64628; Q64630;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 15-JUN-1999 (Rel. 38, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE Sero transferrin precursor (transferrin) (Siderophilin) (Beta-1-metal
 binding globulin).
 DE Name=Trf;
 GN Rattus norvegicus (Rat).
 OS Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=Mistar; TISSUE=Mammary gland;
 RX MEDLINE=95234054; PubMed=7717992;
 RA Berriva H., Pierce A., Codderville B., Gonzalez F., Benaisa M.,
 Leiger D., Wernuszeki J.M., Spik G., Pambianco M.;
 RT "rat mammary-gland transferrin: nucleotide sequence, phylogenetic
 RT analysis and glycan structure.";
 RL Biochem. J. 307:47-55(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=Mistar; TISSUE=Liver;
 RX MEDLINE=96208933; PubMed=8829802; DOI=10.1016/0305-0491(95)02068-3;
 RA Hosino A., Hisayasu S., Shimada T.;
 RT "Complete sequence analysis of rat transferrin and expression of
 RT transferrin but not lactoferrin in the digestive glands.";
 RL Comp. Biochem. Physiol. 113B:491-497(1996).
 RN [3]
 RP SEQUENCE OF 7-295 FROM N.A. (ISOFORM 2).
 RX MEDLINE=84307580; PubMed=6236811;
 RA Aldred A.R., Howlett G.J., Schreiber G.;
 RT "Synthesis of rat transferrin in Escherichia coli containing a
 RT recombinant bacteriophage.";
 RL Biochem. Biophys. Res. Commun. 122:960-965(1984).
 RN [4]
 RP SEQUENCE OF 521-698 FROM N.A.
 RX MEDLINE=87053639; PubMed=3023031;
 RA Huggenvik J.I., Idzerda R.L., Haywood L., Lee D.C., McKnight G.S.,
 Grissold M.D.;
 RT "Transferrin messenger ribonucleic acid: molecular cloning and
 RT hormonal regulation in rat Sertoli cells.";
 RL Endocrinology 120:332-340(1987).
 RN [5]
 RP SEQUENCE OF 20-47.
 RX MEDLINE=80049855; PubMed=500689;
 RA Schreiber G., Dryburgh H., Millership A., Matsuda Y., Inglis A.,
 Phillips J., Edwards K., Mages J.;
 RT "The synthesis and secretion of rat transferrin.";
 RL J. Biol. Chem. 254:12013-12019(1979).

RN [6]
 RP SEQUENCE OF 20-30 AND 642-653.
 RX PubMed=3046655;
 RA Pirves L.R., Purves M., Linton N., Brandt W., Johnson G., Jacobs P.;
 RT "Properties of the transferrin associated with rat intestinal
 RT mucosa.";
 RL Biochim. Biophys. Acta 966:318-327(1988).
 RN [7]
 RP SEQUENCE OF 89-102, 232-243 AND 404-411.
 RX PubMed=1791188;
 RA Cavanaugh P.G., Nicolson G.L.;
 RT "Lung-derived growth factor that stimulates the growth of lung-
 RT metastasizing tumor cells: identification as transferrin.";
 RL J. Cell. Biochem. 47:261-271(1991).
 CC -1- FUNCTION: Transferrin are iron binding transport proteins which
 CC can bind two atoms of ferric iron in association with the binding
 CC of an anion, usually bicarbonate. It is responsible for the
 CC transport of iron from sites of absorption and heme degradation to
 CC those of storage and utilization. Serum transferrin may also have
 CC a further role in stimulating cell proliferation.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P12346-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P12346-2; Sequence=VSP_011840;
 CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>
 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL: X77158; CA54403.1; -;
 DR EMBL: D38380; BAA07458.1; -;
 DR EMBL: M26113; AAA42266.1; -;
 DR EMBL: M27966; AAA42267.1; -;
 DR PIR: S49163; S49163.
 DR HSSP: P19134; ITFD.
 DR GlycoSuiteDB: P12346; -;
 DR InterPro: IPR001156; Peptidase_S60.
 DR Pfam: PF00405; Transferrin; 2.
 DR PRINTS: PR00422; TRANSFERRIN.
 DR SMART: SM00094; TR_FER; 2.
 DR PROSITE: PS00205; TRANSFERRIN_1; 1.
 DR PROSITE: PS00206; TRANSFERRIN_2; 2.
 DR PROSITE: PS00207; TRANSFERRIN_3; 2.
 KW Alternative splicing; Direct protein sequencing; Glycoprotein;
 KW Itron transport; Metal-binding; Repeat; Signal; Transport.
 FT SIGNAL 1 19
 FT CHAIN 20 698 Serotransferrin.
 FT REPEAT 20 355 1.
 FT REPEAT 356 698 2.
 FT DISULFID 28 67 By similarity.
 FT DISULFID 38 58 By similarity.
 FT DISULFID 137 213 By similarity.
 FT DISULFID 156 350 By similarity.
 FT DISULFID 177 193 By similarity.
 FT DISULFID 180 196 By similarity.
 FT DISULFID 190 198 By similarity.
 FT DISULFID 246 260 By similarity.
 FT DISULFID 363 395 By similarity.
 FT DISULFID 373 386 By similarity.
 FT DISULFID 420 693 By similarity.
 FT DISULFID 435 656 By similarity.
 FT DISULFID 471 542 By similarity.

```

FT DISULFID 495 684 By similarity.
FT DISULFID 505 519 By similarity.
FT DISULFID 516 525 By similarity.
FT DISULFID 582 586 By similarity.
FT DISULFID 634 639 By similarity.
FT METAL 82 82 Iron 1 (By similarity).
FT METAL 114 114 Iron 1 (By similarity).
FT METAL 207 207 Iron 1 (By similarity).
FT METAL 268 268 Iron 1 (By similarity).
FT METAL 410 410 Iron 2 (By similarity).
FT METAL 447 447 Iron 2 (By similarity).
FT METAL 536 536 Iron 2 (By similarity).
FT METAL 604 604 Iron 2 (By similarity).
FT BINDING 139 139 Carbonate 1 (By similarity).
FT BINDING 143 143 Carbonate 1 (By similarity).
FT BINDING 145 145 Carbonate 1 (via amide nitrogen) (By
FT BINDING 146 146 Carbonate 1 (via amide nitrogen) (By
FT BINDING 473 473 Carbonate 2 (By similarity).
FT BINDING 477 477 Carbonate 2 (By similarity).
FT BINDING 479 479 Carbonate 2 (via amide nitrogen) (By
FT BINDING 480 480 Carbonate 2 (via amide nitrogen) (By
FT CARBOHYD 512 512 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 65 266 Missing (in isoform 2).
FT CONFLICT 57 57 /Prid=VSP_011840.
FT CONFLICT 110 110 A -> R (in Ref. 1).
FT CONFLICT 318 354 P -> R (in Ref. 1).
FT CONFLICT 380 380 AFCCYCVPPRMDELRLVGHSYVTAIRNREGVCPEAS ->
FT CONFLICT 691 691 RFLRLRAPKDGLOAVRPOLCHCHSKSGSCPD (in
FT CONFLICT 696 697 Ref. 1).
FT CONFLICT 698 AA; 76363 MW; DDFC2C1918E2A1B0E CRC64;
SQ SEQUENCE

Query Match 78.3%; Score 90; DB 1; Length 698;
Best Local Similarity 81.8%; Pred. No. 4.3e-05;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADAMSIDGG 22
Db 391 STEDCIDKIVNGEADAMSIDGG 412

RESULT 13
Q7TNX0 PRELIMINARY; PRT; 698 AA.
AC Q7TNX0;
DT 01-OCT-2003 (TRENBLREL. 25, Created)
DT 01-OCT-2003 (TRENBLREL. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLREL. 26, Last annotation update)
DE Liver regeneration-related protein LRRG03.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu C.S., Li W.Q., Li Y.C., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
RA Yang K.J., Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F.,
RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL; AY327504; AAP97736.1; -.
DR HSP; P02787; IBP5.
DR GO; GO:0005576; C:extracellular; IEA.

```

```

DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006825; P:iron ion transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin_2.
DR SMART; SM00094; TR_FER_2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Iron transport; Metal-binding; Transport.
SQ SEQUENCE 698 AA; 76395 MW; B91AB841CA447194 CRC64;

Query Match 78.3%; Score 90; DB 2; Length 698;
Best Local Similarity 81.8%; Pred. No. 4.3e-05;
Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADAMSIDGG 22
Db 391 STEDCIDKIVNGEADAMSIDGG 412

RESULT 14
TRFL_HUMAN STANDARD; PRT; 711 AA.
AC P02788; O00756; Q16780; Q16785; Q16786; Q16789; Q81U92; Q81ZH6;
AC O8TCD2; Q96K24; Q96K25; Q9H1Z3;
DT 21-JUL-1996 (Rel. 01, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Lactoferrin precursor (Lactoferrin) [Contains: Kallistocin-1;
DE Lactoferrin A; Lactoferrin B; Lactoferrin C].
GN Name=Lf; Synonyms=LF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=90384839; PubMed=2402455;
RA Rey M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
RT "Complete nucleotide sequence of human mammary gland lactoferrin.";
RL Nucleic Acids Res. 18:5288-5288 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cho Y.Y.;
RL Theils (1994), Genetic Engineering Research Institute / Taejon, Korea.
RN [3]
RP SEQUENCE FROM N.A.
RA Conneely O.M.;
RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Liang Q., Jimenez-Plores R., Richardson T.;
RL Molecular cloning and sequence analysis of human lactoferrin.";
RL Submitted (DEC-1991) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Wei X., Han J., Rado T.A.;
RL "Human neutrophil lactoferrin coding and 5' flanking region DNA
RL sequences.";
RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Cheng H., Chen X., Huan L.;
RL "cDNA cloning and sequence analysis of human lactoferrin.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
RN [7]

```

RP SEQUENCE FROM N.A., AND VARIANTS THR-30 AND ARG-48.
RA Kaplan J.B., Fine D.H.; amino acid polymorphism in the antibacterial
RT "characterization of an amino acid polymorphism in the antibacterial
RL domain of human lactoferrin.";
RN Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A., AND VARIANTS THR-30, ARG-48 AND ASP-580.
RC TISSUE=Mammary gland;
RA Shi Y.-Q., Zhang Y., Zheng Y.-M.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A., AND VARIANTS THR-30; ARG-48 AND ASP-580.
RC TISSUE=Semenal vesicle;
RA Baekar Singh S., Saravanan K., Paramasivam M., Srinivasan A.,
RL Singh T.P.;
RN Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Krauss R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haile F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullen S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs S., Sanchez
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalek A., Smallue D.E.,
RA Scheraga J., Scheraga J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [11]
RP SEQUENCE OF 1-15 FROM N.A.
RX MEDLINE=93155571; PubMed=1480183; DOI=10.1210/me.6.11.1969;
RA Tang C.T., Liu Y., Yang N., Walmer D., Panella T.;
RT "Differential molecular mechanism of the estrogen action that
RT regulates lactoferrin gene in human and mouse.";
RL Mol. Endocrinol. 6:1969-1981 (1992).
RN [12]
RP SEQUENCE OF 3-711 FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=90326549; PubMed=2374734;
RA Powell M.J., Ogden J.E.;
RL "Nucleotide sequence of human lactoferrin cDNA.";
RN [13]
RP SEQUENCE OF 20-711.
RX MEDLINE=8507667; PubMed=6510420;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Schentgen F.,
RA Legend D., Spik G., Montreuil J., Jolles P.;
RT "Human lactoferrin: amino acid sequence and structural
RT comparisons with other transferrins.";
RL Eur. J. Biochem. 145:659-666 (1984).
RN [14]
RP PRELIMINARY SEQUENCE OF 20-73; 134-171, 257-278 AND 347-530.
RX MEDLINE=92046817; PubMed=6796460; DOI=10.1016/0005-2795(81)90016-7;
RA Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
RA Jolles P.;
RT "The present state of the human lactoferrin sequence. Study and
RT alignment of the cyanogen bromide fragments and characterization of N-
RL Biochim. Biophys. Acta 670:243-254 (1981).
RN [15]
RP SEQUENCE OF 609-711.
RX MEDLINE=82262043; PubMed=7049727; DOI=10.1016/0014-5793(82)80229-9;
RA Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
RA Jolles P.;
RT "An 88 amino acid long C-terminal sequence of human
RT lactoferrin.";
RL FEBS Lett. 142:107-110 (1982).
RN [16]
RP SEQUENCE OF 436-711 FROM N.A.
RX MEDLINE=88001031; PubMed=3477300;
RA Rado T.A., Wei X., Benz E.J. Jr.;
RT "Isolation of lactoferrin cDNA from a human myeloid library and
RT expression of mRNA during normal and leukemic myelopoiesis.";
RL Blood 70:989-993 (1987).
RN [17]
RP SEQUENCE OF 237-711 FROM N.A.
RA McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
RA Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
RA Gnoj L., La Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
RA Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
RA Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
RA Sagripanti J.L.;
RN Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [18]
RP SYNTHESIS OF 172-202 (KALIOCIN-1).
RX PubMed=12693969; DOI=10.1023/A:1022657630698;
RA Viejo-Diaz M., Andres M.T., Perez-Gil J., Sanchez M., Pierno J.F.;
RT "Potassium efflux induced by a new lactoferrin-derived peptide
RT mimicking the effect of native human lactoferrin on the bacterial
RT cytoplasmic membrane.";
RL Biochimica 68:217-227 (2003).
RN [19]
RP CHARACTERIZATION OF LACTOFERROXINS.
RX MEDLINE=9116929; PubMed=1369293;
RA Tani F., Ito K., Chiba H., Yoshikawa M.;
RT "Isolation and characterization of oploid antagonist peptides derived
RT from human lactoferrin.";
RL Agric. Biol. Chem. 54:1803-1810 (1990).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
RX MEDLINE=90064528; PubMed=2585506;
RA Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
RT "Structure of human lactoferrin: crystallographic structure analysis
RT and refinement at 2.8-A resolution.";
RL J. Mol. Biol. 209:711-734 (1989).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX PubMed=15299793;
RA Haridas M., Anderson B.F., Baker E.N.;
RT "Structure of human ferric lactoferrin refined at 2.2-A
RT resolution.";
RL Acta Crystallogr. D 51:629-646 (1995).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
RX MEDLINE=97156796; PubMed=9003186; DOI=10.1021/bj961908y;
RA Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedle J.W.,
RA Baker E.N.;
RT "Mutagenesis of the histidine ligand in human lactoferrin: iron
RT binding properties and crystal structure of the histidine-
RT 253--methionine mutant.";
RL Biochemistry 36:341-346 (1997).
RN [23]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE=99190892; PubMed=10089347; DOI=10.1107/S0907444998011226;
RA Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
RT "Structure of recombinant human lactoferrin expressed in Aspergillus
RT awamori.";
RL Acta Crystallogr. D 55:403-407 (1999).
RN [24]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=99192677; PubMed=10089508; DOI=10.1107/S0907444998004417;
RA Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.;
RT "Structure of human apolactoferrin at 2.0-A resolution. Refinement and

RT analysis of ligand-induced conformational change."
 RL Acta Crystallogr. D 54:1319-1335 (1998).
 [25]
 RP VARIANTS THR-30 AND ARG-48.
 RX MEDLINE=9091914; PubMed=9873069;

Query Match 78.3%; Score 90; DB 1; Length 711;
 Best Local Similarity 73.9%; Pred. No. 4.3e-05;
 Matches 17; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADAMSJDGG 23
 ||||| : |||||
 Db 396 TTEDCIATLVKGEADAMSJDGG 418

RESULT 15

ID 07TMC7 PRELIMINARY; PRT; 979 AA.
 AC 07TMC7;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Ab2-417 (CC1-8).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xu C.S., Li W.Q., Li Y.C., Chang C.F., Zhao L.F., Ma H., Wang L.,
 RA Wang S.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y., Yang K.J.,
 RA Yan H.M., Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RA Xu C.S., Li W.Q., Li Y.C., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,
 RA Yang K.J., Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F.,
 RA Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Transferrins are iron binding transport proteins which
 bind ferric iron in association with the binding of an anion,
 usually bicarbonate (By similarity).
 CC -!- DOMAIN: Composed of two homologous domains (By similarity).
 CC -!- SIMILARITY: Belongs to the transferrin family.
 CC EMBL; AY325241; AAP92615.1; -;
 DR EMBL; AY325241; AAP92615.1; -;
 DR HSSP; P02787; 1B3E.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0008199; F:ferric iron binding; IEA.
 DR GO; GO:0006879; P:iron ion homeostasis; IEA.
 DR GO; GO:0006826; P:iron ion transport; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro: IPR001156; Peptidase_S60.
 DR Pfam: PF00405; Transferrin; 2.
 DR SMART; SM00094; TR_FER; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 1.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 2.
 DR Iron transport; Metal-binding; Transport.
 SQ SEQUENCE 979 AA; 107411 MW; 5BE80A6A1DD67D09 CRC64;

Query Match 78.3%; Score 90; DB 2; Length 979;
 Best Local Similarity 81.8%; Pred. No. 6.2e-05;
 Matches 18; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TTEDSIKIMNGEADAMSJDGG 22
 :|||:|||||
 Db 377 TTEDCIATLVKGEADAMSJDGG 398

Search completed: November 1, 2005, 12:54:30
 Job time : 113.632 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 13:32:37 ; Search time 162 Seconds
(without alignments)
54.910 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115
Sequence: 1 TTEDSIAKIMNGSADMSLDGFR 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 750623

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	115	100.0	23	8	ADG46076	Adg46076 Human CDT
2	77	67.0	21	6	ABP74737	Abp74737 Proteome
3	77	67.0	21	8	ADR15960	Adr15960 Transferr
4	77	67.0	21	8	ADR15901	Adr15901 Transferr
5	68	59.1	13	8	ADG46093	Adg46093 Human CDT
6	67	58.3	19	2	AAR71072	Aar71072 Draculin
7	65	56.5	13	8	ADG46092	Adg46092 Human CDT
8	62	53.9	13	8	ADG46090	Adg46090 Human CDT
9	62	53.9	13	8	ADG46091	Adg46091 Human CDT
10	59	51.3	18	8	ADR19359	Adr19359 TRPI derl
11	36	31.3	7	8	ADR15885	Adr15885 Transferr
12	34	29.6	12	4	AU68027	Au68027 Human Bre
13	34	29.6	12	4	AU68103	Au68103 Human Bre
14	34	29.6	12	4	AU68052	Au68052 Human Bre
15	34	29.6	12	4	AA884372	Aa884372 Splice-va
16	34	29.6	12	6	ABP88991	Abp88991 EtD82 cel
17	34	29.6	12	6	ABP72825	Abp72825 Human lac
18	34	29.6	12	8	ADH89361	Adh89361 Human tcr
19	34	29.6	12	8	ADK15871	Adk15871 Neutrophil
20	34	29.6	12	8	ADL70737	Adl70737 Neutrophil
21	34	29.6	12	8	ADL24415	Adl24415 Neutrophil
22	34	29.6	17	2	AA891738	Aa891738 HBR4 immu
23	34	28.7	14	8	ADR15908	Adr15908 Transferr
24	33	28.7	15	8	ADS13210	Adsl3210 Human rbe
25	33	28.7	16	8	ADR15849	Adr15849 Transferr

26	32	27.8	8	2	AAR71074	Aar71074 Draculin
27	32	27.8	12	8	ADS13221	Adsl3221 Human rbe
28	32	27.8	15	7	ADC79140	Adc79140 PAPA pill
29	32	27.8	19	8	ADK50523	Adk50523 Human car
30	32	27.8	21	8	ADK50529	Adk50529 Human car
31	32	27.8	22	3	AA851606	Aa851606 Yada homo
32	32	27.8	22	5	AB804567	Ab804567 Hepatitis
33	31	27.0	14	5	AB892749	Ab892749 CnCR31A a
34	31	27.0	15	3	AA661731	Aa661731 Arabidops
35	31	27.0	15	8	ADR15969	Adr15969 Transferr
36	31	27.0	16	2	AAV51787	Aav51787 H. influe
37	31	27.0	16	3	AAW54131	Aaw54131 Polioviru
38	31	27.0	16	3	AAV80389	Aav80389 H. influe
39	31	27.0	17	2	AA877971	Aa877971 H. influe
40	31	27.0	17	2	AAV51786	Aav51786 H. influe
41	31	27.0	17	2	AAW54130	Aaw54130 Polioviru
42	31	27.0	17	3	AAV80388	Aav80388 H. influe
43	31	27.0	18	2	AA850003	Aa850003 Extracell
44	31	27.0	20	2	AA860731	Aa860731 Lolium pe
45	31	27.0	20	2	AA871556	Aa871556 LPI-17, p

ALIGNMENTS

RESULT 1
ID ADG46076 standard; peptide; 23 AA.
AC ADG46076;
XX
XX
DT 25-MAR-2004 (first entry)
XX
DE Human CDT peptide fragment #2.
XX
XX antibody; carbohydrate-deficient transferrin; CDT;
KM non-glycosylated transferrin; alcoholic; alcoholic; diagnosis; human.
XX
OS Homo sapiens.
XX
XX BP1378521-A1.
PN
XX
PD 07-JAN-2004.
XX
PF 19-MAY-2003; 2003EP-00011334.
XX
XX 05-JUL-2002; 2002DE-01030550.
XX
PA (DADE-) DADE BEHRING MARBURG GMBH.
PI Althaus H;
XX
DR WPI; 2004-073743/08.
XX
PT New antibody specific for carbohydrate-deficient transferrin, useful for
PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.
XX
PS Claim 4; SEQ ID NO 2; 21pp; German.
XX
XX This invention describes a novel antibody that, in aqueous solution,
XX binds selectively to carbohydrate-deficient transferrin (CDT) without
XX having to bind CDT to a solid phase. The invention also describes an
XX antibody that binds selectively to CDT at regions containing the
XX sequence VVARSMGKEDLIWEL, TTEDSIAKIMNGSADMSLDGFR, SKLSMGSLNSEEPN and
XX YEKLYGEEYKXAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
XX using the antibodies of the invention. The antibodies of the invention
XX are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
XX antibodies are obtained by immunisation with non-glycosylated
XX transferrin, or a fragment, then generation of hybridomas by standard
XX fusion of spleen and myeloma cells. Hybridomas are then selected for
XX production of antibodies that specifically bind CDT from the aqueous
XX phase. The antibodies are useful for diagnosis of alcoholism, CDT, which

CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcohols. The antibodies allow direct detection of CDT in solution,
CC eliminating the need for immobilising it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
CC fragments used in the method of the invention.

CC Sequence 23 AA;

Query Match 100.0%; Score 115; DB 8; Length 23;

Best Local Similarity 100.0%; Pred. No. 4e-11; Mismatches 0; Gaps 0;

Matches 23; Conservative 0; Indels 0; Indels 0; Gaps 0;

Db 1 TTEDSIKIMNGEADAMSIDGDF 23

RESULT 2

ABP74737 standard; peptide; 21 AA.

AC ABP74737;

DT 03-FEB-2003 (first entry)

DE Proteome analysis related peptide #22.

KM Proteome analysis; isolation; determination; diagnostic assay; detection;

KM protein marker; identification; metastatic; invasive cancer;

KM differential expression; signalling pathway; chromatography.

OS Homo sapiens.

OS Synthetic.

PN MO200277016-A2.

PF 22-MAR-2002; 2002WO-EP003368.

PR 22-MAR-2001; 2001US-0278171P.

PR 12-SEP-2001; 2001US-0318749P.

PR 20-SEP-2001; 2001US-0323999P.

PA (VLA-A-) VLAAWS INTERUNIVERSITAIR INST BIOTECHNOG.

PI Vandekerckhove J, Gevaert K;

DR WPI; 2003-067379/06.

PT Method for isolation of peptides from complex mixture of peptides

PT involves specific chemical and/or enzymatic alteration of at least one

PT type of peptide.

PS Example 19; Page 138; 193pp; English.

CC The present invention describes a method (M1) for the isolation of a
CC subset of peptides from a protein peptide mixture (P1). M1 involves: (a)
CC separating the protein peptide mixture into fractions of peptides via
CC chromatography; (b) chemically, or enzymatically, or chemically and
CC enzymatically, altering at least one amino acid of at least one of the
CC peptides in each fraction, thereby generating a subset of altered
CC peptides; and (c) isolating the altered (flagged) peptides out of each
CC fraction via chromatography, where the chromatography of steps (a) and
CC (c) is performed with the same type of chromatography. M1 can be used for
CC the isolation and determination of peptides from protein peptide
CC mixtures. M1 can also be used in diagnostic assays for detection of the
CC presence, the absence or a variation in expression level of at least one
CC protein marker or a specific set of proteins indicative of a disease
CC state. M1 can be used for identifying target proteins present in
CC metastatic and invasive cancers, in differential expression of proteins
CC in transgenic mice, identification of proteins that are upregulated or
CC down regulated in disease tissues, in identification of intracellular

CC changes in cells with physiological changes such as metabolic shift, in
CC the identification of biomarkers in cancers and in the identification of
CC signalling pathways. The method is gel-free methodology for qualitative
CC and quantitative proteome analysis without the need for multidimensional
CC chromatography and without the use of affinity tags. ABP74714 to ABP75190
CC represent peptide sequences used in the exemplification of the present
CC invention

CC Sequence 21 AA;

Query Match 67.0%; Score 77; DB 6; Length 21;

Best Local Similarity 100.0%; Pred. No. 4.4e-05; Mismatches 0; Gaps 0;

Db 9 INNGEADAMSIDGDF 23

1 INNGEADAMSIDGDF 15

RESULT 3

ADR15960 standard; peptide; 21 AA.

AC ADR15960;

DT 04-NOV-2004 (first entry)

DE Transferrin peptide fragment #118.

KM glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.

OS Synthetic.

PN MO2004070389-A1.

PF 19-AUG-2004.

PF 06-FEB-2004; 2004WO-GB000480.

PR 06-FEB-2003; 2003GB-00002740.

PA (AXIS-) AXIS-SHIELD ASA.

PI Rye PD;

DR WPI; 2004-625547/60.

PT Assay for differentiating protein isoforms to determine their

PT concentrations in sample e.g. blood, involves contacting the sample with

PT proteolytic enzyme to produce peptide fragment by proteolysis followed by

PT detecting.

PS Disclosure; Page 17; 30pp; English.

CC The present invention describes an assay for a protein having at least
CC two isoforms with different glycosylation patterns. The assay involves
CC contacting a sample containing the protein with a proteolytic enzyme,
CC followed by detecting the content or relative content of at least one
CC peptide fragment produced by proteolysis. Also described is a kit for the
CC assay method comprising the proteolytic enzyme and a substrate bound
CC specific binding partner (S1) for at least 2 of the isoforms of the
CC proteins. The method can be used for assaying isoforms of proteins
CC according to their glycosylation pattern to determine their concentration
CC or relative concentration in the sample or material (e.g. blood). The
CC method avoids use of antibodies for distinguishing between glycosylated
CC isoforms of the proteins. The present sequence represents a transferrin
CC peptide fragment which is used in the exemplification of the present
CC invention.

CC Sequence 21 AA;

Query Match 67.0%; Score 77; DB 8; Length 21;

Best Local Similarity 100.0%; Pred. No. 4.4e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 INNGEADAMSJDGGF 23
| | | | | | | | | |
Db 1 INNGEADAMSJDGGF 15

RESULT 4

ADRI5901
ID ADRI5901 standard; peptide; 21 AA.

XX ADR15901;

AC ADR15901;

DT 04-NOV-2004 (first entry)

DE Transferrin peptide fragment #59.

XX glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.

OS Synthetic.

PN WO2004070389-A1.

PD 19-AUG-2004.

PF 06-FEB-2004; 2004WO-GB000480.

PR 06-FEB-2003; 2003GB-00002740.

PA (AXIS-) AXIS-SHIELD ASA.

PI Rye PD;

DR WPI; 2004-625547/60.

XX Assay for differentiating protein isoforms to determine their

PT concentrations in sample e.g. blood, involves contacting the sample with

PT proteolytic enzyme to produce peptide fragment by proteolysis followed by

XX detecting.

PS Disclosure; Page 15; 30pp; English.

XX The present invention describes an assay for a protein having at least

CC two isoforms with different glycosylation patterns. The assay involves

CC contacting a sample containing the protein with a proteolytic enzyme,

CC followed by detecting the content or relative content of at least one

CC peptide fragment produced by proteolysis. Also described is a kit for the

CC assay method comprising the proteolytic enzyme and a substrate bound

CC specific binding partner (SI) for at least 2 of the isoforms of the

CC proteins. The method can be used for assaying isoforms of proteins

CC according to their glycosylation pattern to determine their concentration

CC or relative concentration in the sample or material (e.g. blood). The

CC method avoids use of antibodies for distinguishing between glycosylated

CC isoforms of the proteins. The present sequence represents a transferrin

CC peptide fragment which is used in the exemplification of the present

XX invention.

XX SQ Sequence 21 AA;

Query Match 67.0%; Score 77; DB 8; Length 21;

Best Local Similarity 100.0%; Pred. No. 4.4e-05;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 INNGEADAMSJDGGF 23
| | | | | | | | | |
Db 1 INNGEADAMSJDGGF 15

RESULT 5

ADG46093
ID ADG46093 standard; peptide; 13 AA.

XX ADG46093;

XX 25-MAR-2004 (first entry)

DT Human CDT peptide fragment #19.

XX antibody; carbohydrate-deficient transferrin; CDT;

XX non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.

XX Homo sapiens.

XX BP1378521-A1.

PN 07-JAN-2004.

PD 19-MAY-2003; 2003EP-00011334.

PF 05-JUL-2002; 2002DE-01030550.

PR (DADE-) DADE BEHRING MARBURG GMBH.

PA Althaus H;

PD WPI; 2004-073743/08.

PT New antibody specific for carbohydrate-deficient transferrin, useful for

PT diagnosis of alcoholism, can bind its target in solution, eliminating

PT need for immobilization.

PS Example 7; Page 15; 21pp; German.

XX This invention describes a novel antibody that, in aqueous solution,

CC binds selectively to carbohydrate-deficient transferrin (CDT) without

CC having to bind CDT to a solid phase. The invention also describes an

CC antibody that binds selectively to CDT at regions containing the

CC sequences VVARSWGKEDJIMEL, TTEDSIKINNGEADAMSJDGGF, SLSMSGGLNSEPN and

CC VEXYLDEEVKAV (ADG46075-ADG46078) and an immunoassay for detecting CDT

CC using the antibodies of the invention. The antibodies of the invention

CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The

CC antibodies are obtained by immunisation with non-glycosylated

CC transferrin, or a fragment, then generation of hybridomas by standard

CC fusion of spleen and myeloma cells. Hybridomas are then selected for

CC production of antibodies that specifically bind CDT from the aqueous

CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which

CC lacks glycosylation at Asn413 and/or Asn 611, is present only in

CC alcoholics. The antibodies allow direct detection of CDT in solution,

CC eliminating the need for immobilising it on a solid phase (as required

CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide

CC fragments used in the method of the invention.

XX SQ Sequence 13 AA;

Query Match 59.1%; Score 68; DB 8; Length 13;

Best Local Similarity 100.0%; Pred. No. 0.00069;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 NGEADAMSJDGGF 23
| | | | | | | | | |
Db 1 NGEADAMSJDGGF 13

AAAR71072
ID AAAR71072 standard; peptide; 19 AA.

XX AAAR71072;

AC 25-MAR-2003 (revised)

DT 15-NOV-1995 (first entry)

DE Draculin peptide #35.

XX Anticoagulant; Draculin; saliva; vampire bat; inhibition; factor IX;

XX factor X; blood coagulation cascade; serine protease inhibitor; PMFS;

KW acute myocardial infarction; deep vein thrombosis; pulmonary embolism;
 KW unstable angina; transient ischemic attack; peripheral vascular; DFP;
 KW bypass occlusion; disseminated intravascular coagulation.
 XX
 OS Desmodus rotundus.
 XX
 PN WO9505836-A1.
 XX
 PD 02-MAR-1995.
 XX
 PF 22-AUG-1994; 94WO-US009488.
 XX
 PR 20-AUG-1993; 93US-00109807.
 XX
 PA (RHON) RHONE POULENC RORER PHARM INC.
 XX
 PI Hemker H, Apitz-Castro R, Beguin S;
 XX
 DR WPI; 1995-106668/14.
 XX
 PT New anticoagulant protein, draculin, from vampire bat saliva - and
 PT related nucleic acid, vectors, transformed cells and probes, for treating
 PT myocardial infarction, etc.
 XX
 PS Example 8; Page 35; 107pp; English.
 XX
 CC The sequences given in AAR71038-84 represent peptide fragments derived
 CC from the anticoagulant protein, Draculin. Draculin is isolated from the
 CC saliva of vampire bats and is distinct from other known anticoagulants in
 CC that it inhibits both factors IX and X of the blood coagulation cascade.
 CC The anticoagulant activity is not inhibited by serine protease inhibitors
 CC such as PMFS or DPP. The molecular weight of Draculin ranges from 75-90
 CC kD and may be used in treatment of acute myocardial infarction, deep vein
 CC thrombosis, pulmonary embolism, unstable angina, transient ischemic
 CC attacks, peripheral vascular or bypass occlusions and disseminated
 CC intravascular coagulation. These peptide fragments were derived from
 CC Draculin by cleavage with chymotrypsin and overlapping peptide fragments
 CC were compared to determine the complete amino acid sequence of Draculin.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX
 SQ Sequence 19 AA;
 Query Match 58.3%; Score 67; DB 2; Length 19;
 Best Local Similarity 80.0%; Pred. No. 0.0016;
 Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 9 INNGEADAMSIDGCF 23
 DB 1 VLKGEADAMSIDGCF 15
 RESULT 7
 ADG46092
 ID ADG46092 standard; peptide; 13 AA.
 XX
 AC ADG46092;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human CDT peptide fragment #18.
 XX
 KW antibody; carbohydrate-deficient transferrin; CDT;
 KW non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.
 XX
 OS Homo sapiens.
 XX
 PN EPI378521-A1.
 XX
 PD 07-JAN-2004.
 XX
 PF 19-MAY-2003; 2003EP-00011334.
 XX
 PR 05-JUL-2002; 2002DE-01030550.

XX
 PA (DADE-) DADE BEHRING MARBURG GMBH.
 XX
 PI Althaus H;
 XX
 DR WPI; 2004-073743/08.
 XX
 PT New antibody specific for carbohydrate-deficient transferrin, useful for
 PT diagnosis of alcoholism, can bind its target in solution, eliminating
 PT need for immobilization.
 XX
 PS Example 7; Page 15; 21pp; German.
 XX
 CC This invention describes a novel antibody that, in aqueous solution,
 CC binds selectively to carbohydrate-deficient transferrin (CDT) without
 CC having to bind CDT to a solid phase. The invention also describes an
 CC antibody that binds selectively to CDT at regions containing the
 CC sequences VVARSWGKEDLIWEL, ITEDSIKIMNGEADAMSIDGCF, SKUSWGSGLNDEPN and
 CC YERYLGEYRVAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
 CC using the antibodies of the invention. The antibodies of the invention
 CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
 CC antibodies are obtained by immunisation with non-glycosylated
 CC transferrin, or a fragment, then generation of hybridomas by standard
 CC fusion of spleen and myeloma cells. Hybridomas are then selected for
 CC production of antibodies that specifically bind CDT from the aqueous
 CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
 CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
 CC alcoholics. The antibodies allow direct detection of CDT in solution,
 CC eliminating the need for immobilising it on a solid phase (as required
 CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
 CC fragments used in the method of the invention.
 XX
 SQ Sequence 13 AA;
 Query Match 56.5%; Score 65; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.0021;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 9 INNGEADAMSIDG 21
 DB 1 INNGEADAMSIDG 13
 RESULT 8
 ADG46090
 ID ADG46090 standard; peptide; 13 AA.
 XX
 AC ADG46090;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE Human CDT peptide fragment #16.
 XX
 KW antibody; carbohydrate-deficient transferrin; CDT;
 KW non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.
 XX
 OS Homo sapiens.
 XX
 PN EPI378521-A1.
 XX
 PD 07-JAN-2004.
 XX
 PF 19-MAY-2003; 2003EP-00011334.
 XX
 PR 05-JUL-2002; 2002DE-01030550.
 XX
 PA (DADE-) DADE BEHRING MARBURG GMBH.
 XX
 PI Althaus H;
 XX
 DR WPI; 2004-073743/08.
 XX
 PT New antibody specific for carbohydrate-deficient transferrin, useful for

PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.
XX
PS Example 7; Page 15; 21pp; German.
XX
CC This invention describes a novel antibody that, in aqueous solution,
CC binds selectively to carbohydrate-deficient transferrin (CDT) without
CC having to bind CDT to a solid phase. The invention also describes an
CC antibody that binds selectively to CDT at regions containing the
CC sequence VVARSGKEDLIWEL, TTEDSIKINMGADMSLDGF, SKLSGSGINLSEPN and
CC YKRYLGEERYKAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
CC using the antibodies of the invention. The antibodies of the invention
CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
CC antibodies are obtained by immunisation with non-glycosylated
CC transferrin, or a fragment, then generation of hybridomas by standard
CC fusion of spleen and myeloma cells. Hybridomas are then selected for
CC production of antibodies that specifically bind CDT from the aqueous
CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcoholics. The antibodies allow direct detection of CDT in solution,
CC eliminating the need for immobilising it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
CC fragments used in the method of the invention.
SO
XX
SO Sequence 13 AA:
Query Match 53.9%; Score 62; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 SIKINMGADAM 17
DB 1 SIKINMGADAM 13
RESULT 9
ADG46091
ID ADG46091 standard; peptide; 13 AA.
XX
AC ADG46091;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human CDT peptide fragment #17.
XX
KW antibody; carbohydrate-deficient transferrin; CDT;
XX non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.
OS Homo sapiens.
XX
PN EP1378521-A1.
XX
PD 07-JAN-2004.
XX
PF 19-MAY-2003; 2003EP-00011334.
XX
PR 05-JUL-2002; 2002DE-01030550.
XX
PA (DADE-) DADE BEHRING MARBURG GMBH.
XX
PI Althaus H,
XX
DR WPI; 2004-073743/08.
XX
PT New antibody specific for carbohydrate-deficient transferrin, useful for
PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.
XX
PS Example 7; Page 15; 21pp; German.
XX
CC This invention describes a novel antibody that, in aqueous solution,
CC binds selectively to carbohydrate-deficient transferrin (CDT) without
CC having to bind CDT to a solid phase. The invention also describes an

CC antibody that binds selectively to CDT at regions containing the
CC sequence VVARSGKEDLIWEL, TTEDSIKINMGADMSLDGF, SKLSGSGINLSEPN and
CC YKRYLGEERYKAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
CC using the antibodies of the invention. The antibodies of the invention
CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
CC antibodies are obtained by immunisation with non-glycosylated
CC transferrin, or a fragment, then generation of hybridomas by standard
CC fusion of spleen and myeloma cells. Hybridomas are then selected for
CC production of antibodies that specifically bind CDT from the aqueous
CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcoholics. The antibodies allow direct detection of CDT in solution,
CC eliminating the need for immobilising it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
CC fragments used in the method of the invention.
SO
XX
SO Sequence 13 AA:
Query Match 53.9%; Score 62; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0063;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 AKINMGADAMSL 19
DB 1 AKINMGADAMSL 13
RESULT 10
ADRI9359
ID ADRI9359 standard; peptide; 18 AA.
XX
AC ADRI9359;
XX
DT 04-NOV-2004 (first entry)
XX
DE TRPI derived human tryptic digest peptide, SEQ ID 21.
XX
KW Tissue damage; chronic; tissue repair-associated protein isoform; TRPI;
XX antitumor; vulnery; chronic dermal ulcer; human; tryptic digest;
XX proteolysis; trypsin.
OS Homo sapiens.
XX
PN WO2004069795-A2.
XX
PD 19-AUG-2004.
XX
PF 02-FEB-2004; 2004WO-US002881.
XX
PR 03-FEB-2003; 2003US-0444600P.
XX
PA (PF12) PFIZER PROD INC.
XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Butt R, Rumpel K, Williams-Jones BI, Herath HMAC, Rohlf C,
PI Bruce JA, Patel TP;
XX
DR WPI; 2004-604404/58.
XX
PT Diagnosing, or monitoring the effect of therapy of, chronic tissue damage
PT (e.g. chronic dermal ulcer) comprises detecting and/or quantifying tissue
PT repair-associated protein isoform in a sample (e.g. wound exudate) from
PT the subject.
XX
PS Claim 7; SEQ ID NO 21; 107pp; English.
XX
CC The invention relates to a novel method for assessing, screening,
CC diagnosing or prognosing chronic tissue damage in a subject, identifying
CC a subject at risk of developing chronic tissue damage, or monitoring the
CC effect of therapy administered to a subject having chronic tissue damage.
CC The method comprises detecting and/or quantifying in a biological sample
CC from the subject a tissue repair-associated protein isoform (TRPI), given
CC in the specification. The invention further comprises: an isolated or

CC recombinant TRPI selected from the proteins listed in the specification;
CC screening for or identifying an agent capable of modulating the
CC expression or activity of the TRPI or a TRPI-related polypeptide; a
CC pharmaceutical composition comprising the TRPI cited above or an active
CC agent that modulates the expression and/or activity of the TRPI or a TRPI
CC -related polypeptide, and a pharmaceutical carrier, vehicle or diluent;
CC and treating chronic tissue damage. The novel compositions have anticancer
CC and vulnerrary activity. The composition and methods are useful for
CC diagnosing, preventing, prognosing and treating chronic tissue damage,
CC such as a chronic dermal ulcer. These may also be used for drug screening
CC or drug development, or for screening or identifying agents capable of
CC modulating the activity of TRPI or TRPI-related polypeptides. This
CC sequence represents a TRPI derived human tryptic digest peptide. The
CC peptide was produced by proteolysis using trypsin of a tissue repair-
CC associated protein isoform of the invention.

XX SQ Sequence 18 AA;

Query Match 51.3%; Score 59; DB 8; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.028;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 G6ADAMSLDGCF 23
DB 1 G6ADAMSLDGGY 12

RESULT 11
ADRI5885
ID ADRI5885 standard; peptide; 7 AA.
XX AC ADR15885;
XX AC ADR15885;
DT 04-NOV-2004 (first entry)
XX DE Transferrin peptide fragment #43.
XX DE Transferrin peptide fragment #43.
XX KM glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.
XX OS Synthetic.
XX PN WO2004070389-A1.
XX PD 19-AUG-2004.
XX PF 06-FEB-2004; 2004MO-GB000480.
XX PR 06-FEB-2003; 2003GB-00002740.
XX PA (AXIS-) AXIS-SHIELD ASA.
XX PI Rye PD;
XX DR WPI; 2004-625547/60.
XX PT Assay for differentiating protein isoforms to determine their
XX PT concentrations in sample e.g. blood, involves contacting the sample with
XX PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
XX PT detecting.

XX PS Disclosure; Page 14; 30pp; English.

XX CC The present invention describes an assay for a protein having at least
XX CC two isoforms with different glycosylation patterns. The assay involves
XX CC contacting a sample containing the protein with a proteolytic enzyme,
XX CC followed by detecting the content or relative content of at least one
XX CC peptide fragment produced by proteolysis. Also described is a kit for the
XX CC assay method comprising the proteolytic enzyme and a substrate bound
XX CC specific binding partner (S1) for at least 2 of the isoforms of the
XX CC proteins. The method can be used for assaying isoforms of proteins
XX CC according to their glycosylation pattern to determine their concentration
XX CC or relative concentration in the sample or material (e.g. blood). The
XX CC method avoids use of antibodies for distinguishing between glycosylated

CC isoforms of the proteins. The present sequence represents a transferrin
CC peptide fragment which is used in the exemplification of the present
CC invention.

XX SQ Sequence 7 AA;

Query Match 31.3%; Score 36; DB 8; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 N6EADAM 17
DB 1 N6EADAM 7

RESULT 12
AAU68027
ID AAU68027 standard; peptide; 12 AA.
XX AC AAU68027;
XX AC AAU68027;
DT 16-JAN-2002 (first entry)
XX DE Human Breast cancer-associated protein isoform, BPI-21 peptide #1.
XX DE Human Breast cancer-associated protein isoform; breast cancer;
XX KM Human; Breast cancer-associated protein isoform; breast cancer;
XX KM immunogen; cytoskeletal; BPI; tryptic digest peptide.
XX OS Homo sapiens.
XX PN WO200171357-A2.
XX PD 27-SEP-2001.
XX PF 20-MAR-2001; 2001MO-GB001219.
XX PR 20-MAR-2000; 2000GB-00006695.
XX PR 24-MAR-2000; 2000GB-00007265.
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PI Herath HMC, O'hare MJ, Page MJ, Parekh RB, Waterfield MD;
XX DR WPI; 2001-611532/70.
XX PT Identifying proteins for clinical screening, diagnosis and prognosis of
XX PT breast cancer, comprises detecting Breast Cancer-Associated Protein
XX PT Isoforms (BPIs) using two-dimensional electrophoresis.

XX PS Claim 9; Page 43; 197pp; English.

XX CC The invention relates to diagnosing, determining the stage or severity,
XX CC or identifying the risk of a subject developing cancer (especially breast
XX CC cancer), or monitoring the effect of therapy on a subject with cancer,
XX CC comprising analysing a test sample using two-dimensional electrophoresis
XX CC and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The
XX CC methods disclosed are used for the diagnosis and prognosis of breast
XX CC cancer, for determining the severity of breast cancer, and for
XX CC identifying a subject at risk of developing breast cancer, and monitoring
XX CC the effect of therapy administered to a subject. Antibodies raised
XX CC against the binding domain of a BPI, the binding domain of a BPI, a
XX CC nucleic acid encoding a BPI, or a nucleic acid that inhibits the function
XX CC of a BPI can be incorporated into a pharmaceutical composition for
XX CC treating or preventing breast cancer. The methods use sensitive and
XX CC specific biomarkers provide early diagnosis of breast cancer, and the
XX CC compositions are more potent, specific, and has a more rapid effect with
XX CC fewer side effects than other prior art methods. The present sequence is
XX CC a tryptic digest peptide from a BPI of the invention

XX SQ Sequence 12 AA;

Query Match 29.6%; Score 34; DB 4; Length 12;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;

Matches 5, Conservative 4, Mismatches 2, Indels 0, Gaps 0;

QY 12 GEADAMSLOG 22
|:|:|:|:|
Db 1 GQLEALQVDDG 11

RESULT 13

AAU68103
ID AAU68103 standard; peptide; 12 AA.

AC AAU68103;
XX

DT 16-JAN-2002 (first entry)
XX

DE Human Breast cancer-associated protein isoform, BPI-7 peptide #2.
XX

KW Human; Breast cancer-associated protein isoform; breast cancer;
XX

KM Immunogen; cytoskeletal; BPI; tryptic digest peptide.
XX

OS Homo sapiens.
XX

PN WO200171357-A2.
XX

PD 27-SEP-2001.
XX

PF 20-MAR-2001; 2001WO-GB001219.
XX

PR 20-MAR-2000; 2000GB-00006695.
XX

PR 24-MAR-2000; 2000GB-00007265.
XX

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX

PI Herath HMAc, O'hare MJ, Page MJ, Parekh RB, Waterfield MD;
XX

DR WPI; 2001-611532/70.
XX

PT Identifying proteins for clinical screening, diagnosis and prognosis of
XX

PT breast cancer, comprises detecting Breast Cancer-Associated Protein
XX

PT isoforms (BPIs) using two-dimensional electrophoresis.
XX

PS Claim 9; Page 44; 197pp; English.
XX

CC The invention relates to diagnosing, determining the stage or severity,
XX

CC or identifying the risk of a subject developing cancer (especially breast
XX

CC cancer), or monitoring the effect of therapy on a subject with cancer,
XX

CC comprising analysing a test sample using two-dimensional electrophoresis
XX

CC and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The
XX

CC methods disclosed are used for the diagnosis and prognosis of breast
XX

CC cancer, for determining the severity of breast cancer, and for
XX

CC identifying a subject at risk of developing breast cancer, and monitoring
XX

CC the effect of therapy administered to a subject. Antibodies raised
XX

CC against the binding domain of a BPI, the binding domain of a BPI, a
XX

CC nucleic acid encoding a BPI, or a nucleic acid that inhibits the function
XX

CC of a BPI can be incorporated into a pharmaceutical composition for
XX

CC treating or preventing breast cancer. The methods use sensitive and
XX

CC specific biomarkers provide early diagnosis of breast cancer, and the
XX

CC compositions are more potent, specific, and has a more rapid effect with
XX

CC fewer side effects than other prior art methods. The present sequence is
XX

CC a tryptic digest peptide from a BPI of the invention
XX

CC
XX

SO Sequence 12 AA;
XX

Query Match 29.6%; Score 34; DB 4; Length 12;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 12 GEADAMSLOG 22
|:|:|:|:|
Db 1 GQLEALQVDDG 11

RESULT 14

AAU68052
ID AAU68052 standard; peptide; 12 AA.

AC AAU68052;
XX

DT 16-JAN-2002 (first entry)
XX

DE Human Breast cancer-associated protein isoform, BPI-3 peptide #1.
XX

KW Human; Breast cancer-associated protein isoform; breast cancer;
XX

KM Immunogen; cytoskeletal; BPI; tryptic digest peptide.
XX

OS Homo sapiens.
XX

PN WO200171357-A2.
XX

PD 27-SEP-2001.
XX

PF 20-MAR-2001; 2001WO-GB001219.
XX

PR 20-MAR-2000; 2000GB-00006695.
XX

PR 24-MAR-2000; 2000GB-00007265.
XX

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX

PI Herath HMAc, O'hare MJ, Page MJ, Parekh RB, Waterfield MD;
XX

DR WPI; 2001-611532/70.
XX

PT Identifying proteins for clinical screening, diagnosis and prognosis of
XX

PT breast cancer, comprises detecting Breast Cancer-Associated Protein
XX

PT isoforms (BPIs) using two-dimensional electrophoresis.
XX

PS Claim 9; Page 43; 197pp; English.
XX

CC The invention relates to diagnosing, determining the stage or severity,
XX

CC or identifying the risk of a subject developing cancer (especially breast
XX

CC cancer), or monitoring the effect of therapy on a subject with cancer,
XX

CC comprising analysing a test sample using two-dimensional electrophoresis
XX

CC and detecting Breast Cancer-Associated Protein Isoforms (BPIs). The
XX

CC methods disclosed are used for the diagnosis and prognosis of breast
XX

CC cancer, for determining the severity of breast cancer, and for
XX

CC identifying a subject at risk of developing breast cancer, and monitoring
XX

CC the effect of therapy administered to a subject. Antibodies raised
XX

CC against the binding domain of a BPI, the binding domain of a BPI, a
XX

CC nucleic acid encoding a BPI, or a nucleic acid that inhibits the function
XX

CC of a BPI can be incorporated into a pharmaceutical composition for
XX

CC treating or preventing breast cancer. The methods use sensitive and
XX

CC specific biomarkers provide early diagnosis of breast cancer, and the
XX

CC compositions are more potent, specific, and has a more rapid effect with
XX

CC fewer side effects than other prior art methods. The present sequence is
XX

CC a tryptic digest peptide from a BPI of the invention
XX

SO Sequence 12 AA;
XX

Query Match 29.6%; Score 34; DB 4; Length 12;
Best Local Similarity 45.5%; Pred. No. 1.7e+02;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 12 GEADAMSLOG 22
|:|:|:|:|
Db 1 GQLEALQVDDG 11

RESULT 15

AAAB4372
ID AAAB4372 standard; peptide; 12 AA.

AC AAAB4372;
XX

DT 22-AUG-2001 (first entry)
XX

DE Splice-variance region of a human transferrin.
XX

```

XX Human; transferrin; autoimmune disease; rheumatoid arthritis;
KM hyperproliferative disorder; neoplasia; cardiovascular disorder;
KM cardiac arrest; cerebrovascular disorder; cerebral ischemia;
KM angiogenesis; nervous system disorder; Alzheimer's disease; infection;
KM ocular disorder; corneal infection; wound healing;
KM epithelial cell proliferation; aging; organ transplant.
XX
OS Homo sapiens.
XX
PN WO200146254-A1.
XX
PD 28-JUN-2001.
XX
PF 21-DEC-2000; 2000WO-US034769.
XX
PR 23-DEC-1999; 99US-0171595P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Shi Y, Choi GH;
XX
DR WPI; 2001-381910/40.
XX
PT Isolated nucleic acid molecule encoding a human transferrin protein is
PT used in preventing, treating or ameliorating a medical condition.
XX
PS Disclosure; Page 11; 290pp; English.
XX
XX The present sequence is a splice-variance region of a transferrin.
CC Transferrin polypeptides and polynucleotides are used to prevent, treat
CC or ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
CC horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or
CC treated include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
CC ocular disorders e.g. corneal infection. The polypeptides can also be
CC used to aid wound healing and epithelial cell proliferation, to prevent
CC skin aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities
XX
SQ Sequence 12 AA;

```

```

Query Match          29.6%; Score 34; DB 4; Length 12;
Best Local Similarity 64.3%; Pred. No. 1.7e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
QY 3 EDSIAKINNGEADA 16
   ||| : |||||
DB 1 EDCIA--LKGEDA 12

```

Search completed: November 1, 2005, 13:48:43
 Job time : 164 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 13:43:13, Search time 41 Seconds

(without alignment)
41.876 Million cell updates/sec

Title: US-10-612-162A-2

Sequence: 1 TTEDSIAKIMNGEADMSLDGCF 23

Scoring table:

BLOSUM62

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 211522

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

Issued, Patents AA:*

- 1: /cgn2_6/pcodata/1/aa/5A_COMB.pep.*
- 2: /cgn2_6/pcodata/1/aa/5B_COMB.pep.*
- 3: /cgn2_6/pcodata/1/aa/6A_COMB.pep.*
- 4: /cgn2_6/pcodata/1/aa/6B_COMB.pep.*
- 5: /cgn2_6/pcodata/1/aa/PC/US_COMB.pep.*
- 6: /cgn2_6/pcodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	29.6	17	2	US-08-484-438-31
2	33	28.7	23	1	US-08-568-147B-14
3	31	27.0	16	1	US-08-487-890A-134
4	31	27.0	16	2	US-08-478-435-134
5	31	27.0	16	2	US-08-337-483-134
6	31	27.0	16	2	US-08-478-373-134
7	31	27.0	16	3	US-08-474-671-134
8	31	27.0	16	3	US-08-483-577A-134
9	31	27.0	16	3	US-08-897-438-134
10	31	27.0	16	3	US-08-637-654-134
11	31	27.0	16	3	US-08-649-518-134
12	31	27.0	17	1	US-08-487-890A-133
13	31	27.0	17	1	US-08-478-435-133
14	31	27.0	17	2	US-08-337-483-133
15	31	27.0	17	2	US-08-478-373-133
16	31	27.0	17	3	US-08-474-671-133
17	31	27.0	17	3	US-08-483-577A-133
18	31	27.0	17	3	US-08-897-438-133
19	31	27.0	17	3	US-08-637-654-133
20	31	27.0	17	3	US-08-649-518-133
21	31	27.0	20	1	US-08-440-861-48
22	30	26.1	13	3	US-09-155-941-23
23	30	26.1	17	3	US-08-454-098-26
24	30	26.1	17	5	PCT-US96-01600-26
25	29	25.2	12	4	US-09-462-118-27
26	29	25.2	13	3	US-09-155-941-15
27	29	25.2	20	1	US-08-241-054-79

28	29	25.2	20	1	US-08-241-054-93	Sequence 93, Appl
29	29	25.2	20	1	US-08-390-156A-37	Sequence 37, Appl
30	29	25.2	20	1	US-08-390-156A-44	Sequence 44, Appl
31	29	25.2	20	1	US-08-439-817-59	Sequence 59, Appl
32	29	25.2	20	1	US-08-439-817-73	Sequence 73, Appl
33	29	25.2	20	1	US-08-485-508-79	Sequence 79, Appl
34	29	25.2	20	1	US-08-485-508-93	Sequence 93, Appl
35	29	25.2	22	3	US-08-256-747C-41	Sequence 41, Appl
36	29	25.2	22	3	US-08-334-130A-41	Sequence 41, Appl
37	28	24.3	16	2	US-08-934-822-127	Sequence 127, App
38	28	24.3	16	2	US-08-933-402-127	Sequence 127, App
39	28	24.3	16	2	US-09-207-621-127	Sequence 127, App
40	28	24.3	16	3	US-08-532-818-127	Sequence 127, App
41	28	24.3	16	3	US-09-231-797-127	Sequence 127, App
42	28	24.3	16	3	US-08-534-224-127	Sequence 127, App
43	28	24.3	16	3	US-08-933-843-127	Sequence 127, App
44	28	24.3	16	3	US-08-934-223-127	Sequence 127, App
45	28	24.3	16	3	US-09-413-492-127	Sequence 127, App

ALIGNMENTS

RESULT 1
US-08-484-438-31
Sequence 31, Application US/08484438
Patent No. 5811098
Patent No. 5811098 5780031
GENERAL INFORMATION:
APPLICANT: Plowman, Gregory D.
APPLICANT: Cuioussou, Jean-Michel
APPLICANT: Shoyab, Mohamed
APPLICANT: Siegall, Clay B.
APPLICANT: Hellstr m, Ingegerd
APPLICANT: Hellstr m, Karl E.
TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,438
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,442
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704
FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-2310
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-484-438-31

Query Match 29.6%; Score 34; DB 2; Length 17;
Best Local Similarity 29.4%; Pred No. 41;
Matches 5; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 6 IAKINGEADAMSLDGG 22
Db 1 LARLEGEDEKEYNADGG 17

RESULT 2
US-08-568-147B-14
Sequence 14, Application US/08568147B
Patent No. 5783422

GENERAL INFORMATION:
APPLICANT: Suminami, Yoshinori
APPLICANT: Kato, Hiroshi
APPLICANT: Sekiguchi, Kiyoshi
APPLICANT: Takeda, Kazumichi
TITLE OF INVENTION: DNA FRAGMENT CODING FOR SQUAMOUS CELL
TITLE OF INVENTION: CARCINOMA-ASSOCIATED ANTIGEN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: USA
ZIP: 11530

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,147B
FILING DATE:
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 800,952

FILING DATE: 02-DEC-1991

ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.

REGISTRATION NUMBER: 31,346

REFERENCE/DOCKET NUMBER: 8425

TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343

TELEFAX: 516-742-4366

TELEX: 230 901 SANS UR

INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-568-147B-14

Query Match 28.7%; Score 33; DB 1; Length 23;
Best Local Similarity 46.2%; Pred No. 86;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 9 INNGEADAMSLDGG 21
Db 5 IFNGDADLSGWTG 17

RESULT 3

US-08-487-890A-134
Sequence 134, Application US/08487890A
Patent No. 5708149

GENERAL INFORMATION:
APPLICANT: Loomore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
FILING DATE: 07-JUN-1993
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116

FILING DATE: 29-DEC-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968

FILING DATE: 08-NOV-1993

ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-466 MIS:jfb

TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155

TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-487-890A-134

Query Match 27.0%; Score 31; DB 1; Length 16;
Best Local Similarity 60.0%; Pred No. 12e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 14 ADAMSLDGGF 23
Db 3 ASTSLDGGF 12

RESULT 4
US-08-478-435-134
Sequence 134, Application US/08478435
Patent No. 5922323

GENERAL INFORMATION:
APPLICANT: Loomore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel

TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,435
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-462 MIS:v9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-478-435-134

Query Match 27.0%; Score 31; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 14 ADAMSIDGCF 23
DB 3 AASTSLGCF 12

RESULT 5
US-08-337-483-134
Sequence 134, Application US/08337483
Patent No. 5922562
GENERAL INFORMATION:
APPLICANT: Loomore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Mordin, Andrew
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada

ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-337-483-134

Query Match 27.0%; Score 31; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 14 ADAMSIDGCF 23
DB 3 AASTSLGCF 12

RESULT 6
US-08-478-373-134
Sequence 134, Application US/08478373
Patent No. 5922841
GENERAL INFORMATION:
APPLICANT: Loomore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Mordin, Andrew
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,373
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:

```

; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
;   NAME: Stewart, Michael I
;   REGISTRATION NUMBER: 24,973
;   REFERENCE/DOCKET NUMBER: 1038-463 MIS:Vg
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (416) 595-1155
;   TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 16 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;
US-08-478-373-134

Query Match      27.0%; Score 31; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      14 ADAMSIDGGF 23
DB      3 ASTTSLEGGF 12

RESULT 7
US-08-474-671-134
; Sequence 134, Application US/08474671
; Patent No. 6008326
; GENERAL INFORMATION:
;   APPLICANT: Loosmore, Sheena
;   APPLICANT: Harkness, Robin
;   APPLICANT: Schryvers, Anthony
;   APPLICANT: Chong, Pele
;   APPLICANT: Gray-Owen, Scott
;   APPLICANT: Yang, Yan-Ping
;   APPLICANT: Murdin, Andrew
;   APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Sim & McBurney
;   STREET: Suite 701, 330 University Avenue
;   CITY: Toronto
;   STATE: Ontario
;   COUNTRY: Canada
;   ZIP: M5G 1R7
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/474,671
;   FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/337,483
;   FILING DATE: 08-NOV-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/175,116
;   FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
;   NAME: Stewart, Michael I
;   REGISTRATION NUMBER: 24,973
;   REFERENCE/DOCKET NUMBER: 1038-465 MIS:Vg
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (416) 595-1155

```

```

; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 16 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;
US-08-474-671-134

Query Match      27.0%; Score 31; DB 3; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      14 ADAMSIDGGF 23
DB      3 ASTTSLEGGF 12

RESULT 8
US-08-483-577A-134
; Sequence 134, Application US/08483577A
; Patent No. 6015688
; GENERAL INFORMATION:
;   APPLICANT: Loosmore, Sheena
;   APPLICANT: Harkness, Robin
;   APPLICANT: Schryvers, Anthony
;   APPLICANT: Chong, Pele
;   APPLICANT: Gray-Owen, Scott
;   APPLICANT: Yang, Yan-Ping
;   APPLICANT: Murdin, Andrew
;   APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Sim & McBurney
;   STREET: Suite 701, 330 University Avenue
;   CITY: Toronto
;   STATE: Ontario
;   COUNTRY: Canada
;   ZIP: M5G 1R7
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Releasee #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/483,577A
;   FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/337,483
;   FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/148,968
;   FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
;   NAME: Stewart, Michael I
;   REGISTRATION NUMBER: 24,973
;   REFERENCE/DOCKET NUMBER: 1038-511
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (416) 595-1155
;   TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 16 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;
US-08-483-577A-134

```

Query Match 27.0%; Score 31; DB 3; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 14 ADAMSJDGF 23
DB 3 ASTTSLJEGF 12

RESULT 9
US-08-897-438-134
; Sequence 134, Application US/08897438
; Patent No. 6262016
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murlin, Andrew
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/897,438
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-897-438-134

Query Match 27.0%; Score 31; DB 3; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 14 ADAMSJDGF 23
DB 3 ASTTSLJEGF 12

DB 3 ASTTSLJEGF 12

RESULT 10
US-08-637-654-134
; Sequence 134, Application US/08637654
; Patent No. 6368727
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena M
; APPLICANT: Harkness, Robin B
; APPLICANT: Schryvers, Anthony B
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murlin, Andrew D
; TITLE OF INVENTION: HAEMOPHILUS TRANSFERRIN RECEPTOR GENES
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/637,654
; FILING DATE: 05-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/CA94/00616
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-637-654-134

Query Match 27.0%; Score 31; DB 3; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 14 ADAMSJDGF 23
DB 3 ASTTSLJEGF 12

RESULT 11
US-08-649-518-134
; Sequence 134, Application US/08649518
; Patent No. 6361779
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murlin, Andrew

```

; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 160
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/649,518
; FILING DATE: 17-MAY-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/337,483
; FILING DATE: 08-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,577
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-608
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-649-518-134
;
Query Match          27.0%; Score 31; DB 3; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      14 ADAMSJDGCF 23
Db      3 ASTTSLEGGF 12

RESULT 12
US-08-487-890A-133
; Sequence 133, Application US/08487890A
; Patent No. 5708149
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6th Floor, 330 University Avenue
```

```

; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,890A
; FILING DATE: 07-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,116
; FILING DATE: 29-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/148,968
; FILING DATE: 08-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Stewart, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 133:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-487-890A-133
;
Query Match          27.0%; Score 31; DB 1; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      14 ADAMSJDGCF 23
Db      3 ASTTSLEGGF 12

RESULT 13
US-08-478-435-133
; Sequence 133, Application US/08478435
; Patent No. 5922323
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Schryvers, Anthony
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Yang, Yan-Ping
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
; NUMBER OF SEQUENCES: 147
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: Suite 701, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,435
; FILING DATE: 07-JUN-1995
```

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-462 MIS:V9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-478-435-133

Query Match 27.0%; Score 31; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 14 ADAMSLEGGF 23
DB 3 ASTTSLEGGF 12

RESULT 14
US-08-337-483-133
Sequence 133, Application US/08337483
Patent No. 5922562
GENERAL INFORMATION:
APPLICANT: Loomore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murlin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-410 MIS:Jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163

INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-337-483-133

Query Match 27.0%; Score 31; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 14 ADAMSLEGGF 23
DB 3 ASTTSLEGGF 12

RESULT 15
US-08-478-373-133
Sequence 133, Application US/08478373
Patent No. 5922841
GENERAL INFORMATION:
APPLICANT: Loomore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murlin, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,373
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-463 MIS:V9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-478-373-133

Query Match 27.0%; Score 31; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 14 ADAMSIDGGF 23
| | | | |
Db 3 ASTTSLEGGF 12

Search completed: November 1, 2005, 13:53:07
Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: November 1, 2005, 13:49:34 ; Search time 163 Seconds
(without alignments)
58.988 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115
Sequence: 1 TTEDSIKIMNGEADMSLDGGR 23

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 400882

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

1: /cgn2_6/prodata/1/pubppa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubppa/US06_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubppa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pep:*
8: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep:*
9: /cgn2_6/prodata/1/pubppa/US09A_PUBCOMB.pep:*
10: /cgn2_6/prodata/1/pubppa/US09B_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubppa/US09C_PUBCOMB.pep:*
12: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB.pep:*
13: /cgn2_6/prodata/1/pubppa/US10_PUBCOMB.pep:*
14: /cgn2_6/prodata/1/pubppa/US10B_PUBCOMB.pep:*
15: /cgn2_6/prodata/1/pubppa/US10C_PUBCOMB.pep:*
16: /cgn2_6/prodata/1/pubppa/US10D_PUBCOMB.pep:*
17: /cgn2_6/prodata/1/pubppa/US10E_PUBCOMB.pep:*
18: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB.pep:*
19: /cgn2_6/prodata/1/pubppa/US11A_PUBCOMB.pep:*
20: /cgn2_6/prodata/1/pubppa/US11_NEW_PUB.pep:*
21: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep:*
22: /cgn2_6/prodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	23	15	US-10-612-162-2
2	77	67.0	21	15	US-10-394-980-20
3	77	67.0	21	18	US-10-952-557-20
4	34	29.6	12	9	US-09-891-126-6
5	34	29.6	12	10	US-09-988-493-10
6	34	29.6	12	14	US-10-266-745-6
7	34	29.6	12	15	US-10-378-094-5
8	34	29.6	12	15	US-10-384-060-4
9	34	29.6	12	15	US-10-231-494-8
10	34	29.6	12	16	US-10-700-330-101
11	33	28.7	15	17	US-10-801-990-1

12	32	27.8	12	17	US-10-801-990-12	Sequence 12, App1
13	31	27.0	14	15	US-10-432-422-88	Sequence 88, App1
14	31	27.0	16	14	US-10-043-344-134	Sequence 134, App
15	31	27.0	17	14	US-10-043-344-133	Sequence 133, App
16	31	27.0	20	11	US-09-855-604-138	Sequence 138, App
17	31	27.0	20	12	US-09-855-604-138	Sequence 138, App
18	30	26.1	15	16	US-10-416-249-415	Sequence 415, App
19	30	26.1	17	10	US-09-880-748-3151	Sequence 3151, App
20	30	26.1	17	15	US-10-293-418-3151	Sequence 3151, App
21	30	26.1	23	18	US-10-862-195-357	Sequence 357, App
22	29	25.2	12	14	US-10-937-042-28	Sequence 28, App1
23	29	25.2	12	14	US-10-247-946-27	Sequence 27, App1
24	29	25.2	12	14	US-10-251-526-27	Sequence 27, App1
25	29	25.2	13	16	US-10-700-330-184	Sequence 184, App
26	29	25.2	13	18	US-10-789-4948-8	Sequence 8, App11
27	29	25.2	13	18	US-10-789-4948-8	Sequence 8, App11
28	29	25.2	20	14	US-10-115-072-18	Sequence 68, App1
29	29	25.2	20	16	US-10-679-033-56	Sequence 18, App1
30	29	25.2	20	18	US-10-862-195-2151	Sequence 56, App1
31	28.5	24.6	19	9	US-09-734-417-4	Sequence 2151, App
32	28	24.3	10	10	US-09-572-4048-448	Sequence 4, App11
33	28	24.3	13	15	US-10-469-837-58	Sequence 448, App
34	28	24.3	13	16	US-10-468-671-51	Sequence 58, App1
35	28	24.3	13	16	US-10-488-671-52	Sequence 51, App1
36	28	24.3	13	16	US-10-488-671-53	Sequence 52, App1
37	28	24.3	13	16	US-10-488-671-54	Sequence 53, App1
38	28	24.3	14	16	US-10-813-638-1337	Sequence 54, App1
39	28	24.3	14	16	US-10-813-638-1337	Sequence 1237, App
40	28	24.3	15	9	US-09-826-290-144	Sequence 1237, App
41	28	24.3	15	15	US-10-813-638-1298	Sequence 144, App
42	28	24.3	15	15	US-10-264-309-193	Sequence 193, App
43	28	24.3	15	16	US-10-416-249-417	Sequence 417, App
44	28	24.3	15	18	US-10-264-309-193	Sequence 193, App
45	28	24.3	16	9	US-09-073-009-41	Sequence 41, App1
			9	9	US-09-023-588-41	Sequence 41, App1

ALIGNMENTS

RESULT 1
US-10-612-162-2
; Sequence 2, Application US/10612162
; Publication No. US20040014145A1
GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
; FILE REFERENCE: 2002/B001
; CURRENT APPLICATION NUMBER: US/10/612,162
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; PRIOR FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-162-2

Query Match 100.0%; Score 115; DB 15; Length 23;
Best Local Similarity 100.0%; Pred. No. 5.5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTEDSIKIMNGEADMSLDGGR 23
|||||
Db 1 TTEDSIKIMNGEADMSLDGGR 23
|||||

RESULT 2
US-10-394-980-20

Db 1 GQLEALQVDSG 11

```
RESULT 6
US-10-266-745-6
; Sequence 6, Application US/10266745
; Publication No. US20030149256A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PTO35P1
; CURRENT APPLICATION NUMBER: US/10/266,745
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/891,126
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: PCT/US00/34769
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/171,595
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-266-745-6
```

Query Match 29.6%; Score 34; DB 14; Length 12;
Best Local Similarity 64.3%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 3 EDSIAKIMGEADA 16
Db 1 EDCIA--LKGEADA 12

```
RESULT 7
US-10-378-094-5
; Sequence 5, Application US/10378094
; Publication No. US20030221201A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: LAI, Char-Huei
; APPLICANT: SADEGH, Homayoun
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5001-01-US
; CURRENT APPLICATION NUMBER: US/10/378,094
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Neutrophil lactoferrin splice variant
US-10-378-094-5
```

Query Match 29.6%; Score 34; DB 15; Length 12;
Best Local Similarity 64.3%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 3 EDSIAKIMGEADA 16
Db 1 EDCIA--LKGEADA 12

```
RESULT 8
US-10-384-060-4
; Sequence 4, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGH, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Neutrophil splice variant sequence
US-10-384-060-4
```

Query Match 29.6%; Score 34; DB 15; Length 12;
Best Local Similarity 64.3%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 3 EDSIAKIMGEADA 16
Db 1 EDCIA--LKGEADA 12

```
RESULT 9
US-10-231-494-8
; Sequence 8, Application US/10231494
; Publication No. US20040023334A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Lactoferrin splice variant sequence
US-10-231-494-8
```

Query Match 29.6%; Score 34; DB 15; Length 12;
Best Local Similarity 64.3%; Pred. No. 1.6e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 3 EDSIAKIMGEADA 16
Db 1 EDCIA--LKGEADA 12

RESULT 10
US-10-700-330-101
; Sequence 101, Application US/10700330
; Publication No. US20040203022A1
; GENERAL INFORMATION:
; APPLICANT: Heratch, Mudiyanselage Athula Chandrasiri Heratch
; APPLICANT: Page, Martin John
; TITLE OF INVENTION: Proteins and Genes For Diagnosis And Treatment of ErbB2-Related C
; FILE REFERENCE: 2543-1-031
; CURRENT APPLICATION NUMBER: US/10/700,330
; CURRENT FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: GB 0110886.9
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: GB 0128183.1
; PRIOR FILING DATE: 2001-11-23
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-330-101

Query Match 29.6%; Score 34; DB 16; Length 12;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 12 G6ADAMSLDGG 22
|:|:|:|
DB 1 GQLEALQVDGG 11

RESULT 11
US-10-801-990-1
; Sequence 1, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
; APPLICANT: Kantor, Aaron B.
; APPLICANT: Schulman, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121
; CURRENT APPLICATION NUMBER: US/10/801,990
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-1

Query Match 28.7%; Score 33; DB 17; Length 15;
Best Local Similarity 87.5%; Pred. No. 3e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTEDSIAX 8
|:|:|:|
DB 8 TTEDCIAX 15

RESULT 12
US-10-801-990-12
; Sequence 12, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
; APPLICANT: Kantor, Aaron B.
; APPLICANT: Schulman, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121

; CURRENT APPLICATION NUMBER: US/10/801,990
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-12

Query Match 27.8%; Score 32; DB 17; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 SLDDGF 23
|:|:|:|
DB 1 SLDDGF 6

RESULT 13
US-10-432-422-88
; Sequence 88, Application US/10432422
; Publication No. US20040076981A1
; GENERAL INFORMATION:
; APPLICANT: Syngenta Participations AG
; APPLICANT: Cornell Research Foundation, Inc.
; APPLICANT: Yoder, Olen
; APPLICANT: Turgeon, Barbara G.
; APPLICANT: Lu, Shen-wen
; TITLE OF INVENTION: Fungal Iron Reductase Gene
; FILE REFERENCE: 1360.017MO1
; CURRENT APPLICATION NUMBER: US/10/432,422
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: US 60/252,732
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 60/252,649
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 210
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Cochliobolus heterostrophus
US-10-432-422-88

Query Match 27.0%; Score 31; DB 15; Length 14;
Best Local Similarity 66.7%; Pred. No. 5.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 15 DAMSLDGGF 23
|:|:|:|
DB 6 DSPSLSGF 14

RESULT 14
US-10-043-344-134
; Sequence 134, Application US/10043344
; Publication No. US20030080806A1
; GENERAL INFORMATION:
; APPLICANT: Loomore, Sheena M.
; APPLICANT: Harkness, Robin E.
; APPLICANT: Schryvers, Anthony B.
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
; APPLICANT: Mordin, Andrew D.
; APPLICANT: Klein, Michael H.
; TITLE OF INVENTION: TRANSFERIN RECEPTOR GENES
; FILE REFERENCE: 1038-1221 MIS
; CURRENT APPLICATION NUMBER: US/10/043,344
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: 08/649,518

! PRIOR FILING DATE: 1996-05-17
! NUMBER OF SEQ ID NOS: 160
! SOFTWARE: PatentIn Ver. 2.1
! SEQ ID NO 134
! LENGTH: 16
! TYPE: PRT
! ORGANISM: Haemophilus influenzae
US-10-043-344-134

Query Match 27.0%; Score 31; DB 14; Length 16;
Best Local Similarity 60.0%; Pred. No. 6.8e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 14 ADAMSIDGGF 23
| :|||
Db 3 ASTTSLEGGF 12

RESULT 15
US-10-043-344-133
! Sequence 133. Application US/10043344
! Publication No. US20030088086A1
! GENERAL INFORMATION:
! APPLICANT: Loosmore, Sheena M.
! APPLICANT: Harkness, Robin E.
! APPLICANT: Schryvers, Anthony B.
! APPLICANT: Chong, Pele
! APPLICANT: Gray-Owen, Scott
! APPLICANT: Mordin, Andrew D.
! APPLICANT: Klein, Michel H.
! TITLE OF INVENTION: TRANSFERRIN RECEPTOR GENES
! FILE REFERENCE: 1038-1221 MIS
! CURRENT APPLICATION NUMBER: US/10/043,344
! PRIOR FILING DATE: 2002-07-01
! PRIOR APPLICATION NUMBER: 08/649,518
! PRIOR FILING DATE: 1996-05-17
! NUMBER OF SEQ ID NOS: 160
! SOFTWARE: PatentIn Ver. 2.1
! SEQ ID NO 133
! LENGTH: 17
! TYPE: PRT
! ORGANISM: Haemophilus influenzae
US-10-043-344-133

Query Match 27.0%; Score 31; DB 14; Length 17;
Best Local Similarity 60.0%; Pred. No. 7.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 14 ADAMSIDGGF 23
| :|||
Db 3 ASTTSLEGGF 12

Search completed: November 1, 2005, 14:05:54
Job time : 167 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 13:40:49 ; Search time 38 seconds

(without alignments)
58.236 Million cell updates/sec

Title: US-10-612-162A-2

Perfect score: 115
Sequence: 1 TTEDSTAKINGEADMSLDGCF 23Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 4495

Minimum DB seq length: 0
Maximum DB seq length: 23Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	31	27.0	16	2	A44823	synaptosomal-assoc
2	28	24.3	23	2	S54339	cytochrome P450 CY
3	27	23.5	22	2	H83991	hypothetical prote
4	26	22.6	16	2	A29501	fibrinopeptide A -
5	26	22.6	16	2	B24180	fibrinogen alpha c
6	26	22.6	16	2	A24180	fibrinogen alpha c
7	26	22.6	16	2	B28854	fibrinopeptide A -
8	26	22.6	16	2	C28854	fibrinopeptide A -
9	26	22.6	16	2	A28854	fibrinopeptide A -
10	25	21.7	11	2	C53652	rhlR protein - Pse
11	25	21.7	13	2	S03879	6-phosphofructokin
12	25	21.7	20	4	IS3672	somatostatin - syn
13	25	21.7	21	2	S16073	alanine-tRNA ligase
14	24	20.9	11	4	S19015	hypothetical prote
15	24	20.9	12	2	PH1172	T-cell receptor al
16	24	20.9	12	2	E64573	hypothetical prote
17	24	20.9	15	2	S26516	T-cell receptor al
18	24	20.9	16	2	PH1453	T-cell receptor al
19	24	20.9	18	2	S30346	4-hydroxybenzoate-
20	23	20.0	12	2	FQ0730	unidentified 5.4/3
21	23	20.0	15	2	PH1807	T cell receptor al
22	23	20.0	16	2	D83794	hypothetical prote
23	23	20.0	17	2	A44896	heat shock protein
24	23	20.0	18	2	S09086	proteasome chain 5
25	23	20.0	19	2	A49192	transferrin - bu
26	23	20.0	19	2	A39504	octamer-binding pr
27	23	20.0	20	2	S65135	xanthine dehydroge
28	23	20.0	21	2	S09088	proteasome chain 7
29	23	20.0	22	2	S08990	calcimedlin, 67K -

30	22	19.1	10	2	PT0309	Ig heavy chain CRD
31	22	19.1	10	2	C39572	sperm-activating p
32	22	19.1	11	2	A35594	buccalin - Cal1for
33	22	19.1	18	2	PH1349	Ig heavy chain DJ
34	22	19.1	18	2	I78841	thrombopoietin rec
35	22	19.1	20	2	B61333	chymotrypsin (EC 3
36	22	19.1	20	2	S53440	glutathione-bindin
37	22	19.1	20	2	A56899	serum heterodimer,
38	22	19.1	21	2	S33868	quinadine acid 4-o
39	22	19.1	22	2	S06487	glycine cleavage s
40	21	18.3	10	2	E41946	T-cell receptor ga
41	21	18.3	10	2	C60787	sperm-activating p
42	21	18.3	13	2	PC2369	unidentified 85K p
43	21	18.3	15	2	PA0075	fructose-bisphosph
44	21	18.3	16	2	H29501	fibrinopeptide A -
45	21	18.3	2	2	S01669	RNA N-glycosidase

ALIGNMENTS

RESULT 1

A44823

N: synaptosomal-associated protein SNAP-25 peptide 108 - rabbit (fragment)

C: Species: Oryctolagus cuniculus (domestic rabbit)

C: Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996

C: Accession: A44823

R: Loewy, A.; Liu, W.S.; Baillinger, C.; Willard, M.B.

J. Neurosci. 11, 3412-3421, 1991

A: Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is

A: Reference number: A44823; PMID:92044785; PMID:1941090

A: Accession: A44823

A: Status: preliminary

A: Molecule type: protein

A: Residues: 1-16 <LOE>

A: Experimental source: visual tissue

A: Note: sequence extracted from NCBI backbone (NCBIF:64256)

C: Keywords: membrane trafficking

Query Match 27.0%; Score 31; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 13 EADMSLDGCF 23

DB 4 ERSQMAISGCF 14

RESULT 2

S54339

cytochrome P450 CYP2A7AS - human

C: Species: Homo sapiens (man)

C: Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999

C: Accession: S54339

R: Ding, S.; Lake, B.G.; Friedberg, T.; Wolf, C.R.

Biochem. J. 306, 161-166, 1995

A: Title: Expression and alternative splicing of the cytochrome P-450 CYP2A7.

A: Reference number: S54338; PMID:95169049; PMID:7864805

A: Accession: S54339

A: Status: preliminary

A: Molecule type: mRNA

A: Residues: 1-23 <DIN>

Query Match 24.3%; Score 28; DB 2; Length 23;
Best Local Similarity 54.5%; Pred. No. 6e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 DSTAKINGEA 14

DB 6 DSTIMKVSQGVA 16

RESULT 3
 H83991
 hypochlorite protein BH2736 [imported] - *Bacillus halodurans* (strain C-125)
 C:Species: *Bacillus halodurans*
 C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: H83991
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hirono
 Nucleic Acids Res. 28, 4317-4331, 2000
 A:Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
 A:Reference number: AB6550; MUID:20512582; PMID:11058132
 A:Accession: H83991
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-52 <STO>
 A:Cross-references: UNIPROT:O9KCB3; GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BA064
 C:Genetics:
 A:Gene: BH2736

Query Match	23.5%	Score 27;	DB 2;	Length 22;
Best Local Similarity	31.2%	Pred. No.	8.2e+02;	
Matches	5;	Conservative	5;	Mismatches 6; Indels 0; Gaps 0;
Oy	4	DSIAKINGGEADAMSL	19	
	:::::	:::::	:::::	
Db	7	ETIKUMEGIFVARI	22	

```

RESULT 4
A29501
fibrinopeptide A - baboon
C:Species: Papio sp. (baboon)
C:Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 26-Jan-1996
C:Accession: A29501
R:Blomback, B.; Blomback, M.; Hann, C.
unpublished results, cited by Blomback, B., in Chemotaxonomy and Ser
A:Reference number: A29501
A:Accession: A29501
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-16 <BLO>
;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

```

Query Match	22.6%	Score 25;	DB 2;	Length 16;
Best Similarity	45.5%	Pred. No.	8.2e+02;	
Local				
Matches	5;	Conservative	2;	Mismatches 4; Indels 0; Gaps 0;
Oy	12	GEADAMSLDGG	22	
Db	4	GGGDFLAECCG	14	

```

RESULT 5
B24180
fibrinogen alpha chain - red guenon (Fragment)
N/Contains: Fibrinopeptide A
C/Species: Erythrocebus patas (red guenon, hussar)
C/Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 09-Jul-2004
C/Accession: B24180
R/Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A/Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (Erythrocebus patas), and baboons.
A/Reference number: A91990; MUID:85289140; PMID:3928610
A/Accession: B24180
A/Molecule type: protein
A/Residues: 1-16 <NAK>
A/Cross-References: UNIPROT:P12803
A/Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

```

Query Match	22.6%	Score 26;	DB 2;	Length 16;
Best Local Similarity	45.5%	Pred. NO.	8.2e+02;	
Matches	5;	Conservative	4;	Indels 0;
		Mismatches	0;	Gaps 0;

QY	12	GEADAMSLDGG	22
		:::	:::
Db	4	GEEDFLAEGGG	14

RESULT 6
A24180
Fibrinogen alpha chain - Japanese macaque (fragment)
N/Contains: Fibrinopeptide A
C/Species: Macaca fuscata (Japanese macaque)
C/Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 09-Jul-2004
C/Accession: A24180
R/Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A>Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (Papio anubis), and baboons.
A/Reference number: A91990; MUID:85289140; PMID:3928610
A/Accession: A24180
A/Molecule type: protein
A/Residues: 1-16 <NA>
A/Cross-references: UNIPROT:P12803
C/Superfamily: Fibrinogen alpha chain, fibrinogen disulfide ring homology

Query Match	22.6%	Score 26;	DB 2;	length 16;
Best Local Similarity	45.5%	Fred. No.	8.7e+02;	
Matches	5;	Mismatches	4;	Indels 0;
				Gaps 0;

QY	12	GEADAMSLDGG	22
		::	
Db	4	GEGDFLAEGGG	14

RESULT 7
B28854
Fibrinopeptide A - hamadryas baboon
C:Species: Papio hamadryas (hamadryas baboon)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C:Accession: B28854
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus aethiopicus)
#:Reference number: A91973; MUID:84161822; PMID:6423671

Query Match	22.6%	Score 26;	DB 2;	Length 16;
Best Local Similarity	45.5%	Pred. No. 8	.2e+02;	
Matches	5;	Conservative	2;	Mismatches 4;
				Indels 0;
				Gaps 0;

QY	12	GEADAMSLDGG	22
		:::	:::
Db	4	GEGDFLAEGGG	14

RESULT 8
C28854
fibrinopeptide A - gelada baboon
C:Species: Theropithecus gelada (gelada baboon)
C:Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C:Accession: C28854
R:Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A:Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropithecus gelada)
A:Reference number: A91973; MUID:84161822; PMID:6423621
A:Accession: C28854
A:Molecule type: Protein
A:Residues: 1-16 <NA>
A:Cross-references: UNIPROT:P12803
;Superfamily: fibrinogen alpha chain, fibrinogen disulfide ring homology

Query Match 22.6%; Score 26; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 8.2e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 12 G6ADAMSLDGG 22
DB 4 G6GDPLAEGGG 14

RESULT 9
A28854
Fibrinopeptide A - olive baboon
C/Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C/Accession: A28854
R; Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A/Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit
A/Reference number: A91973; MUID:64161822; PMID:6423621
A/Accession: A28854
A/Molecule type: protein
A/Residues: 1-16 <NAK>
A/Cross-references: UNIPROT:P12803
C/Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 22.6%; Score 26; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 8.2e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 12 G6ADAMSLDGG 22
DB 4 G6GDPLAEGGG 14

RESULT 10
C53652
rhlr protein - Pseudomonas aeruginosa (fragment)
C/Species: Pseudomonas aeruginosa
C/Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
C/Accession: C53652
R; Ochener, U.A.; Flechter, A.; Reiser, J.
J. Biol. Chem. 269, 19787-19795, 1994
A/Title: Isolation, characterization, and expression in Escherichia coli of the Pseudom
A/Reference number: A53652; MUID:94321521; PMID:8051059
A/Accession: C53652
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-11 <OCH>
A/Cross-references: UNIPROT:P54292; GB:L28170
C/Superfamily: eda regulatory protein

Query Match 21.7%; Score 25; DB 2; Length 11;
Best Local Similarity 71.4%; Pred. No. 7.7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 17 MSUDGPF 23
DB 1 MRNDGPF 7

RESULT 11
S03879
6-phosphofructokinase (EC 2.7.1.11) B - rabbit (fragment)
N/Alternate names: phosphofructo-1-kinase B
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C/Accession: S03879
R; Valaitis, A.P.; Foe, L.G.; Kwiatkowski, D.; Latshaw, S.P.; Kemp, R.G.
Biochim. Biophys. Acta 995, 187-194, 1989
A/Title: The sites of phosphorylation of rabbit brain phosphofructo-1-kinase by cyclic A
A/Reference number: S03878; MUID:89194250; PMID:2539199
C/Accession: S03879

A/Molecule type: protein
A/Residues: 1-13 <VAL>
A/Cross-references: UNIPROT:Q7M3F5
A/Note: the sequence from the summary is inconsistent with that from table 1 and Fig. 4
C/Keywords: glycolysis; phosphotransferase

Query Match 21.7%; Score 25; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 9.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 16 AMSLDGPF 23
DB 6 SLMDKGF 13

RESULT 12
I53672
somatotropin - synthetic
C/Species: synthetic
C/Date: 07-Jun-1996 #sequence_revision 31-Jul-1997 #text_change 19-May-2000
C/Accession: I53672
R; Bogostian, G.; Bilyeu, K.; O'Neill, J.P.
Gene 133, 17-22, 1993
A/Title: Genome rearrangements by residual IS10 elements in strains of Escherichia coli
A/Reference number: I53672; MUID:9404791; PMID:8224890
A/Accession: I53672
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-20 <BOG>
A/Cross-references: GB:S67119; NID:9455674; PIDN:AA82847.1; PID:9455675
A/Note: partial sequence of bovine somatotropin synthesized and expressed in Escherichi

Query Match 21.7%; Score 25; DB 4; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.5e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 AMSLDGPF 23
DB 4 AMSLSGLF 11

RESULT 13
S16073
alanyl-tRNA ligase (EC 6.1.1.7) - rat (fragment)
N/Alternate names: alanyl-tRNA synthetase
C/Species: Rattus norvegicus (Norway rat)
C/Date: 19-Mar-1997 #sequence_revision 24-Oct-1998 #text_change 09-Jul-2004
C/Accession: S16073
R; Dignam, J.D.; Dignam, S.S.; Brumley, L.L.
Eur. J. Biochem. 198, 201-210, 1991
A/Title: Alanyl-tRNA synthetase from Escherichia coli, Bombyx mori and Rattus rattus. Exi
A/Reference number: S16072; MUID:91249799; PMID:2040280
A/Accession: S16073
A/Molecule type: protein
A/Residues: 1-21 <DIG>
A/Cross-references: UNIPROT:P50475
C/Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis

Query Match 21.7%; Score 25; DB 2; Length 21;
Best Local Similarity 55.6%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 G6ADAMSLD 20
DB 3 G6EDLIMLD 11

RESULT 14
S19015
hypothetical protein 11 ruvc-yebc intergenic region - Escherichia coli
C/Species: Escherichia coli
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: S19015

R;Sharples, G.J.; Lloyd, R.G.
J. Bacteriol. 173, 7711-7715, 1991
A;Title: Resolution of Holliday junctions in Escherichia coli: identification of the ruv
A;Reference number: S19013; MUID:92041688; PMID:1657895
A;Accession: S19015
A;Molecule type: DNA
A;Residues: 1-11 <SHA>
A;Cross-references: UNIPROT:Q47420; EMBL:X59551; NID:942172; PIDN:CAA42127.1; PID:942174
C;Comment: This is the hypothetical translation of a sequence that was not reported as a

Query Match 20.9%; Score 24; DB 4; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 AKINGBA 14
Db 4 AKQONGDA 11

RESULT 15

PH1172
T-cell receptor alpha chain V region (Cw3/Cas15) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1172
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: PH1172
A;Status: Preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>

Query Match 20.9%; Score 24; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 DGGF 23
Db 5 DGGF 8

Search completed: November 1, 2005, 13:49:26
Job time : 39 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 13:41:28 ; Search time 168 Seconds
(without alignments)
70.106 Million cell updates/sec

Title: US-10-612-162A-2
Perfect score: 115
Sequence: 1 TTEDSIATKIMNGEADMSLDGCF 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 14769

Minimum DB seq length: 0
Maximum DB seq length: 23

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	40	34.8	12	2	Q8AUP7	Q8AUP7 salmo salar
2	40	34.8	12	2	Q8AUP8	Q8AUP8 salmo trutta
3	37	32.2	18	2	Q38573	Q38573 bacterioph
4	34	29.6	8	2	Q9QVFP4	Q9QVFP4 ratius sp.
5	28	24.3	18	2	Q9UCRF6	Q9UCRF6 homo sapien
6	27.5	23.9	21	2	Q6S8FO	Q6S8FO musa acumin
7	27	23.5	12	2	Q6PAJ9	Q6PAJ9 mus musculu
8	27	23.5	19	2	Q7RLN8	Q7RLN8 plasmodium
9	27	23.5	22	2	Q9K9B3	Q9K9B3 bacillus ha
10	26	22.6	12	2	Q801G7	Q801G7 choriostoneu
11	26	22.6	14	2	Q798V0	Q798V0 bacillus su
12	26	22.6	16	1	FIBA_CERAE	FIBA_CERAE cercopilhec
13	26	22.6	16	1	FIBA_ERYPA	FIBA_ERYPA erythrocebu
14	26	22.6	16	1	FIBA_MACPA	FIBA_MACPA macaca fasc
15	26	22.6	16	1	FIBA_MACPU	FIBA_MACPU macaca fusc
16	26	22.6	16	1	FIBA_PAPNU	FIBA_PAPNU macaca muli
17	26	22.6	16	1	FIBA_PAPPA	FIBA_PAPPA papio anubi
18	26	22.6	16	1	FIBA_PAPHA	FIBA_PAPHA papio hamad
19	26	22.6	16	1	FIBA_THRGE	FIBA_THRGE theropithec
20	26	22.6	20	2	Q9UCM7	Q9UCM7 homo sapien
21	26	22.6	20	2	Q99JF5	Q99JF5 mus musculu
22	25.5	22.2	18	2	Q9PSI6	Q9PSI6 gallus galli
23	25.5	22.2	22	2	Q85513	Q85513 chlamydia t
24	25.5	22.2	22	2	Q85515	Q85515 chlamydia t
25	25	21.7	10	2	Q9TU33	Q9TU33 canis fami
26	25	21.7	11	2	Q9NFX0	Q9NFX0 dirosophila
27	25	21.7	13	1	TEIA_RANBO	TEIA_RANBO rana boylii
28	25	21.7	13	2	Q7M3F5	Q7M3F5 oycocolegus
29	25	21.7	15	2	Q91XV8	Q91XV8 ratius norv
30	25	21.7	18	2	Q69Y10	Q69Y10 homo sapien
31	25	21.7	19	2	Q8V1G6	Q8V1G6 escherichia

32	25	21.7	19	2	Q99144	Q99144 human adeno
33	25	21.7	19	2	Q99146	Q99146 human adeno
34	25	21.7	19	2	Q99148	Q99148 human adeno
35	25	21.7	19	2	Q99150	Q99150 human adeno
36	25	21.7	19	2	Q99152	Q99152 human adeno
37	25	21.7	19	2	Q99154	Q99154 human adeno
38	25	21.7	19	2	Q99156	Q99156 human adeno
39	25	21.7	19	2	Q99158	Q99158 human adeno
40	25	21.7	20	2	Q9TR70	Q9TR70 urus arcto
41	25	21.7	20	2	Q9S8B8	Q9S8B8 lupinus alb
42	25	21.7	20	2	Q53370	Q53370 escherichia
43	25	21.7	20	2	Q64976	Q64976 alfalfa mos
44	25	21.7	21	1	SYA RAT	SYA RAT ratius norv
45	25	21.7	21	2	Q9R592	Q9R592 zymomonas m

ALIGNMENTS

RESULT 1
Q8AUP7 PRELIMINARY; PRT; 12 AA.
AC Q8AUP7;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Transferrin (Fragment).
OS Salmo salar (Atlantic salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxId=8030;
RN [1]
RP MEDLINE=2135992; PubMed=12140239;
RA Aunes A., Templeton A.R., Guyonard R., Alexandrino P.;
RT "The role of nuclear genes in intraspecific evolutionary inference:
RT genealogy of the transferrin gene in the brown trout.";
RL Mol. Biol. Evol. 19:1272-1287(2002).
DR EMBL; AF488839; ANI17020.1; -;
DR EMBL; AF488847; ANI17025.1; -;
FT NON_TER 1
FT 1
SQ SEQUENCE 12 AA; 1201 MW; 8C28335257D05DDA CRC64;
Query Match 34.8%; Score 40; DB 2; Length 12;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Caps 0;
QY 13 EADMSLDG 22
Db 3 EADMSLDG 12
RESULT 2
Q8AUP8 PRELIMINARY; PRT; 12 AA.
AC Q8AUP8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Transferrin (Fragment).
OS Salmo trutta (Brown trout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxId=8032;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2135992; PubMed=12140239;
RA Aunes A., Templeton A.R., Guyonard R., Alexandrino P.;
RT "The role of nuclear genes in intraspecific evolutionary inference:
RT genealogy of the transferrin gene in the brown trout.";

RL Mol. Biol. Evol. 19:1272-1287(2002).
DR EMBL; AF488871; AANI17030.1; -
DR EMBL; AF488871; AANI17040.1; -
DR EMBL; AF488871; AANI17045.1; -
DR EMBL; AF488871; AANI17050.1; -
DR EMBL; AF488895; AANI17055.1; -
DR EMBL; AF488903; AANI17060.1; -
DR EMBL; AF488911; AANI17065.1; -
DR EMBL; AF488919; AANI17071.1; -
DR EMBL; AF488927; AANI17076.1; -
DR EMBL; AF488935; AANI17081.1; -
DR EMBL; AF488943; AANI17086.1; -
DR EMBL; AF488951; AANI17091.1; -
DR EMBL; AF488959; AANI17095.1; -
DR EMBL; AF488967; AANI17101.1; -
DR EMBL; AF488975; AANI17106.1; -
DR EMBL; AF488983; AANI17111.1; -
DR EMBL; AF488991; AANI17116.1; -
DR EMBL; AF488999; AANI17121.1; -
DR EMBL; AF489007; AANI17126.1; -
DR EMBL; AF489015; AANI17131.1; -
DR EMBL; AF489023; AANI17136.1; -
DR EMBL; AF489031; AANI17141.1; -
DR EMBL; AF489039; AANI17146.1; -
DR EMBL; AF489047; AANI17151.1; -
DR EMBL; AF489055; AANI17156.1; -
DR EMBL; AF489063; AANI17161.1; -
DR EMBL; AF489071; AANI17166.1; -
DR EMBL; AF489079; AANI17171.1; -
DR EMBL; AF489087; AANI17176.1; -
DR EMBL; AF489095; AANI17181.1; -
DR EMBL; AF488863; AANI17035.1; -
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1231 MW; 8C2833524BA05DDA CRC64;

Query Match 34.8%; Score 40; DB 2; Length 12;
Best Local Similarity 70.0%; Pred. No. 31;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 13 EADMSLDG 22
DB 3 EADATVDDG 12

RESULT 3
Q38573 PRELIMINARY; PRT; 18 AA.
ID Q38573;
AC Q38573;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Coat protein (Fragment).
OS Bacteriophage KUI.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Levivirinae.
OX NCB1_Taxid=12021;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96207403; PubMed=8615017; DOI=10.1006/viro.1996.0174;
RA Groeneweld H., Oudot F., van Duin J.V.;
RT "RNA phage KUI has an insertion of 18 nucleotides in the start codon of its lysate gene";
RL Virology 218:141-147(1996).
DR EMBL; S81763; AAD14371.1; -
DR HSPF; P07234; IUNA.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
KW Coat protein.
FT NON_TER 1 1
SQ SEQUENCE 18 AA; 1825 MW; 2D4092DC26D8904 CRC64;

Query Match 32.2%; Score 37; DB 2; Length 18;

Best Local Similarity 56.2%; Pred. No. 1.4e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 8 KIMGEADMSLDG 23
DB 1 KIGNPVDAISSQSG 16

RESULT 4
Q9QVF4 PRELIMINARY; PRT; 8 AA.
ID Q9QVF4;
AC Q9QVF4;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE TRANSFERRIN-PEPTIDE 60 (Fragment).
OS Rattus sp.; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Eukaryota; Metazoa; Chordata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCB1_Taxid=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92165927; PubMed=1791188;
RA Cavanaugh P.G., Nicolson G.L.;
RT "Lung-derived growth factor that stimulates the growth of lung-metastasizing tumor cells: identification as transferrin";
RL J. Cell. Biochem. 47:261-271(1991).
FT NON_TER 1 1
SQ SEQUENCE 8 AA; 778 MW; 9D744735B6DDAD CRC64;

Query Match 29.6%; Score 34; DB 2; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.6e+06;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 ADAMSIDG 21
DB 1 ADAMSIDG 8

RESULT 5
Q9UCF6 PRELIMINARY; PRT; 18 AA.
ID Q9UCF6;
AC Q9UCF6;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Low-affinity interleukin-4 receptor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_Taxid=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93271485; PubMed=8499634;
RA Fawcett W.C., Spriggs M.K., Rauch C.T., Clifford K.N., Macduff B.M., Ziegler S.F., Schooley K.A., Mohler K.M., March C.J., Armitage R.J.;
RT "Identification of a distinct low-affinity receptor for human interleukin-4 on pre-B cells";
RL Blood 81:2998-3005(1993).
SQ SEQUENCE 18 AA; 1853 MW; F047FBA0F773B5 CRC64;

Query Match 24.3%; Score 28; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 3.6e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 14 ADAMSIDG 21
DB 11 SDLSLDG 18

RESULT 6
Q6S8FO

```

ID 0688F0 PRELIMINARY; PRT; 21 AA.
AC 0688F0;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Putative 26S proteasome regulatory subunit 8 (Fragment).
OS Musa acuminata (Banana).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
OC Musa.
OX NCBI_TaxID=4641;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pulp;
RA Bacter W.A., do Nascimento J.R.O., Lajolo F.M., Purgatto E.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY63021; AAR88784.1; -
DR GO; GO:0005829; Cytoisol; IEA.
KM Proteasome.
FT NON TER
SQ SEQUENCE 21 AA; 2519 MW; E877B80AC269BA4E CRC64;

Query Match 23.9%; Score 27.5; DB 2; Length 21;
Best Local Similarity 43.8%; Pred. No. 5.1e+03;
Matches 7; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 5 SIANKNGEADA-MSL 19
DB 1 AVAKVMKKEKTERKNSL 16

RESULT 7
ID 06PAJ9 PRELIMINARY; PRT; 12 AA.
AC 06PAJ9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE D1W6U476 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RL MDLLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
RA Datchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunterane P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywicki M.I., Skelton U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Straubeberg R.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC060257; AAH60257.1; -

```

```

SQ SEQUENCE 12 AA; 1262 MW; DFE49D95A4D33DC2 CRC64;

Query Match 23.5%; Score 27; DB 2; Length 12;
Best Local Similarity 54.5%; Pred. No. 3.3e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 IMGEADAMSL 19
DB 1 MLNSVAKAMSL 11

RESULT 8
ID 07RLN8 PRELIMINARY; PRT; 19 AA.
AC 07RLN8;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
CN Name=PY02502;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17XNL;
RX PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Anguolli S.V., Suh B.B., Koolij T.W., Perlea M.,
RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallom S.J., van Aken S.B., Riedmiller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,
RA Florens L., Yates F.R. III, Raine J.D., Sinden R.E., Harris M.A.,
RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
RA Carucci D.J.;
RT "Genome sequence and comparative analysis of the model rodent malaria
RT parasite Plasmodium yoelii yoelii."
RL Nature 419:512-519(2002).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABL0100686; EAA21950.1; -
KM Hypothetical protein.
FT NON TER
SQ SEQUENCE 19 AA; 2174 MW; 42DBA0B172A783F CRC64;

Query Match 23.5%; Score 27; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 5.5e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 TTEDSIKANG 12
DB 2 TTTEAIKANG 13

RESULT 9
ID 09K9B3 PRELIMINARY; PRT; 22 AA.
AC 09K9B3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE BH2736 protein.
GN OrderedLocNames=BH2736;
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=8665;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C-125;
RL MDLLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RX

```

RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.,
 RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus*
 RT *halodurans* and genomic sequence comparison with *Bacillus subtilis*."
 RL Nucleic Acids Res. 28:4337-4331(2000).
 DR EMBL; AF001516; BAB06455.1; -.
 DR PIR; H83991; H83991.
 KM Complete proteome.
 SQ SEQUENCE 22 AA; 2527 MW; 471D4FD20D0D9C39 CRC64;
 Query Match 23.5%; Score 27; DB 2; Length 22;
 Best Local Similarity 31.2%; Pred. No. 6.4e+03;
 Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 4 DSIAKIMGEADMSL 19
 Db 7 ETIKKLMEGIFDVATI 22

RESULT 10
 Q801G7 PRELIMINARY; PRT; 12 AA.
 ID Q801G7;
 AC Q801G7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Mini-cistron protein.
 OS *Chlorostemonura fumiferana* nuclear polyhedrosis virus (CEMPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=208973;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX Pubmed=14671115; DOI=10.1128/JVI.78.1.329-339.2004;
 RA Chen T., Sahni D., Carstens E.B.;
 RT "Characterization of the interaction between P143 and LEF-3 from two
 RT different baculovirus species: *Chlorostemonura fumiferana*
 RT nucleopolyhedrovirus LEF-3 can complement *Autographa californica*
 RT nucleopolyhedrovirus LEF-3 in supporting DNA replication.";
 RL J. Virol. 78:329-339(2004).
 DR EMBL; AF127530; AAF36457.1; -.
 SQ SEQUENCE 12 AA; 1252 MW; C878D87A88B2CDD9 CRC64;
 Query Match 22.6%; Score 26; DB 2; Length 12;
 Best Local Similarity 80.0%; Pred. No. 4.7e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 19 LDGGF 23
 Db 1 MDGGF 5

RESULT 11
 Q798V0 PRELIMINARY; PRT; 14 AA.
 ID Q798V0;
 AC Q798V0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE glpT and glpQ genes for glycerol 3-phosphate permease and
 DE glycerophosphoryl diester phosphodiesterase (Fragment).
 OS *Bacillus subtilis*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR95;
 RX MEDLINE=94282317; Pubmed=8012593;
 RA Nilsson R.P., Beijer L., Rutberg B.;
 RT "The glpT and glpQ genes of the glycerol regulon in *Bacillus*
 RT *subtilis*.";
 RL Microbiology 140:723-730(1994).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BR95;
 RA Nilsson R.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z26522; CAA81293.1; -.
 DT NON TER 1
 SQ SEQUENCE 14 AA; 1416 MW; 801FFDSFF58E05 CRC64;
 Query Match 22.6%; Score 26; DB 2; Length 14;
 Best Local Similarity 33.3%; Pred. No. 5.6e+03;
 Matches 3; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 8 KIMNGEADA 16
 Db 1 QILNGSEA 9

RESULT 12
 FIBA_CERAE STANDARD; PRT; 16 AA.
 ID FIBA_CERAE;
 AC P68112; P12803;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Fibrinogen alpha chain (Contains: Fibrinopeptide A) (Fragment).
 GN Name=FGA;
 OS *Cercopithecus aethiops* (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE.
 RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
 RT "Studies on fibrinopeptides from primates.";
 RL Acta Chem. Scand. 19:1788-1789(1965).
 CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -1- SUBUNIT: Hexamer containing 2 sets of 3 nonidentical chains
 CC (alpha, beta and gamma), linked to each other by disulfide bonds.
 CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.
 KM Blood coagulation; Direct protein sequencing; Plasma.
 FT NON TER 16
 FT PEPTIDE 1
 FT FIBRINOPEPTIDE A.
 SQ SEQUENCE 16 AA; 1551 MW; 49E8CBB63EA04DD3 CRC64;
 Query Match 22.6%; Score 26; DB 1; Length 16;
 Best Local Similarity 45.5%; Pred. No. 6.5e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 12 GEADMSLDGG 22
 Db 4 GEGDPLAEGGG 14

RESULT 13
 FIBA_ERYPA STANDARD; PRT; 16 AA.
 ID FIBA_ERYPA;
 AC P68112; P12803;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Fibrinogen alpha chain (Contains: Fibrinopeptide A) (Fragment).
 GN Name=FGA;
 OS *Erythrocybus patas* (Red guenon) (Cercopithecus patas).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Erythrocybus.

THIS PAGE BLANK (USPTO)

CC lacks glycosylation at Asn413 and/or Asn 611. is present only in
CC alcohols. The antibodies allow direct detection of CDT in solution,
CC eliminating the need for immobilising it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
CC fragments used in the method of the invention.

CC Sequence 15 AA;

Query Match 100.0%; Score 74; DB 8; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SKLSMGSLNLSERN 15
| | | | | | | | | | | | | | | | |
DB 1 SKLSMGSLNLSERN 15

RESULT 2
ADG46094
ID ADG46094 standard; peptide; 13 AA.

AC ADG46094;

DT 25-MAR-2004 (first entry)

DE Human CDT peptide fragment #20.

KM antibody; carbohydrate-deficient transferrin; CDT;
KW non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.

OS Homo sapiens.

PN EPI378521-A1.

PD 07-JAN-2004.

PF 19-MAY-2003; 2003EP-00011334.

PR 05-JUL-2002; 2002DE-01030550.

PA (DADE-) DADE BEHRING MAREBURG GMBH.

PI Althaus H;

DR WPI; 2004-073743/08.

PT New antibody specific for carbohydrate-deficient transferrin, useful for
PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.

PS Example 7; Page 15; 21pp; German.

CC This invention describes a novel antibody that, in aqueous solution,
CC binds selectively to carbohydrate-deficient transferrin (CDT) without
CC having to bind CDT to a solid phase. The invention also describes an
CC antibody that binds selectively to CDT at regions containing the
CC sequence VVARSMGGKEDLDIWL, TTEDSIJAKINGGADMSLDGGF, SKLSMGSLNLSERN and
CC YEKXIGERYVAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
CC using the antibodies of the invention. The antibodies of the invention
CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
CC antibodies are obtained by immunisation with non-glycosylated
CC transferrin, or a fragment, then generation of hybridomas by standard
CC fusion of spleen and myeloma cells. Hybridomas are then selected for
CC production of antibodies that specifically bind CDT from the aqueous
CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcohols. The antibodies allow direct detection of CDT in solution,
CC eliminating the need for immobilising it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
CC fragments used in the method of the invention.

XX Sequence 13 AA;

Query Match 87.8%; Score 65; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 LSMGSLNLSERN 15
| | | | | | | | | | | | | | | | |
DB 1 LSMGSLNLSERN 13

RESULT 3
ADH89392
ID ADH89392 standard; protein; 42 AA.

AC ADH89392;

DT 15-APR-2004 (first entry)

DE Human transferrin protein domain SegID36.

KM fusion protein; transferrin protein; glycosylation;
KW antibody variable region; cytotatic; antibacterial; virucide;

KW antiparasitic; immunosuppressive; antiarthritic; gene therapy;
KW septic shock; endotoxic shock; cachexia syndrome; bacterial infection;

KW viral infection; parasitic infection; neoplasm; autoimmune disease;
KW arthritis; graft rejection; human.

OS Homo sapiens.

PN US2003226155-A1.

PD 04-DEC-2003.

PF 10-MAR-2003; 2003US-00384060.

PR 30-AUG-2001; 2001US-0315745P.

PR 30-NOV-2001; 2001US-0334059P.

PR 30-AUG-2002; 2002US-00231494.

PR 30-AUG-2002; 2002US-0406977P.

PA (BIOR-) BIOREXIS PHARM CORP.

PI Sadeghi H, Prior CP, Turner A;

DR WPI; 2004-022093/02.

PT New fusion protein comprising a transferrin protein exhibiting reduced
PT glycosylation fused to at least one antibody variable region, useful for
PT preparing a composition for treating e.g., septic shock, neoplasm or
PT autoimmune disease.

PS Example 2; SEQ ID NO 36; 82pp; English.

CC This invention relates to a novel fusion protein which comprises a
CC transferrin protein exhibiting reduced glycosylation fused to at least
CC one antibody variable region. The invention may be useful for the
CC development of compounds with cytostatic, antibacterial, virucide,
CC antiparasitic, immunosuppressive or antiarthritic activity. In addition,
CC the sequences disclosed may be useful for gene therapy. The fusion
CC protein is useful for preparing a composition for treating a disease or
CC disease symptom in a patient for example septic shock, endotoxic shock,
CC cachexia syndrome associated with bacterial, viral or parasitic
CC infections, neoplasm, autoimmune disease, arthritis or adverse effects
CC associated with treatment for preventing graft rejection. The present
CC sequence is that of a domain of the human transferrin protein which was
CC used in the exemplification of the invention.

XX Sequence 42 AA;

Query Match 81.1%; Score 60; DB 8; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.0035;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSLNLSERN 15


```

XX PN WO2003060089-A2.
XX XX
XX PD 24-JUL-2003.
XX XX
XX PF 14-JAN-2003; 2003WO-US001485.
XX XX
XX PR 14-JAN-2002; 2002US-0348769P.
XX PR 18-JAN-2002; 2002US-0350701P.
XX PR 19-MAR-2002; 2002US-0366059P.
XX PR 10-MAY-2002; 2002US-0379907P.
XX PA
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Kable AE, Griffin JA, Gorvad AE, Becha SD, Richardson TW;
XX PI Emerling BM, Chien D, Jin P, Chawla NK, Yue H, Khare R, Margulis JP;
XX PI Tang YT;
XX DR WPI; 2003-598523/56.
XX DR N-PSDB; ACF35812.
XX PT New human metalloproteins and polynucleotides, useful for diagnosing,
XX PT treating or preventing autoimmune or inflammatory disorders (e.g. AIDS,
XX PT allergy or anemia), multiple sclerosis, osteoarthritis, cancer or
XX PT hepatitis.
XX PS Claim 1; Page 146-148; 153pp; English.
XX XX
XX CC The invention relates to novel human metalloproteins (MEPR) and encoding
XX CC polynucleotides. The human MEPR polypeptides, polynucleotides and
XX CC modulators are useful for diagnosing, treating or preventing disorders
XX CC associated with aberrant expression of MEPR, particularly cell
XX CC proliferative disorders (e.g. arteriosclerosis, atherosclerosis,
XX CC cirrhosis, hepatitis, paroxysmal nocturnal hemoglobinuria, polycythemia
XX CC vera, porphyria, primary chromocytopenia or cancer), developmental
XX CC disorders (e.g. renal tubular acidosis, anemia or mental retardation),
XX CC neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or
XX CC epilepsy), autoimmune/inflammatory disorders (e.g. AIDS, allergies,
XX CC asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease,
XX CC diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout,
XX CC Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome,
XX CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
XX CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
XX CC bacterial, fungal, parasitic, protozoan or helminthic infections. The
XX CC polynucleotides encoding MEPR are useful for creating transgenic animals
XX CC to model human disease. Sequences ABR82316-323 represent the human MEPR
XX CC polypeptides of the invention
XX SQ
XX Sequence 575 AA;
XX
XX Query Match 81.1%; Score 60; DB 6; Length 575;
XX Best Local Similarity 85.7%; Pred. No. 0.065;
XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 KLSMGSGLNLSEPN 15
XX DB 392 KLCMGSGLNLCEPN 405

```

```

RESULT 7
ABM83782
ID ABM83782 standard; protein; 609 AA.
XX
XX AC ABM83782;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:4031.
XX
XX KM gene therapy; human diagnostic and therapeutic polynucleotide; dtthp.
XX
XX OS Homo sapiens.
XX

```

```

PN PN WO2004023973-A2.
XX XX
XX PD 25-MAR-2004.
XX XX
XX PF 12-SEP-2003; 2003WO-US028227.
XX XX
XX PR 12-SEP-2002; 2002US-0410259P.
XX PR 12-SEP-2002; 2002US-0410260P.
XX XX
XX PA (INCY-) INCYTE CORP.
XX
XX PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
XX PI Harshborne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV;
XX PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
XX PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;
XX PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve IL;
XX PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitek UA, Kirton ES;
XX PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
XX PI Patury S, Shi X, Suarez CJ;
XX
XX DR WPI; 2004-329368/30.
XX DR N-PSDB; ACN42434.
XX
XX PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
XX PT in diagnosing a condition, disease or disorder associated with human
XX PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
XX PT in gene mapping.
XX
XX PS Claim 27; Page; 190pp; English.
XX XX
XX CC The invention relates to novel diagnostic and therapeutic polynucleotides
XX CC selected from one of the 2722 sequences defined in the specification. A
XX CC polynucleotide of the invention may have a use in gene therapy. The human
XX CC polynucleotide and therapeutic polynucleotides (dtthp) or polypeptides may be
XX CC used to diagnose a particular condition, disease or disorder associated
XX CC with human molecules, e.g. cell proliferative disorders,
XX CC autoimmune/inflammatory disorders, developmental disorders, endocrine
XX CC disorder, neurological disorders, gastrointestinal disorders, or
XX CC infections caused by virus, bacteria, fungi or parasite. The dtthp
XX CC molecules may also be used in genetic mapping, in identifying individuals
XX CC from minute biological samples, in detecting single nucleotide
XX CC polymorphisms, as molecular weight markers, and for somatic or germline
XX CC gene therapy. The present sequence represents a dtthp protein of the
XX CC invention. Note: The sequence data for this patent is not represented in
XX CC the printed specification, but was obtained in electronic format directly
XX CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX SQ
XX Sequence 609 AA;
XX
XX Query Match 81.1%; Score 60; DB 8; Length 609;
XX Best Local Similarity 85.7%; Pred. No. 0.07;
XX Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 KLSMGSGLNLSEPN 15
XX DB 444 KLCMGSGLNLCEPN 457

```

```

RESULT 8
ABM83781
ID ABM83781 standard; protein; 627 AA.
XX
XX AC ABM83781;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX DE Human diagnostic and therapeutic pprotein SEQ ID NO:4030.
XX
XX KM gene therapy; human diagnostic and therapeutic polynucleotide; dtthp.
XX
XX OS Homo sapiens.
XX
XX PN WO2004023973-A2.

```



```
XX 12-SEP-2003; 2003WO-US028227.
PF 12-SEP-2002; 2002US-0410259P.
XX 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
XX (INCY-) INCYTE CORP.
PA
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Harbshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV,
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP,
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Geregin EH,
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Valt UA, Kirtton ES,
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
PI Patursy S, Shi X, Suarez CJ,
XX
XX WPI; 2004-329368/30.
DR N-PSDB; ACN42430.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 27; Page; 190pp; English.
PS
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 643 AA;
Query Match 81.1%; Score 60; DB 8; Length 643;
Best Local Similarity 85.7%; Pred. No. 0.074;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGNLSEPN 15
Db 478 KLCMSGSLNLCFNP 491
```

```
RESULT 11
ABM83783
ID ABM83783 standard; protein; 645 AA.
```

```
XX AC ABM83783;
XX
XX 18-NOV-2004 (first entry)
XX
XX Human diagnostic and therapeutic pproetin SEQ ID NO:4032.
XX
XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
XX Homo sapiens.
XX
XX MO2004023973-A2.
XX
XX 25-MAR-2004.
XX
```

```
PF 12-SEP-2003; 2003WO-US028227.
XX 12-SEP-2002; 2002US-0410259P.
XX 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
XX (INCY-) INCYTE CORP.
PA
XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Harbshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV,
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP,
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Geregin EH,
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Valt UA, Kirtton ES,
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
PI Patursy S, Shi X, Suarez CJ,
XX
XX WPI; 2004-329368/30.
DR N-PSDB; ACN42435.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 27; Page; 190pp; English.
PS
XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 645 AA;
Query Match 81.1%; Score 60; DB 8; Length 645;
Best Local Similarity 85.7%; Pred. No. 0.074;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGNLSEPN 15
Db 462 KLCMSGSLNLCFNP 475
```

```
RESULT 12
AAU02938
ID AAU02938 standard; protein; 646 AA.
```

```
XX AC AAU02938;
XX
XX 12-SEP-2001 (first entry)
XX
XX Angiotensin converting enzyme (ACEV) splice variant protein #38.
XX
XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
XX granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
XX platelet-derived endothelial cell growth factor; cardiovascular disease;
XX cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
XX vasorelaxant intestinal polypeptide receptor 2; arteriosclerosis; cancer;
XX myocardial infarction; coronary arterial thrombosis; renal disease;
XX diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
XX multiple sclerosis; immune complex nephritis; deep vein thrombosis;
XX nonarctoidotic pulmonary granulomatous disease; endothelial abnormality;
```

KW vascular disorder; asbestosis.
XX
OS Homo sapiens.
XX
FN WO200136632-A2.
XX
PD 25-MAY-2001.
XX
PF 17-NOV-2000; 2000WO-IL000766.
XX
PR 17-NOV-1999; 99IL-00132978.
PR 10-DEC-1999; 99IL-00133455.
XX
PA (COMP-) COMPUGEN LTD.
XX
PI Levine Z, David A, Azar I, Khosravi R, Bernstein J;
XX
DR WPI; 2001-336004/35.
DR N-PSDB; AAS06038.
XX
PT Novel alternative splicing variants e.g. variant of angiotensin
PT converting enzyme (ACEV), useful in identifying candidate compounds
PT capable of binding to the variant and to detect anti-variant antibodies.
XX
PS Claim 4; Fig 38; 519pp; English.
XX
CC The sequence represents an angiotensin converting enzyme splice variant
CC (ACEV) polypeptide. The polypeptides of the invention include variants of
CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
CC inhibitor 1C, cellular tumour antigen p53, and vasoactive intestinal
CC polypeptide receptor 2. The polypeptides and their associated nucleic
CC acids are useful for identification of variant sequences and detection of
CC candidate compounds capable of binding the molecules. The sequences of
CC the invention can be used in the treatment and diagnosis of various
CC disorders including cardiovascular diseases such as arteriosclerosis,
CC myocardial infarction and coronary arterial thrombosis, renal diseases
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
CC immune disorders such as immune complex nephritis, multiple sclerosis,
CC cancer, sarcoidosis, nonaroidotic pulmonary granulomatous diseases such
CC as asbestosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis
XX
SQ Sequence 646 AA:
XX
Query Match 81.1%; Score 60; DB 4; Length 646;
Best Local Similarity 85.7%; Pred. No. 0.075;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSWGSGLINSEPN 15
DB 463 KLCWGSGLINCEPN 476

RESULT 13
ABM83780
ID ABM83780 standard; protein; 646 AA.
XX
AC ABM83780;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic protein SEQ ID NO:4029.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dthp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.

XX
PR 12-SEP-2002; 2002US-0410259P.
PR 12-SEP-2002; 2002US-0410260P.
XX
XX (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Brune CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH,
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LU;
PI Lagace RE, Spito PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
DR WPI; 2004-329368/30.
DR N-PSDB; ACN42432.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
PS Claim 27; Page; 190pp; English.
XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders, endocrine
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dthp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dthp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX
SQ Sequence 646 AA:
XX
Query Match 81.1%; Score 60; DB 8; Length 646;
Best Local Similarity 85.7%; Pred. No. 0.075;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSWGSGLINSEPN 15
DB 463 KLCWGSGLINCEPN 476

RESULT 14
AAU02937
ID AAU02937 standard; protein; 665 AA.
XX
AC AAU02937;
XX
DT 12-SEP-2001 (first entry)
XX
DE Angiotensin converting enzyme (ACEV) splice variant protein #37.
XX
KW Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW nonaroidotic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; asbestosis.

XX The present sequence is the protein sequence of human transferrin (Tf),
 CC minus the signal peptide. The invention relates to modified Tf fusion
 CC proteins comprising at least one therapeutic protein, polypeptide or
 CC peptide, in which the Tf portion is engineered to extend the serum half-
 CC life or bioavailability of the molecule. The modified Tf fusion protein
 CC preferably comprises a human Tf moiety that has been modified to reduce
 CC or prevent glycosylation, iron binding and/or transferrin receptor
 CC binding, having at least one amino acid substitution, deletion or
 CC addition in the hinge region, or at residues Asp-63, Gly-65, Tyr-95, Tyr-
 CC 188, Lys-206, His-207, His-249, Asp-392, Tyr-426, Tyr-514, Tyr-517, His-
 CC 585, Thr-120, Arg-124, Ala-126, Gly-127, Thr-452, Arg-456, Ala-458 and
 CC Gly-459, or a mutation which prevents glycosylation at Asn-413 or Asn-611
 CC (all claimed). Nucleic acids encoding such fusion proteins, vectors, host
 CC cells and transgenic animals which produce the fusion protein in their
 CC serum or milk are also claimed. The modified fusion protein is useful for
 CC treating a disease or disease symptom, or for delivering a therapeutic
 CC agent complexed to the ferric iron of transferrin to the inside of a cell
 CC or across the blood-brain barrier. The modified fusion protein, or a
 CC nucleic acid encoding it, can be used in the diagnosis, prognosis, or a
 CC prevention and/or treatment of diseases and/or disorders of the
 CC endocrine, nervous, immune, respiratory, cardiovascular, reproductive and
 CC digestive systems, diseases and/or disorders relating to the blood or to
 CC cell proliferation, inflammatory conditions, and to treat viral, fungal,
 CC bacterial or parasitic infection
 CC
 XX
 SQ Sequence 679 AA;

Query Match 81.1%; Score 60; DB 6; Length 679;
 Best Local Similarly 85.7%; Pred. No. 0.079;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 KLSMGSGLNSEPN 15
 |||||||||
 Db 496 KLCMGSGLNLCERN 509

Search completed: November 1, 2005, 12:48:53
 Job time : 86.8088 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:37:09 ; Search time 22.0588 Seconds
(without alignments)
50.761 Million cell updates/sec

Title: US-10-612-162A-3

Perfect score: 74
Sequence: 1 SKLSMGSGLNLESPN 15

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A COMB pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B COMB pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A COMB pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B COMB pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTCUS COMB pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1 pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	81.1	698	2	US-08-175-158A-2
2	60	81.1	698	4	US-09-439-740-2
3	60	81.1	1074	2	US-08-470-058-2
4	60	81.1	1074	3	US-09-037-188-2
5	60	81.1	1074	3	US-09-285-310-2
6	60	81.1	1410	3	US-08-470-058-4
7	60	81.1	1410	3	US-09-037-188-4
8	60	81.1	1410	3	US-09-285-310-4
9	52	70.3	696	6	5262177-4
10	52	70.3	696	6	5262177-4
11	46	62.2	439	4	US-09-248-796A-15968
12	43	58.1	1969	4	US-09-418-710-72
13	43	58.1	1969	4	US-09-839-479-71
14	43	58.1	1972	4	US-09-418-710-21
15	43	58.1	1972	4	US-09-839-479-21
16	41	55.4	148	4	US-09-711-164-464
17	41	55.4	148	4	US-09-248-796A-20574
18	40.5	54.7	504	4	US-09-469-039A-11966
19	40	54.1	125	3	US-08-480-173A-50
20	40	54.1	125	3	US-08-484-408A-50
21	40	54.1	170	2	US-08-683-262B-49
22	40	54.1	170	2	US-09-361-707-49
23	40	54.1	174	2	US-08-683-262B-38
24	40	54.1	174	2	US-08-683-262B-39
25	40	54.1	174	2	US-08-683-262B-42
26	40	54.1	174	2	US-08-683-262B-43
27	40	54.1	174	2	US-08-683-262B-44

28	40	54.1	174	2	US-08-683-262B-45	Sequence 45, Appl
29	40	54.1	174	2	US-08-683-262B-46	Sequence 46, Appl
30	40	54.1	174	2	US-08-683-262B-47	Sequence 47, Appl
31	40	54.1	174	2	US-08-683-262B-48	Sequence 48, Appl
32	40	54.1	174	3	US-08-480-173A-48	Sequence 48, Appl
33	40	54.1	174	3	US-08-484-408A-48	Sequence 48, Appl
34	40	54.1	174	3	US-09-361-707-38	Sequence 38, Appl
35	40	54.1	174	3	US-09-361-707-39	Sequence 39, Appl
36	40	54.1	174	3	US-09-361-707-42	Sequence 42, Appl
37	40	54.1	174	3	US-09-361-707-43	Sequence 43, Appl
38	40	54.1	174	3	US-09-361-707-44	Sequence 44, Appl
39	40	54.1	174	3	US-09-361-707-45	Sequence 45, Appl
40	40	54.1	174	3	US-09-361-707-46	Sequence 46, Appl
41	40	54.1	174	3	US-09-361-707-47	Sequence 47, Appl
42	40	54.1	174	3	US-09-361-707-48	Sequence 48, Appl
43	40	54.1	174	6	5204096-5	Patent No. 5204096
44	40	54.1	174	6	5204096-5	Patent No. 5204096
45	40	54.1	358	4	US-09-328-352-7579	Sequence 7579, Ap

ALIGNMENTS

RESULT 1
US-08-175-158A-2

Sequence 2, Application US/08175158A
Patent No. 5986067

GENERAL INFORMATION:

APPLICANT: FUNK, Walter D.
APPLICANT: MAGGILIVRAY, Ross T.A.

APPLICANT: WOODWORTH, Robert C.
TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-

NUMBER OF SEQUENCES: 7
TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510

CITY: Boston
STATE: Massachusetts

COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/175,158A

FILING DATE: 28-DEC-1993
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/832,029

FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:

NAME: Deconati, Giulio A.
REGISTRATION NUMBER: 31,503

REFERENCE/DOCKET NUMBER: UVI-005CP2
TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 698 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-175-158A-2

Query Match 81.1%; Score 60; DB 2; Length 698;
Best Local Similarity 85.7%; Pred. No. 0.018;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSGLNISEPN 15
DB 515 KLCMGSGGLNICEPN 528

RESULT 2

US-09-439-740-2
Sequence 2, Application US/09439740
Patent No. 6825037
GENERAL INFORMATION:
APPLICANT: FUNK, Walter D.
APPLICANT: MACGILLIVRAY, Ross T.A.
APPLICANT: MASON, Anne B.
APPLICANT: WOODWORTH, Robert C.
TITLE OF INVENTION: RECOMBINANT TRANSFERRIN HALF-
TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/439,740
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/175,158
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: UVI-005CPE2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 698 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-439-740-2

Query Match 81.1%; Score 60; DB 4; Length 698;
Best Local Similarity 85.7%; Pred. No. 0.018;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNISEPN 15
DB 515 KLCMGSGGLNICEPN 528

RESULT 3

US-08-470-058-2
Sequence 2, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
TITLE OF INVENTION: of a Selected Substance Into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.

STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-2

Query Match 81.1%; Score 60; DB 2; Length 1074;
Best Local Similarity 85.7%; Pred. No. 0.029;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNISEPN 15
DB 891 KLCMGSGGLNICEPN 904

RESULT 4

US-09-037-188-2
Sequence 2, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemontt, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-2

Query Match 81.1%; Score 60; DB 3; Length 1074;
Best Local Similarity 85.7%; Pred. No. 0.029;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 KLSWGSGLNCEPN 15
Db 891 KLSWGSGLNCEPN 904

RESULT 5
US-09-285-310-2
Sequence 2, Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285.310
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-2

Query Match 81.1%; Score 60; DB 3; Length 1074;
Best Local Similarity 85.7%; Pred. No. 0.029;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 KLSWGSGLNCEPN 15
Db 891 KLSWGSGLNCEPN 904

RESULT 6
US-08-470-058-4
Sequence 4, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
of a Selected Substance into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-4

Query Match 81.1%; Score 60; DB 2; Length 1410;
Best Local Similarity 85.7%; Pred. No. 0.04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 KLSWGSGLNCEPN 15
Db 1227 KLSWGSGLNCEPN 1240

RESULT 7
US-09-037-188-4
Sequence 4, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible

Query Match 81.1%; Score 60; DB 3; Length 1074;
Best Local Similarity 85.7%; Pred. No. 0.029;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OPERATING SYSTEM: windows95
SOFTWARE: FASTSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-4

Query Match 81.1%; Score 60; DB 3; Length 1410;
Best Local Similarity 85.7%; Pred. No. 0.04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLSERN 15
DB 1227 KLCMPSGLNLSERN 1240

RESULT 8
US-09-285-310-4
Sequence 4: Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: windows95
SOFTWARE: FASTSEQ for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids

TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-4

Query Match 81.1%; Score 60; DB 3; Length 1410;
Best Local Similarity 85.7%; Pred. No. 0.04;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLSERN 15
DB 1227 KLCMPSGLNLSERN 1240

RESULT 9
5262177-4
Patent No. 5262177
APPLICANT: BROWN, J. OSEPH P.; ESTIN, CHARLES D.; PLOWMAN, GREGORY
D.; HELSTROM, KARL E.; ROSE, TIMOTHY M.; HELSTROM, INGEGARD;
PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
MELANOMA-ASSOCIATED ANTIGEN
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/7230
FILING DATE: 27-JAN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 827,313
FILING DATE: 07-FEB-1986
SEQ ID NO: 4:
LENGTH: 696

Query Match 70.3%; Score 52; DB 6; Length 696;
Best Local Similarity 78.6%; Pred. No. 0.5;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLSERN 15
DB 514 KLCMPSGLNLSERN 527

RESULT 10
5262177-4
Patent No. 5262177
APPLICANT: BROWN, J. OSEPH P.; ESTIN, CHARLES D.; PLOWMAN, GREGORY
D.; HELSTROM, KARL E.; ROSE, TIMOTHY M.; HELSTROM, INGEGARD;
PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
MELANOMA-ASSOCIATED ANTIGEN
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/7230
FILING DATE: 27-JAN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 827,313
FILING DATE: 07-FEB-1986
SEQ ID NO: 4:
LENGTH: 696

Query Match 70.3%; Score 52; DB 6; Length 696;
Best Local Similarity 78.6%; Pred. No. 0.5;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLSERN 15
DB 514 KLCMPSGLNLSERN 527

RESULT 11
US-09-248-796A-15968
Sequence 15968, Application US/09248796A

```
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 15968
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (112)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknc
US-09-248-796A-15968

Query Match          62.2%; Score 46; DB 4; Length 439;
Best Local Similarity 57.1%; Pred. No. 3.6;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SKUSGSLNSEPN 14
|:|||||:|:|
Db 351 SPMSMGAGINWTP 364

RESULT 12
US-09-418-710-72
; Sequence 72, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 72
; LENGTH: 1969
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-72

Query Match          58.1%; Score 43; DB 4; Length 1969;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 SMGSGNLISEPN 15
|:|||||:|:|
Db 1454 SLSSGGLSGN 1465

RESULT 13
US-09-839-479-71
; Sequence 71, Application US/09839479
; Patent No. 6727222
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042002
; CURRENT APPLICATION NUMBER: US/09/839,479
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
```

```
; CURRENT APPLICATION NUMBER: US/09/839,479
; CURRENT FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 1969
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-479-71

Query Match          58.1%; Score 43; DB 4; Length 1969;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 SMGSGNLISEPN 15
|:|||||:|:|
Db 1454 SLSSGGLSGN 1465

RESULT 14
US-09-418-710-21
; Sequence 21, Application US/09418710
; Patent No. 6596482
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042001
; CURRENT APPLICATION NUMBER: US/09/418,710
; CURRENT FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1972
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-418-710-21

Query Match          58.1%; Score 43; DB 4; Length 1972;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 SMGSGNLISEPN 15
|:|||||:|:|
Db 1457 SLSSGGLSGN 1468

RESULT 15
US-09-839-479-21
; Sequence 21, Application US/09839479
; Patent No. 6727222
; GENERAL INFORMATION:
; APPLICANT: Jones, Michael H.
; TITLE OF INVENTION: TRANSCRIPTIONAL REGULATOR
; FILE REFERENCE: 06501-042002
; CURRENT APPLICATION NUMBER: US/09/839,479
; PRIOR FILING DATE: 2001-04-20
; PRIOR APPLICATION NUMBER: US 09/418,710
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: PCT/JP98/01783
```

```

; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: JP 9/310027
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: JP 9/116570
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO: 21
; LENGTH: 1972
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-839-479-21

```

```

Query Match      58.1%; Score 43; DB 4; Length 1972;
Best Local Similarity 75.0%; Pred. No. 75;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 SMGGLNLSEPN 15
      |:|||||
DB      1457 SLGGGLGLSRGN 1468

```

Search completed: November 1, 2005, 12:57:31
 Job time : 23.0588 secs


```
/ Sequence 15, Application US/10378094
/ Publication No. US20030221201A1
/ GENERAL INFORMATION:
/ APPLICANT: PRIOR, Christopher P.
/ APPLICANT: LAI, Char-Huei
/ APPLICANT: SADEGH, Homayoun
/ APPLICANT: TURNER, Andrew
/ TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
/ FILE REFERENCE: 54710-5001-01-US
/ CURRENT APPLICATION NUMBER: US/10/378,094
/ CURRENT FILING DATE: 2003-03-04
/ PRIOR APPLICATION NUMBER: US 10/221,494
/ PRIOR FILING DATE: 2002-08-30
/ PRIOR APPLICATION NUMBER: US 60/334,059
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: US 60/315,745
/ PRIOR FILING DATE: 2001-08-30
/ NUMBER OF SEQ ID NOS: 66
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 15
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ OTHER INFORMATION: C1 subdomain of transferrin
US-10-378-094-15
```

```
Query Match      81.1%; Score 60; DB 15; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.0032;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 KLSMSGSLNLEPN 15
        |||||||
Db      25 KLCMSGSLNLEPN 38
```

```
RESULT 3
US-10-384-060-36
/ Sequence 36, Application US/10384060
/ Publication No. US20030226155A1
/ GENERAL INFORMATION:
/ APPLICANT: SADEGH, Homayoun
/ APPLICANT: PRIOR, Christopher P.
/ APPLICANT: TURNER, Andrew
/ TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
/ FILE REFERENCE: 54710-5004-US
/ CURRENT APPLICATION NUMBER: US/10/384,060
/ CURRENT FILING DATE: 2003-03-10
/ PRIOR APPLICATION NUMBER: US 10/231,494
/ PRIOR FILING DATE: 2002-08-30
/ PRIOR APPLICATION NUMBER: US 60/334,059
/ PRIOR FILING DATE: 2001-11-30
/ PRIOR APPLICATION NUMBER: US 60/315,745
/ PRIOR FILING DATE: 2001-08-30
/ PRIOR APPLICATION NUMBER: US 60/406,977
/ PRIOR FILING DATE: 2002-08-30
/ NUMBER OF SEQ ID NOS: 80
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 36
/ LENGTH: 42
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: C1 domain of human Tf
US-10-384-060-36
```

```
Query Match      81.1%; Score 60; DB 15; Length 42;
Best Local Similarity 85.7%; Pred. No. 0.0032;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 KLSMSGSLNLEPN 15
        |||||||
```

```
Db      25 KLCMSGSLNLEPN 38
```

```
RESULT 4
US-09-891-126-5
/ Sequence 5, Application US/09891126
/ Patent No. US20020072596A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruden et al.
/ TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
/ FILE REFERENCE: PT035PI
/ CURRENT APPLICATION NUMBER: US/09/891,126
/ CURRENT FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: PCT/US00/34769
/ PRIOR FILING DATE: 2000-12-21
/ PRIOR APPLICATION NUMBER: 60/171,595
/ PRIOR FILING DATE: 1999-12-23
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 328
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-891-126-5
```

```
Query Match      81.1%; Score 60; DB 9; Length 328;
Best Local Similarity 85.7%; Pred. No. 0.032;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 KLSMSGSLNLEPN 15
        |||||||
Db      179 KLCMSGSLNLEPN 192
```

```
RESULT 5
US-10-266-745-5
/ Sequence 5, Application US/10266745
/ Publication No. US20030149256A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruden et al.
/ TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
/ FILE REFERENCE: PT035PI
/ CURRENT APPLICATION NUMBER: US/10/266,745
/ CURRENT FILING DATE: 2002-10-09
/ PRIOR APPLICATION NUMBER: US/09/891,126
/ PRIOR FILING DATE: 2001-06-26
/ PRIOR APPLICATION NUMBER: PCT/US00/34769
/ PRIOR FILING DATE: 2000-12-21
/ PRIOR APPLICATION NUMBER: 60/171,595
/ PRIOR FILING DATE: 1999-12-23
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 5
/ LENGTH: 328
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-266-745-5
```

```
Query Match      81.1%; Score 60; DB 14; Length 328;
Best Local Similarity 85.7%; Pred. No. 0.032;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 KLSMSGSLNLEPN 15
        |||||||
Db      179 KLCMSGSLNLEPN 192
```

```
RESULT 6
US-10-378-094-3
/ Sequence 3, Application US/10378094
/ Publication No. US20030221201A1
/ GENERAL INFORMATION:
/ APPLICANT: PRIOR, Christopher P.
```

```

; APPLICANT: LAI, Char-Huei
; APPLICANT: SADEGH, Homayoun
; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5001-01-US
; CURRENT APPLICATION NUMBER: US/10/378,094
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Mature Transferrin Protein
; US-10-378-094-3
```

```

Query Match      81.1%; Score 60; DB 15; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2 KLSMGSGLNSEPN 15
Db      496 KLCMGSGLNLCERN 509
```

```

RESULT 7
; US-10-384-060-3
; Sequence 3, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGH, Homayoun
; APPLICANT: PRIOR, Christopher P.
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Mature Transferrin Protein
; US-10-384-060-3
```

```

Query Match      81.1%; Score 60; DB 15; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2 KLSMGSGLNSEPN 15
Db      496 KLCMGSGLNLCERN 509
```

```

RESULT 8
; US-10-231-494-3
; Sequence 3, Application US/10231494
; Publication No. US20040023334A1
; GENERAL INFORMATION:
; APPLICANT: Prior, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Mature transferrin protein
; US-10-231-494-3
```

```

Query Match      81.1%; Score 60; DB 15; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2 KLSMGSGLNSEPN 15
Db      496 KLCMGSGLNLCERN 509
```

```

RESULT 9
; US-10-429-482-4
; Sequence 4, Application US/10429482
; Publication No. US20040219097A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For The Diagnosis, Imaging and Treatment Of T
; FILE REFERENCE: 2537,000001
; CURRENT APPLICATION NUMBER: US/10/429,482
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-429-482-4
```

```

Query Match      81.1%; Score 60; DB 15; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY      2 KLSMGSGLNSEPN 15
Db      496 KLCMGSGLNLCERN 509
```

```

RESULT 10
; US-10-429-497-4
; Sequence 4, Application US/10429497
; Publication No. US20040219098A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For The Treatment of Tumors
; FILE REFERENCE: 2537,000006
; CURRENT APPLICATION NUMBER: US/10/429,497
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
```

```
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-497-4

Query Match      81.1%; Score 60; DB 16; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 KLSMSGSLNISEPN 15
      || ||||| |||
Db      496 KLCMSGSLNICEPN 509

RESULT 11
US-10-429-515-4
; Sequence 4, Application US/10429515
; Publication No. US20040219099A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods For The Treatment Of Tumors
; FILE REFERENCE: 2537.000005
; CURRENT APPLICATION NUMBER: US/10/429,515
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-515-4

Query Match      81.1%; Score 60; DB 16; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 KLSMSGSLNISEPN 15
      || ||||| |||
Db      496 KLCMSGSLNICEPN 509

RESULT 12
US-10-429-598-4
; Sequence 4, Application US/10429598
; Publication No. US20040219100A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For The Treatment of Tumors
; FILE REFERENCE: 2537.000003
; CURRENT APPLICATION NUMBER: US/10/429,598
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-598-4

Query Match      81.1%; Score 60; DB 16; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 KLSMSGSLNISEPN 15
      || ||||| |||
Db      496 KLCMSGSLNICEPN 509

RESULT 13
US-10-429-635-4
; Sequence 4, Application US/10429635
; Publication No. US20040219101A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Composition Useful For Treatment Of Tumors
; FILE REFERENCE: 2537.000007
; CURRENT APPLICATION NUMBER: US/10/429,635
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-635-4

Query Match      81.1%; Score 60; DB 16; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 KLSMSGSLNISEPN 15
      || ||||| |||
Db      496 KLCMSGSLNICEPN 509

RESULT 14
US-10-429-653-4
; Sequence 4, Application US/10429653
; Publication No. US20040219102A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Compositions For Drug Delivery
; FILE REFERENCE: 2537.000009
; CURRENT APPLICATION NUMBER: US/10/429,653
; CURRENT FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-653-4

Query Match      81.1%; Score 60; DB 16; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 KLSMSGSLNISEPN 15
      || ||||| |||
Db      496 KLCMSGSLNICEPN 509

RESULT 15
US-10-429-659-4
; Sequence 4, Application US/10429659
; Publication No. US20040219103A1
; GENERAL INFORMATION:
; APPLICANT: Sandhu, Jasbir
; TITLE OF INVENTION: Methods Useful For The Diagnosis, Imaging and Treatment Of Tumor
; FILE REFERENCE: 2537.000004
; CURRENT APPLICATION NUMBER: US/10/429,659
; CURRENT FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-429-659-4

Query Match      81.1%; Score 60; DB 16; Length 679;
Best Local Similarity 85.7%; Pred. No. 0.071;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2 KLSMSGSLNISEPN 15
      || ||||| |||
```

Tue Nov 1 17:05:15 2005

us-10-612-162a-3.rapb

Page 5

Db 496 KLCMGSGLNLCBPN 509

Search completed: November 1, 2005, 13:26:07
Job time : 76.8824 secB

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:35:39 ; Search time 15.2206 Seconds
(without alignments)
94.822 Million cell updates/sec

Title: US-10-612-162A-3

Perfect score: 74

Sequence: 1 SKXSMGSLNLSRPN 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	60	81.1	698	1	TFHUP
2	41	55.4	148	2	C65068
3	41	55.4	163	2	C91092
4	41	55.4	163	2	G85937
5	40	54.1	382	2	T13474
6	40	54.1	384	2	T13469
7	40	54.1	400	1	SAVLA
8	40	54.1	400	2	S35528
9	40	54.1	445	2	S43492
10	40	54.1	448	2	D71852
11	40	54.1	448	2	H64663
12	40	54.1	516	2	T27845
13	39	52.7	338	2	C89991
14	39	52.7	400	1	UQ1575
15	39	52.7	400	1	SAVLKS
16	39	52.7	400	1	SAVLVD
17	39	52.7	494	2	T02523
18	39	52.7	545	2	JC2500
19	39	52.7	610	2	A96701
20	39	52.7	915	2	S24577
21	39	52.7	1268	2	AB0204
22	39	52.7	3828	2	T13857
23	38	51.4	289	2	T48108
24	38	51.4	293	2	T40702
25	38	51.4	311	2	T42088
26	38	51.4	316	2	T49376
27	38	51.4	317	1	S67781
28	38	51.4	322	2	S43453
29	38	51.4	465	2	G90961

30	38	51.4	465	2	G85809	flagellar capping
31	38	51.4	468	2	A64956	flagellar hook-ax
32	38	51.4	768	2	AH1085	hypothetical prote
33	38	51.4	769	1	WZBE54	gene 54 protein -
34	38	51.4	1021	2	T05901	hypothetical prote
35	38	51.4	2212	2	A41098	calcium channel pr
36	37.5	50.7	431	2	F95236	prg system, ITC co
37	37.5	50.7	431	2	H98100	hypothetical prote
38	37	50.0	106	2	T20860	hypothetical prote
39	37	50.0	124	2	B27632	T-cell receptor al
40	37	50.0	152	2	F71973	hypothetical prote
41	37	50.0	282	2	S31463	probable integrase
42	37	50.0	325	2	T35318	probable dehydroge
43	37	50.0	335	2	C95118	hypothetical prote
44	37	50.0	335	2	A97988	hypothetical prote
45	37	50.0	344	1	RWRTC2	T-cell surface gly

ALIGNMENTS

RESULT 1
TFHUP
transferrin precursor (validated) - human
N:Alternate names: siderophilin
C:Species: Homo sapiens (man)
C>Date: 15-Oct-1982 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: A20981; A92417; A94044; A23090; A22739; I51959; I63133; I54011; I68160; A0
R/Yang, F.; Lum, J.B.; McGill, J.R.; Moore, C.M.; Naylor, S.L.; van Bregt, P.H.; Baldwi.
Proc. Natl. Acad. Sci. U.S.A. 81, 2752-2756, 1984
A>Title: Human transferrin: cDNA characterization and chromosomal localization.
A/Reference number: A20981; PMID:84194084; PMID:6585826
A/Content: variant C
A/Accession: A20981
A/Molecule type: mRNA
A/Residues: 1-698 <YAN>
A/Cross-references: UNIPROT:P02787; EMBL:M12530; NID:G339452; PIDN:AAA61140.1; PID:G339
R/McGillivray, R.T.A.; Mendez, E.; Shevale, J.G.; Sinha, S.K.; Linbeck-Zins, J.; Brew
J. Biol. Chem. 258, 3543-3553, 1983
A>Title: The primary structure of human serum transferrin. The structures of seven cyan
A/Reference number: A92417; PMID:83160878; PMID:6833213
A/Accession: A92417
A/Molecule type: protein
A/Residues: 20-263, 'E', 265-328, 'N', 330-379, 'SD', 382-435, 'D', 437-557, 'T', 559-560, 'P', 562
A/Note: the sequence shown is the predominant electrophoretic genetic variant (C or TfC)
R/Park, I.; Schaeffer, E.; Sidoli, A.; Baralle, F.E.; Cohen, G.N.; Zakin, M.M.
Proc. Natl. Acad. Sci. U.S.A. 82, 3149-3153, 1985
A>Title: Organization of the human transferrin gene: direct evidence that it originated
A/Reference number: A94044; PMID:85216459; PMID:3858812
A/Accession: A94044
A/Molecule type: DNA
A/Residues: 73-263, 'E', 265-328, 'N', 330-562 <PAR>
A/Cross-references: EMBL:M1361
R/Adrian, G.S.; Korinek, B.W.; Bowman, B.H.; Yang, F.
Gene 49, 167-175, 1986
A>Title: The human transferrin gene: 5' region contains conserved sequences which match
A/Reference number: A23090; PMID:87192006; PMID:3106157
A/Accession: A23090
A/Molecule type: DNA
A/Residues: 1-72, 291-300 <ADR>
A/Cross-references: EMBL:M5673
R/Uzan, G.; Fraim, M.; Park, I.; Beemond, C.; Maessen, G.; Trepac, J.S.; Zakin, M.M.; K
Biochem. Biophys. Res. Commun. 119, 273-281, 1984
A>Title: Molecular cloning and sequence analysis of cDNA for human transferrin.
A/Reference number: A32739; PMID:84153910; PMID:6322780
A/Accession: A32739
A/Molecule type: mRNA
A/Residues: 422-690, 'G', 692-698 <UZA>
A/Cross-references: EMBL:M12525; NID:G339468; PIDN:AAA61142.1; PID:G339469
R/McGillivray, R.T.A.; Mendez, E.; Sinha, S.K.; Sutton, M.R.; Linbeck-Zins, J.; Brew,
Proc. Natl. Acad. Sci. U.S.A. 79, 2504-2508, 1982

A>Title: The complete amino acid sequence of human serum transferrin.
A:Reference number: A93911; MUID:8222166; PMID:6553407
A:Contents: annotation; disulfide bonds
R:Herberberger, C.L.; Larson, U.L.; Arnold, B.; Roestek, P.R.
Ann. N. Y. Acad. Sci. 646, 140-154, 1991
A>Title: A cloned gene for human transferrin.
A:Reference number: I51959; MUID:9221399; PMID:1809186
A:Accession: I51959
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-698 <RES>
A:Cross-references: GB:S95936; NID:G248647; PIDN:AA61233.1; PID:G248648
R:Duguid, J.R.; Bohmont, C.W.; Liu, N.G.; Tourtellotte, W.W.
Proc. Natl. Acad. Sci. U.S.A. 86, 7260-7264, 1989
A>Title: Changes in brain gene expression shared by scrapie and Alzheimer disease.
A:Reference number: I48174; MUID:89386721; PMID:2780570
A:Accession: I63133
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 636-696 <RE2>
A:Cross-references: GB:M26641; NID:G339988; PIDN:AA61233.1; PID:G339989
R:Schoeffler, E.; Lucero, M.A.; Jeltch, J.M.; Py, M.C.; Levin, M.U.; Chambon, P.; Cohen, Gene 56, 109-116, 1987
A>Title: Complete structure of the human transferrin gene. Comparison with analogous chi
A:Reference number: I54011; MUID:88056305; PMID:3678832
A:Accession: I54011
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-72 <RE3>
A:Cross-references: GB:M17611; NID:G339480; PIDN:AA61147.1; PID:G339485
A:Accession: I68160
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 564-698 <RE4>
A:Cross-references: GB:M17614; NID:G339483; PIDN:AA61148.1; PID:G339486
C:Comment: Each of the two repetitive domains binds a ferric ion and a bicarbonate anion
C:Genetic8:
A:Gene: GDB:TF
A:Cross-references: GDB:120432; OMIM:190000
A:Map position: 3q21-3q21
A:Intons: 15/1; 72/3; 119/1; 166/1; 212/2; 231/1; 290/3; 350/1; 401/3; 433/1; 444/1; 49
C:Function:
A:Description: binds iron for delivery into cells
A:Superfamily: transferrin; transferrin repeat homology
C:Keywords: duplication; glycoprotein; iron transport; metal binding; plasma
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-698/Product: transferrin #status experimental <MAT>
F:20-350/Domain: transferrin repeat homology <TRH2>
F:356-686/Domain: transferrin repeat homology <TRH2>
F:28-67,38-58,137-213,156-350,177-193,180-196,190-198,246-260,358-615,364-396,374-387,42
F:432,630/Binding site: carbohydrate (Aan) (covalent) #status experimental
Query Match 81.1%; Score 60; DB 1; Length 698;
Best Local Similarity 85.7%; Pred. No. 0.0087;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNLSEPN 15
DB 515 KLCMSGGLNLSEPN 528
RESULT 2
C65068
hypothetical protein b2850 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
A:Accession: C65068
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
Science 277, 1453-1462, 1997
A>Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: C65068

A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-148 <BLAT>
A:Cross-references: UNIPROT:Q46786; GB:AE000369; GB:U00096; NID:G2367168; PIDN:AACT5889
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: Escherichia coli hypothetical protein b2850
Query Match 55.4%; Score 41; DB 2; Length 148;
Best Local Similarity 66.7%; Pred. No. 4.8;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNLSE 13
DB 35 KITMSGGLNLYIE 46
RESULT 3
C91092
hypothetical protein EC93707 [imported] - Escherichia coli (strain O157:H7, substrain RI
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
A:Accession: C91092
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasaawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: C91092
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-163 <HAY>
A:Cross-references: UNIPROT:Q8X6H8; GB:BA000007; PIDN:BA937130.1; PID:G13363179; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetic8:
A:Gene: EC93707
C:Superfamily: Escherichia coli hypothetical protein b2850
Query Match 55.4%; Score 41; DB 2; Length 163;
Best Local Similarity 66.7%; Pred. No. 5.4;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNLSE 13
DB 35 KITMSGGLNLYIE 46
RESULT 4
G85937
hypothetical protein Z4171 [imported] - Escherichia coli (strain O157:H7, substrain EDL9
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
A:Accession: G85937
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Llm, A.; Dinalaata, E.; Potamoultis, K.; Apodaca,
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: G85937
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-163 <STO>
A:Cross-references: UNIPROT:Q8X6H8; GB:AE005174; NID:G12517343; PIDN:AA657963.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetic8:
A:Gene: Z4171
C:Superfamily: Escherichia coli hypothetical protein b2850
Query Match 55.4%; Score 41; DB 2; Length 163;
Best Local Similarity 66.7%; Pred. No. 5.4;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 KLSMGSGLNLSE 13
DB 35 KITMSGGLNLYIE 46

large surface antigen - hepatitis B virus (subtype adr)
N:Contains: major surface antigen; middle surface antigen
C:Species: hepatitis B virus, HBV
C:Date: 14-Nov-1993 #sequence_revision 14-Nov-1993 #text_change 09-Jul-2004
C:Accession: A03705; S04569; JQ2107; PQ0608
R:Onda, Y.; Onda, H.; Saadad, R.; Igarashi, K.; Sugino, Y.; Nishioaka, K.
Nucleic Acids Res. 11, 1747-1757, 1983
A:Title: The complete nucleotide sequences of the cloned hepatitis B virus DNA; subtype
A:Reference number: A93460; MUID:63168919; PMID:6300776
A:Accession: A03705
A:Molecule type: DNA
A:Residues: 1-400 <ONO>
A:Cross-references: UNIPROT:P03140; GB:V00867
R:Rho, H.M.; Kim, K.; Hyun, S.W.; Kim, Y.S.
Nucleic Acids Res. 17, 2124, 1989
A:Title: The nucleotide sequence and reading frames of a mutant hepatitis B virus subtype
A:Accession: S04569
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-50, 'R', 52-66, 'Y', 69-129, 'V', 131-142, 'P', 144-164, 'S', 166-176, 'S', 178-338,
A:Cross-references: EMBL:X1193
R:Norder, H.; Hammas, B.; Ise, S.D.; Bile, K.; Courouce, A.M.; Mushwar, I.K.; Magnus
J. Gen. Virol. 74, 1341-1346, 1993
A:Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A:Reference number: JQ2044; MUID:93329382; PMID:8336122
A:Accession: JQ2107
A:Molecule type: DNA
A:Residues: 175-400 <NOR>
A:Experimental source: genogroup C, subtype adr, strain PBHadr4
R:Norder, H.; Courouce, A.M.; Magnus, L.O.
J. Gen. Virol. 73, 3141-3145, 1992
A:Title: Molecular basis of hepatitis B virus serotype variations within the four major
A:Reference number: PQ0453; MUID:93107848; PMID:1469353
A:Accession: PQ0608
A:Molecule type: DNA
A:Residues: 275-354 <NO2>
A:Experimental source: subtype adtg+, Bau
C:Genetics:
A:Gene: pre-S1/pre-S2/S
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: glycoprotein; surface antigen
P:120-400/Product: middle surface antigen (gene pre-S2/S) #status predicted <NSA>
P:175-400/Product: major surface antigen (gene S) #status predicted <MSA>
P:115,123,177/Binding site: carbohydrate (Asn) #status predicted

Query Match 54.1%; Score 40; DB 1; Length 400;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 SKLMSGQLNSEPN 15
||| ||| ||| |||
Db 6 SKPRQGWGTNLNVN 20

RESULT 8
S35528
N:Alternate names: hepatitis B virus (subtype adr)
N:Alternate names: envelope protein; HBs antigen
N:Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mids)
C:Species: hepatitis B virus, HBV
A:Variety: subtype adr
C:Date: 09-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S35528
R:Mukaike, M.; Kunazawa, T.; Hoshi, A.; Kawaguchi, R.; Hikiji, K.
Nucleic Acids Res. 20, 6105, 1992
A:Title: The complete nucleotide sequence of hepatitis B virus, subtype adr (SRADR) and
A:Reference number: S35527; MUID:9306607; PMID:1461746
A:Accession: S35528
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-400 <MKU>
A:Cross-references: UNIPROT:Q81108; EMBL:D12980; NID:G221500; PTDN:BAA02359.1; PID:G2215

A:Experimental source: subtype adr
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
 C:Genetics:
 A:Gene: S
 A:Insertions: 165/2
 C:Superfamily: hepatitis B virus surface antigen
 C:Keywords: surface antigen
 F:1-400/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
 F:1-119/Domin: pre-S1 domain #status predicted <PRE1>
 F:1120-400/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <F>
 F:1120-174/Domin: pre-S2 domain #status predicted <PRE2>
 F:1175-400/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match 54.1% Score 40; DB 2; Length 400;
 Best Local Similarity 60.0%; Pred. No. 22;
 Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 SKLMSGSLNLEPN 15
 |||
 Db 6 SKPRQMGNTNLSVPN 20

RESULT 9
 S43492
 surface antigen - hepatitis B virus (subtype adr)
 N:Alternate names: Hbs antigen
 N:Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mid
 C:Species: hepatitis B virus, HBV
 A:Variety: subtype adr
 C:Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C:Accession: S43492; PNO601; PNO602
 R:Loncarevic, I.F.; Zentgraf, H.; Schroeder, C.H.
 Nucleic Acids Res. 18, 4940, 1990
 A:Title: Sequence of a replication competent hepatitis B virus genome with a prex open r
 A:Reference number: S12558; MUID:90370503; PMID:2395664
 A:Accession: S43492
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-445 <LON>
 A:Cross-references: UNIPROT:Q67953; EMBL:X52939; NID:g457780; PIDN:CAA37114.1; PID:g4577
 A:Experimental source: subtype adr
 R:Mims, L.T.; Solomon, L.R.; Ebert, J.W.; Field, H.
 Biochem. Biophys. Res. Commun. 195, 186-191, 1993
 A:Title: Unique Pres sequence in a gibbon-derived hepatitis B virus variant.
 A:Reference number: PNO601; MUID:93371402; PMID:8363598
 A:Accession: PNO601
 A:Molecule type: protein
 A:Residues: 57-95 <MIM>
 A:Accession: PNO602
 A:Molecule type: protein
 A:Residues: 165-196 <M12>
 C:Genetics:
 A:Gene: S
 A:Insertions: 210/3
 C:Superfamily: hepatitis B virus surface antigen
 C:Keywords: surface antigen
 F:1-445/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
 F:1-164/Domin: pre-S1 domain #status predicted <PRE1>
 F:1165-445/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <F>
 F:1165-219/Domin: pre-S2 domain #status predicted <PRE2>
 F:120-445/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match 54.1% Score 40; DB 2; Length 445;
 Best Local Similarity 60.0%; Pred. No. 25;
 Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 SKLMSGSLNLEPN 15
 |||
 Db 51 SKPRQMGNTNLSVPN 65

RESULT 10
 D71852

probable signal recognition particle protein - Helicobacter pylori (strain J99)
 C:Species: Helicobacter pylori
 A:Variety: strain J99
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
 C:Accession: D71852
 R:Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.;
 ; Ivers, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, O.; Taylor, D.E.; Vovis, G.F.;
 Nature 397, 176-180, 1999
 A:Title: Genomic sequence comparison of two unrelated isolates of the human gastric path
 A:Reference number: A71800; MUID:99120557; PMID:9923682
 A:Accession: D71852
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-448 <ARN>
 A:Cross-references: UNIPROT:Q9ZK62; GB:AE001535; GB:AE001439; NID:g4155664; PIDN:AA00665
 A:Experimental source: strain J99
 C:Genetics:
 A:Gene: fth
 C:Superfamily: signal recognition particle 54k protein

Query Match 54.1% Score 40; DB 2; Length 448;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 2 KLSMSGSLNLEPN 15
 :|:|:|:|:|:|:|:|
 Db 394 RIALGSGLEVSEIN 407

RESULT 11
 H64663
 signal recognition particle protein - Helicobacter pylori (strain 26695)
 C:Species: Helicobacter pylori
 C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
 C:Accession: H64663
 R:Tomb, J.F.; White, O.; Kervavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
 Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalil, H.G.; Glodek, A.; McKen
 son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watney, L.
 Nature 388, 539-547, 1997
 A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
 A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
 A:Reference number: A64520; MUID:97394467; PMID:9252185
 A:Accession: H64663
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-448 <TOM>
 A:Cross-references: UNIPROT:P56005; GB:AE000621; GB:AE000511; NID:g2314301; PIDN:AA00819
 C:Superfamily: signal recognition particle 54k protein

Query Match 54.1% Score 40; DB 2; Length 448;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 7; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 2 KLSMSGSLNLEPN 15
 :|:|:|:|:|:|:|:|
 Db 394 RIALGSGLEVSEIN 407

RESULT 12
 T27845
 hypothetical protein ZK402.5 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T27845
 R:Favella, T.
 submitted to the EMBL Data Library, November 1995
 A:Description: The sequence of C. elegans cosmid ZK402.
 A:Reference number: Z20429
 A:Accession: T27845
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-516 <FAV>
 A:Cross-references: UNIPROT:Q23477; EMBL:U40956; PIDN:AAA81756.1; CESP:ZK402.5

C:Genetics: A:Gene: CBSP:ZK402.5
A:Intron: 28/2; 122/2; 160/2; 248/2; 420/3
C:Superfamily: Caenorhabditis elegans hypothetical protein Y57A10A.h

Query Match Best Local Similarity 54.1%; Score 40; DB 2; Length 516;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 2 KLSMGSGNLSEPN 14
Db 476 KISRGGGLNSSPP 488

RESULT 13
CB9991
hypothetical protein SA1812 (imported) - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
A:Accession: CB9991
R:Kuroda, M.; Ohka, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogunc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiratsuku, K.
Lance 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: AB9758; MUID:21311952; PMID:11418146
A:Accession: CB9991
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-338 <KIR>
A:Cross-references: UNIPROT:Q99SN8; GB:BA000018; PID:g13701799; PIDN:BAB3092.1; GSPDB:G
C:Genetics: A:Experimental source: strain N315
A:Gene: SA1812
C:Superfamily: Leukocidin

Query Match Best Local Similarity 52.7%; Score 39; DB 2; Length 338;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

OY 1 SKLSMGSGNLSEPN 15
Db 86 AKGTIGSGLRIDPN 100

RESULT 14
JQ1575
major surface antigen - hepatitis B virus
N:Alternate names: envelope protein; HBs antigen
N:Contains: surface envelope pre-S1 (large envelope protein); surface antigen pre-S2 (mid
C:Species: hepatitis B virus, HBV
A:Variety: subtype adw2
C:Date: 31-Dec-1993 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
A:Accession: S47411; JQ1575
R:Plucieniczak, A.
submitted to the EMBL Data Library, August 1994
A:Description: Molecular cloning and sequencing of two complete genomes of polish isolat
A:Reference number: S47404
A:Accession: S47411
A:Molecule type: DNA
A:Residues: 1-400 <PIU>
A:Cross-references: UNIPROT:Q67896; EMBL:Z35717; NID:g527440; PIDN:CAA64792.1; PID:g5274
A:Experimental source: subtype adw2
R:Notter, H.; Hammas, B.; Loefdahl, S.; Courouce, A.M.; Magnus, L.O.
J. Gen. Virol. 73, 1201-1208, 1992
A:Title: Comparison of the amino acid sequences of nine different serotypes of hepatitis
A:Reference number: JQ1570; MUID:92268879; PMID:1586323
A:Accession: JQ1575
A:Molecule type: DNA
A:Residues: 175-400 <NOB>
A:Cross-references: GB:X75666; NID:g416074; PIDN:CAA53362.1; PID:g416075
A:Experimental source: subtype adw2, strain p6
C:Genetics:

```

A:Gene: S
A:Introns: 122/3
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: glycoprotein; surface antigen
F.1-400/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1>
F.1-119/Domain: pre-S1 domain #status predicted <PR1>
F.120-400/Product: surface antigen pre-S2 (middle envelope protein) #status predicted <PRS2>
F.120-174/Domain: pre-S2 domain #status predicted <PRS2>
F.175-400/Product: surface antigen S (small envelope protein) #status predicted <PSD>
F.117/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          52.7%; Score 39; DB 1; Length 400;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 SKLMSGGLNISEPN 15
      |||-----|||
DB      6 SKPRKMGNTLSVNP 20

RESULT 15
SAVLKS
large surface antigen - hepatitis B virus (subtype adw, strain 991)
N:Contains: major surface antigen; middle surface antigen
C:Species: hepatitis B virus, HBV
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S10383
R:Koechel, H.G.; Schueler, A.; Lottmann, S.; Thomsen, R.
submitted to the EMBL Data Library, February 1990
A:Reference number: S10380
A:Accession: S10383
A:Molecule type: DNA
A:Residues: 1-400 <KOE>
A:Cross-references: UNIPROT:P17101; EMBL:X51970; NID:g155012; PIDN:CAA6230.1; PID:G90
C:Genetics:
A:Gene: pre-S1/pre-S2/S
A:Introns: 123/2
C:Superfamily: hepatitis B virus surface antigen
C:Keywords: glycoprotein; surface antigen
F.120-400/Product: middle surface antigen (gene pre-2/S) #status predicted <DSA>
F.175-400/Product: major surface antigen (gene S) #status predicted <MSA>
F.115,123,177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          52.7%; Score 39; DB 1; Length 400;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY      1 SKLMSGGLNISEPN 15
      |||-----|||
DB      6 SKPRKMGNTLSVNP 20

Search completed: November 1, 2005, 12:55:50
Job time : 18.2206 secs

```

THIS PAGE BLANK (USPTO)

RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=2228657; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Struhsberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buelow K.H., Scheffer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McEran K.U., Malek U.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shcherchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[17]
RP SEQUENCE OF 99-698 FROM N.A.
RC TISSUE=Fetal liver;
RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
RA He F.;
RT "Functional prediction of the coding sequences of 33 new genes deduced
RT by analysis of cDNA clones from human fetal liver";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
[8]
RP SEQUENCE OF 422-698 FROM N.A.
RX MEDLINE=84153910; PubMed=6322780;
RA Uzan G., Frain M., Park I., Beemond C., Maessen G., Trepac J.S.,
RA Zakin M.M., Kahn A.;
RT "Molecular cloning and sequence analysis of cDNA for human
RT transferrin";
RL Biochem. Biophys. Res. Commun. 119:272-281 (1984).
[9]
RP SEQUENCE OF 20-698.
RX MEDLINE=83160878; PubMed=6833213;
RA McGillivray R.T.A., Mendez E., Shevale J.G., Sinha S.K.,
RA Linbeck-Zins J., Brew K.;
RT "The primary structure of human serum transferrin. The structures of
RT seven cyanogen bromide fragments and the assembly of the complete
RT structure";
RL J. Biol. Chem. 258:3543-3553 (1983).
[10]
RP SEQUENCE OF 73-698 FROM N.A.
RX MEDLINE=85216459; PubMed=3858812;
RA Park I., Schaeffer E., Sidoli A., Baralle F.E., Cohen G.N.,
RA Zakin M.M.;
RT "Organization of the human transferrin gene: direct evidence that it
RT originated by gene duplication";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3149-3153 (1985).
[11]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=87066744; PubMed=3786138;
RA Lucero M.A., Schaeffer E., Cohen G.N., Zakin M.M.;
RT "The 5' region of the human transferrin gene: structure and potential
RT regulatory sites";
RL Nucleic Acids Res. 14:8692-8692 (1986).
[12]
RP SEQUENCE OF 1-72 AND 291-300 FROM N.A.
RX MEDLINE=87192006; PubMed=3106157; DOI=10.1016/0378-1119(86)90277-5;
RA Adrian G.S., Korinek B.W., Bowman B.H., Yang F.;
RT "The human transferrin gene: 5' region contains conserved sequences
RT which match the control elements regulated by heavy metals,
RT glucocorticoids and acute phase reaction";
RL Gene 49:167-175 (1986).
[13]
RP SEQUENCE OF 45-72 FROM N.A.

RX MEDLINE=20392111; PubMed=10931525;
DOI=10.1002/1097-4547(20000815)61:4<388::AID-JNR53.0.CO;2-Q;
RA de Arriba Zepa G.A., Saleh M.-C., Fernandez P.M., Guillou F.,
RA Espinosa de los Monteros A., de Velles J., Zakin M.M., Baron B.;
RT "Alternative splicing prevents transferrin secretion during
RT differentiation of a human oligodendrocyte cell line";
RL J. Neurosci. Res. 61:388-395 (2000).
[14]
RP SEQUENCE OF 564-624 FROM N.A., AND VARIANT TF*2.
RC TISSUE=Brain;
RX MEDLINE=97418135; PubMed=9272172;
RA Namakata K., Oyama F., Imagawa M., Itara Y.;
RT "Human transferrin (TF): a single mutation at codon 570 determines TF
RT C1 or TF C2 variant";
RL Hum. Genet. 100:457-458 (1997).
[15]
RP SEQUENCE OF 564-624 FROM N.A.
RA Tsuchida S., Ikemoto S., Kajil E.;
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
[16]
RP SEQUENCE OF 636-696 FROM N.A.
RX MEDLINE=89386721; PubMed=2780570;
RA Duguid J.R., Belmont C.W., Liu N.G., Tourtelotte W.W.;
RT "Changes in brain gene expression shared by scrapie and Alzheimer
RT disease";
RL Proc. Natl. Acad. Sci. U.S.A. 86:7260-7264 (1989).
[17]
RP SEQUENCE OF 263-266; 454-458; 531-538 AND 589-595.
RC TISSUE=Heart;
RX MEDLINE=96007936; PubMed=7498159;
RA Kovalyov L.I., Shishkin S.S., Efimochkin A.S., Kovalyova M.A.,
RA Ershova E.S., Egorov T.A., Musalyamov A.K.;
RT "The major protein expression profile and two-dimensional protein
RT database of human heart";
RL Electrophoresis 16:1160-1169 (1995).
[18]
RP DISULFIDE BONDS.
RX MEDLINE=82222166; PubMed=6953407;
RA McGillivray R.T.A., Mendez E., Sinha S.K., Sutton M.R.,
RA Linbeck-Zins J., Brew K.;
RT "The complete amino acid sequence of human serum transferrin";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2504-2508 (1982).
[19]
RP MUTAGENESIS.
RX MEDLINE=92031536; PubMed=1932003;
RA Woodworth R.C., Mason A.B., Funk W.D., McGillivray R.T.A.;
RT "Expression and initial characterization of five site-directed mutants
RT of the N-terminal half-molecule of human transferrin";
RL Biochemistry 30:10824-10829 (1991).
[20]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 22-350.
RX MEDLINE=98272665; PubMed=9609685; DOI=10.1021/b1980355j; Baker H.,
RA McGillivray R.T.A., Moore S.A., Chen J., Anderson B.F.,
RA Luo Y., Bewley M.C., Smith C.A., Murphy M.E.P., Wang Y., Mason A.B.,
RA Woodworth R.C., Brayer G.D., Baker E.N.;
RT "Two high-resolution crystal structures of the recombinant N-lobe of
RT human transferrin reveal a structural change implicated in iron
RT release";
RL Biochemistry 37:7919-7928 (1998).
[21]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-350.
RX MEDLINE=98434369; PubMed=9760232; DOI=10.1021/b19812064j; Baker H.,
RA Jeffrey P.D., Bewley M.C., McGillivray R.T.A., Mason A.B.,
RA Woodworth R.C., Baker E.N.;
RT "Isand-induced conformational change in transferrins: crystal
RT structure of the open form of the N-terminal half-molecule of human
RT transferrin";
RL Biochemistry 37:13978-13986 (1998).
[22]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 23-352.
RX MEDLINE=99155227; PubMed=10029548; DOI=10.1021/b19824543j; Baker H.,
RA Bewley M.C., Tam B.M., Grewal J., He S., Shewry S., Murphy M.E.P.,
RA Mason A.B., Woodworth R.C., Baker E.N., McGillivray R.T.A.;

RT "X-ray crystallography and mass spectroscopy reveal that the N-lobe of human transferlin expressed in *Pichia pastoris* is folded correctly but

Query Match 81.4%; Score 60; DB 1; Length 698;
Best Local Similarity 85.7%; Pred. No. 0.059;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLEPN 15
DB 515 KLSMGSGLNLEPN 528

RESULT 2

Q9E952 PRELIMINARY; PRT; 400 AA.
AC Q9E952;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Large surface antigen.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirine.
OC NCBI_Taxid=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20528423; PubMed=11074474;
RX DOI=10.1002/1096-9071(200012)62:4<456::AID-JMV10-3.0.CO;2-3;
RA Suganuchi F., Mizokami M., Orito E., Ohno T., Kato H., Maki M.,
RA Suzuki H., Ojika K., Ueda R.;
RT "Hepatitis B virus infection among residents of a nursing home for the
RT elderly: seroepidemiological study and molecular evolutionary
RT analysis."
RT J. Med. Virol. 62:456-462(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Suganuchi F.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL:AB042246; BAB17298.1; -.
DR PIR:JQ2094; JQ2094.
DR PIR:JQ2095; JQ2095.
DR PIR:JQ2096; JQ2096.
DR PIR:JQ2097; JQ2097.
DR PIR:JQ2098; JQ2098.
DR PIR:JQ2099; JQ2099.
DR PIR:JQ2100; JQ2100.
DR PIR:JQ2101; JQ2101.
DR PIR:JQ2102; JQ2102.
DR PIR:JQ2106; JQ2106.
DR PIR:JQ2108; JQ2108.
DR PIR:JQ2109; JQ2109.
DR PIR:JQ2111; JQ2111.
DR PIR:JQ2112; JQ2112.
DR PIR:JQ2116; JQ2116.
DR GO:GO:0016032; P:Viral life cycle; IEA.
DR InterPro:IPR000349; Hepvir_surtag.
DR Pfam:PF00695; VMSA; 1.
KW Antigen.

QY SEQUENCE 400 AA; 43655 MW; 3B22DF329A8266C6 CRC64;

Query Match 63.5%; Score 47; DB 2; Length 400;
Best Local Similarity 66.7%; Pred. No. 7.6;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KLSMGSGLNLEPN 15
DB 6 SKLRGSGMTNLSVFN 20
RESULT 3
Q943K6 PRELIMINARY; PRT; 521 AA.
AC Q943K6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Putative SLT1 protein (ion homeostasis related protein)
DE (Sodium/lithium tolerance protein).
GN Name=P0031D11.29; Synonyms=P0408C03.13;
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Enarthrodidae; Oryzaceae; Oryza.
OX NCBI_Taxid=39947;
RN [1]
RP SEQUENCE FROM N.A.

RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Saketa K., Baba T., Katayose Y.,
RA Wu J., Nilmura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayaishi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijiya S., Honda M., Ichikawa Y., Iidoma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karsawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang X., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1."
RL Nature 420:312-316(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA Antoine W., Stewart J.M., de los Reyes B.G.;
RT "Evolution of SLT gene family: a new subclass of plant-specific heat
RT shock proteins."
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Antoine W., Stewart J.M., de los Reyes B.G.;
RT "Posttranslational modification of the rice SLT proteins is required
RT for chaperone activity under stress conditions."
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL:AP003231; BAB67895.1; -.
DR EMBL:AP003241; BAB93215.1; -.
DR EMBL:AF672599; AAT81168.1; -.
DR Gramene:Q943K6; -.
DR InterPro:IPR008978; HSP20_chap.
DR InterPro:IPR000834; Peptidase_M14.
DR PROSITE:PS00133; CARBOXYPEPT_ZN_2; UNKNOWN 1.
DR PROSITE:PS00133; CARBOXYPEPT_ZN_2; UNKNOWN 1.
SQ SEQUENCE 521 AA; 58300 MW; 4CA7F68BB35F570 CRC64;

Query Match 63.5%; Score 47; DB 2; Length 521;
Best Local Similarity 71.4%; Pred. No. 10;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KLSMGSGLNLEPN 15
DB 303 KLSMGSGLNLEPN 316

RESULT 4

Q8U2T2 PRELIMINARY; PRT; 823 AA.
AC Q8U2T2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE G-protein coupled receptor.
GN Name=GACGR1;
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_Taxid=5476;
RN [1]

```

RP SEQUENCE FROM N.A.
RX PubMed=15302825;
RA Miwa T., Takagi Y., Shinozaki M., Yun C.W., Schell W.A., Perfect J.R.,
RA Kumagai H., Tamaki H.;
RT "Gp1, a putative G-protein-coupled receptor, regulates morphogenesis
RT and hypha formation in the pathogenic fungus Candida albicans.";
RL Eukaryotic Cell 3:919-931(2004).
DR EMBL, AB084519; BAC22916.1; -.
DR GO, GO:0004872; P:receptor activity; IEA.
DR InterPro, IPR02048; EF-hand.
DR PROSITE, PS00018; EF_HAND; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 823 AA; 92340 MW; 4B3A61EBDD6E709 CRC64;

Query Match
Best Local Similarity 57.1%; Score 46; DB 2; Length 823;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SKLMSGGLNISEPN 14
Db 656 SPMSGAGINWTEP 669

RESULT 5
Q7PD10 PRELIMINARY; PRT; 368 AA.
AC Q7PD10;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE ENSANG00000015427 (ENSANGP0000006590) (Fragment).
GN Name=ENSANG00000015427; Synonyms=ENSANG0000004992;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles genome Sequencing Consortium;
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
FT EMBL; AAB01008192; EAA03293.2; -.
FT NON_TER 1 368
FT NON_TER 368 368
SQ SEQUENCE 368 AA; 40792 MW; 8D3D3663C0A29CF CRC64;

Query Match
Best Local Similarity 58.1%; Score 43; DB 2; Length 368;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ISMSGGLNISEPN 15
Db 147 ISLGLGLNPADPN 159

RESULT 6
Q8NC87 PRELIMINARY; PRT; 796 AA.
AC Q8NC87;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLU90414.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Isegaki T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,

```

```

RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Negahari K.,
RA Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Niimiya K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, AK074895; BAC11274.1; -.
DR HSSP; Q9UG0.1P62.
DR GO, GO:0003577; P:DNA binding; IEA.
DR GO, GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro, IPR01011; FIVE_PHD_Znf.
DR InterPro, IPR01965; Znf_PHD.
DR Pfam; PF00628; PHD; 1.
DR SMART; SM00249; PHD; 1.
DR PROSITE, PS0016; ZF_PHD_2; 1.
FT NON_TER 796 796
SQ SEQUENCE 796 AA; 88462 MW; 2EDB8BCAF9720C1E CRC64;

Query Match
Best Local Similarity 58.1%; Score 43; DB 2; Length 796;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 SMGSGLNISEPN 15
Db 416 SLGSGLGISEGN 427

RESULT 7
BA2B HUMAN STANDARD; PRT; 1972 AA.
AC Q9UIF8; Q96EAL; Q96S08; Q9P252; Q9Y4N8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bromodomain adjacent to zinc finger domain 2B (hMMLP4).
GN Name=BA2B2; Synonyms=K1A1176;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Testis;
RX MEDLINE=20130112; PubMed=10662543; DOI=10.1006/geno.1999.6071;
RA Jones M.H., Hamana N., Nezu J., Shiwan M.;
RT "A novel family of bromodomain genes.";
RL Genomics 63:40-45(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RA Ohara O., Nagase T., Kikuno R.;
RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 753-1972 FROM N.A.
RX MEDLINE=20277482; PubMed=10819331;
RA Nagase T., Kikuno R., Ishikawa K., I., Hirosewa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:143-150(2000).
RN [4]
RP SEQUENCE OF 1-776 FROM N.A. (ISOFORM 1).
RC TISSUE=Melanoma;
RA Ansoorge W., Winkner U., Mewes H.-W., Weil B., Wiemann S.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 1-799 FROM N.A. (ISOFORM 2).
RC TISSUE=Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

```


Db 1457 SLGSGGLSEGN 1468

RESULT 8

Q6FMKO: PRELIMINARY; PRT; 307 AA.
 ID 06FMKO: PRELIMINARY; PRT; 307 AA.
 AC Q6FMKO: PRELIMINARY; PRT; 307 AA.
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE Similar to sp|Q04013 Saccharomyces cerevisiae YMR241w.
 GN ORFNames=CAGL0K07436g;
 OS Candida glabrata CBS138.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Mitoportic Saccharomycetales; Candida.
 NCBI_TaxID=284593;
 OX NCBI_TaxID=284593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBS138;
 RG Genolevures;

RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marc C., Neveglisse C., Talla E.,
 RA Goffard N., Frangoul L., Aigle M., Anhouard V., Babour A., Barde V.,
 RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleyaesten C.,
 RA Bolgerme A., Boyer J., Catolico L., Confanioleri F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
 RA Nicoud J.M., Nikolaki M., Octas S., Oster-Kalogeropoulos O.,
 RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zenou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudon B., Scarpelli C., Galliard C., Weisenbach J.,
 RA Winkler P., Souciet J.L.;
 RT "Genome evolution in yeasts."
 RL Nature 430:35-44(2004).
 CC -1 SIMILARITY: Belongs to the mitochondrial carrier family.
 DR EMBL: CB380957; CAG61507.1; -;
 DR GO: GO:0016020; C:membrane; IEA.
 DR GO: GO:0005488; F:binding; IEA.
 DR GO: GO:0006810; P:transport; IEA.
 DR InterPro: IPR001993; Mitoch carrier.
 DR Pfam: PF00153; Mito car; 2.
 DR PROSITE: PS00920; SOLCAR; 2.
 KW Transmembrane; Transport.
 SQ SEQUENCE 307 AA; 33587 MW; 1A5859ADDBA74C47 CRC64;

Query Match 56.8%; Score 42; DB 2; Length 307;
 Best Local Similarity 61.5%; Pred. No. 47;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SKLWSGSLNLEP 13
 Db 13 SNLLGAGLNLSE 25

RESULT 9

Q8GPA0: PRELIMINARY; PRT; 428 AA.
 ID Q8GPA0: PRELIMINARY; PRT; 428 AA.
 AC Q8GPA0: PRELIMINARY; PRT; 428 AA.
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Epa110.
 GN Name=epa110;
 OS Streptococcus thermophilus.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 NCBI_TaxID=1308;
 OX NCBI_TaxID=1308;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Rallu F., Ehrlich D.S., Renault P.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF454501; AAN63800.1; -;
 SQ SEQUENCE 428 AA; 50454 MW; D2PB3BEED466547 CRC64;

Query Match 56.8%; Score 42; DB 2; Length 428;
 Best Local Similarity 69.2%; Pred. No. 68;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 KLSWGSGLNLEP 14
 Db 20 KKSWSGLNLEP 32

RESULT 10

Q8J289: PRELIMINARY; PRT; 528 AA.
 ID Q8J289: PRELIMINARY; PRT; 528 AA.
 AC Q8J289: PRELIMINARY; PRT; 528 AA.
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE YGL104C.
 OS Kluyveromyces lactic (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22307030; PubMed=12420142;
 RA Takekova M., Sklenar P., Gbelika Y., Breunig K., Subik J.;
 RT "Isolation, heterologal cloning and sequencing of the RPL28 gene in
 RT Kluyveromyces lactic."
 RL Curr. Genet. 42:21-26(2002).
 CC -1 SIMILARITY: Integral membrane protein (By similarity).
 DR EMBL: AF493565; AAN65374.1; -;
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0005351; F:sugar porter activity; IEA.
 DR GO: GO:0005215; F:transporter activity; IEA.
 DR GO: GO:0006643; P:carbohydrate transport; IEA.
 DR InterPro: IPR007114; MFS.
 DR InterPro: IPR005828; Sub_transporter.
 DR InterPro: IPR003663; Sugar_transp.
 DR InterPro: IPR005829; Sug_transporter.
 DR Pfam: PF00083; Sugar tr; 1.
 DR PRINTS: PRO0171; SUGTRNSPORT.
 DR TIGRFAMs: TIGR00879; SP. 1.
 DR PROSITE: PS00850; MFS. 1.
 DR PROSITE: PS00216; SUGAR_TRANSPORT_1; UNKNOWN_1.
 DR PROSITE: PS00217; SUGAR_TRANSPORT_2; UNKNOWN_1.
 KW Sugar transport; Transmembrane; Transport.
 SQ SEQUENCE 528 AA; 58196 MW; 140D6B8E3B26E732 CRC64;

Query Match 56.8%; Score 42; DB 2; Length 528;
 Best Local Similarity 46.7%; Pred. No. 86;
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 SKLWSGSLNLEPN 15
 Db 288 SQMNGSLNLEPNPS 302

RESULT 11

Q6CKZ8: PRELIMINARY; PRT; 528 AA.
 ID Q6CKZ8: PRELIMINARY; PRT; 528 AA.
 AC Q6CKZ8: PRELIMINARY; PRT; 528 AA.
 DT 25-OCT-2004 (TREMBLrel. 28, Created)
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Similarity.
 GN ORFNames=KLA0F06853g;
 OS Kluyveromyces lactic NRRL Y-1140.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.

```

OX NCBI_TaxId=284590;
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RC Genovetres;
RA Dujon B., Sherman D., Flecher G., Durens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boistrame A., Boyer J., Caciolico L., Confanietti H., de Darvar A.,
RA Despons L., Fabre B., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantaye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerest A., Kozul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Niclaud J.M., Nkolleki M., Oztra S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Sweeney D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Weyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA Mancker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RC Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to the sugar transporter family.
DR EMBL: CB382126; CAG98099.1; -.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0005351; F: sugar porter activity; IEA.
DR GO: GO:0005215; F: transporter activity; IEA.
DR GO: GO:0006643; P: carbohydrate transport; IEA.
DR InterPro: IPR007114; MFS.
DR InterPro: IPR005828; Sub_transporter.
DR InterPro: IPR003663; Sugar_transp.
DR InterPro: IPR005829; Sug_transporter.
DR Pfam: PF00083; Sugar_tr; 1.
DR PRINTS: PR00171; SUGTRANSPORT.
DR TIGRfam: TIGR00879; SP; 1.
DR PROSITE: PS50850; MFS; 1.
DR PROSITE: PS00216; SUGAR_TRANSPORT_1; UNKNOWN 1.
DR PROSITE: PS00217; SUGAR_TRANSPORT_2; UNKNOWN 1.
KW Sugar transporter; Transmembrane; Transport.
SQ SEQUENCE 528 AA; 58196 MW; 14068B83E26E732 CRC64;

Query Match 56.8%; Score 42; DB 2; Length 528;
Best Local Similarity 46.7%; Pred. No. 86;
Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 SKLMSGSLNLEPN 15
DB 288 SKMNLGSLNLEPN 302

RESULT 12
Q8U379 PRELIMINARY; PRT; 867 AA.
AC Q8U379;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ATP-dependent RNA helicase, putative.
GN OrderedLocusNames=PF0592;
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxId=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Vci / DSM 3638 / ATCC 43587 / JCM 8422;
RC Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
RT "The complete sequence of the Pyrococcus furiosus genome.";
```

```

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE010181; AAL80716.1; -.
DR GO: GO:0005524; F: ATP binding; IEA.
DR GO: GO:0008026; F: ATP-dependent helicase activity; IEA.
DR GO: GO:0003676; F: nucleic acid binding; IEA.
DR Pfam: PF00270; DEAD; 1.
DR Pfam: PF00271; Helicase_C; 1.
DR SMART: SM00487; DEXDC; 1.
DR SMART: SM00490; HELIC; 1.
KW ATP-binding; Complete proteome; Helicase; Hydrolyase.
SQ SEQUENCE 867 AA; 101122 MW; 8F633D547552448B CRC64;

Query Match 56.8%; Score 42; DB 2; Length 867;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SKLMSGSLNLEPN 15
DB 753 SKMGISGLHAIEN 767

RESULT 13
Q8INF9 PRELIMINARY; PRT; 3358 AA.
ID Q8INF9;
AC Q8INF9;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CG8651-PB (CG8651-PC).
GN Name=trix; ORFNames=CG8651;
OS Drosophila melanogaster (Fruit fly).
OC Diptera; Insecta; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
RA Abriil J.F., Agbayani A., An H.V., Andrews-Planonch C., Baldwin D.,
RA Baillet R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benoe P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotier P.,
RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegem C.,
RA Jalali M., Kalish F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Paclet J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasearan D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
```


RA Pacleeb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
RT melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.B., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celisner S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
RT a genomic perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RN SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miya S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Betman B.P.,
RA Betencourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RN SEQUENCE FROM N.A.
RG Flybase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RN SEQUENCE FROM N.A.
RG Flybase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 SET domain.
DR EMBL; AE003704; AAF5041.2; -;
DR HSSP; O8X235; 1PEG.
DR Flybase; FBgn0003862; trx.
DR GO; GO:0003097; Cytochrome methyltransferase complex; IDA.
DR GO; GO:004800; Cytochrome lysine N-methyltransferase activity. .; IC.
DR GO; GO:0016571; Cytochrome methylation; IDA.
DR InterPro; IPR003889; FYrich_C.
DR InterPro; IPR003888; FYrich_N.
DR InterPro; IPR003616; PostSET.
DR InterPro; IPR001214; SET.
DR InterPro; IPR011382; Trx_SET_Mettrans.
DR InterPro; IPR011965; ZnF_PHD.
DR InterPro; IPR001841; ZnF_ring.
DR Pfam; PF05965; FYRC; 1.
DR Pfam; PF05964; FYRN; 1.
DR Pfam; PF0628; PHD; 3.
DR Pfam; PF0628; PHD; 3.
DR PIRSF; PIRSF010354; Trx_SET; 1.
DR SMART; SM00542; FYRC; 1.
DR SMART; SM00541; FYRN; 1.
DR SMART; SM00249; PHD; 4.
DR SMART; SM00508; PostSET; 2.
DR SMART; SM00184; RING; 4.
DR SMART; SM00317; SET; 1.
DR PROSITE; PS50868; POST_SET; 1.
DR PROSITE; PS50280; SET; 1.
DR PROSITE; PS01359; ZF_PHD_1; 4.
DR PROSITE; PS50016; ZF_PHD_2; 1.
SQ SEQUENCE 3726 AA; 400095 MW; E3DDB8F062BD7796 CRC64;

Query Match 56.8%; Score 42; DB 2; Length 3726;
Best Local Similarity 66.7%; Pred. No. 7.7e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

4 SMGSLINSEPN 15
|:|||||:|:|

Db 2362 SLGSGFPLSQPN 2373

RESULT 15

YGEF_ECOLI

ID YGEF_ECOLI

AC 046786;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Hypothetical protein ygef.

GN Name=ygef; OrderedLocustNames=b2850;

OS Escherichia coli.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=562;

RN (1)

RP SEQUENCE FROM N.A.

RC STRAIN=K12 / MG1655;

RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; U28375; AAA83032.1; -;

DR EMBL; U00096; AAC75889.1; -;

DR PIR; C65068; C65068.

DR Echobase; EB2851; -;

DR Ecogene; EG13036; ygef.

KW Complete proteome; Hypothetical protein.

SQ SEQUENCE 148 AA; 16878 MW; 59D6F53C973614DF CRC64;

Query Match 55.4%; Score 41; DB 1; Length 148;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 KLSGSLINSE 13
|:|||||:|:|
Db 35 KITMGSLINYE 46

Search completed: November 1, 2005, 12:54:33
Job time : 76.4559 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: November 1, 2005, 13:53:15 ; Search time 161 Seconds
(without alignments)
36.034 Million cell updates/sec

Title: US-10-612-162a-3

Perfect score: 74 SKLMSGGLNLEPN 15

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 632537

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	74	100.0	15	8	ADG46077	Adg46077 Human CDT
2	65	87.8	13	8	ADG46094	Adg46094 Human CDT
3	55	74.3	15	8	ADRI5909	Adri5909 Transferr
4	55	74.3	15	8	ADRI5970	Adri5970 Transferr
5	55	74.3	15	8	ADSI3393	Adsi3393 Human rbe
6	55	74.3	15	8	ADSI3389	Adsi3389 Human rbe
7	33	44.6	15	3	AAV70486	AAV70486 Synthesis
8	30	40.5	9	5	ABU08867	Abj08867 Hepatitis
9	30	40.5	9	5	ABU09159	Abj09159 Hepatitis
10	30	40.5	9	8	ADQ12374	Adq12374 Hepatitis
11	30	40.5	10	2	AAK38384	AAK38384 T-cell ep
12	30	40.5	10	2	AAK38384	AAK38384 T-cell ep
13	30	40.5	10	5	ABU06595	Abj06595 Hepatitis
14	30	40.5	10	5	ABU07286	Abj07286 Hepatitis
15	30	40.5	10	5	ABU06082	Abj06082 Hepatitis
16	30	40.5	10	8	ADK37389	Adk37389 Hepatitis
17	30	40.5	10	8	ADK37875	Adk37875 Hepatitis
18	30	40.5	10	8	ADK38506	Adk38506 Hepatitis
19	30	40.5	14	2	AAV23365	AAV23365 CR3 sequ
20	30	40.5	15	2	AAK62914	AAK62914 V-alpha c
21	30	40.5	15	2	AAK94866	AAK94866 Peptide f
22	30	40.5	15	2	AAW43544	AAW43544 Mycobacte
23	30	40.5	15	5	ABJ08961	Abj08961 Hepatitis
24	30	40.5	15	5	ABJ09253	Abj09253 Hepatitis
25	30	40.5	15	8	ADK39233	Adk39233 Hepatitis

26	29	39.2	10	2	AAW21293	AAW21293 Hydroxyne
27	29	39.2	13	4	AAU02673	AAU02673 CDR regio
28	29	39.2	13	4	AAU03316	AAU03316 Fruit fly
29	29	39.2	13	6	ABJ36774	Abj36774 G protein
30	29	39.2	13	6	ABJ36773	Abj36773 G protein
31	29	39.2	13	7	ABW00016	Abw00016 Human G a
32	29	39.2	13	7	ABW00017	Abw00017 Human G a
33	29	39.2	13	7	ADL14646	Adl14646 DmgPCR bl
34	29	39.2	13	7	ADP45271	Adp45271 G alpha c
35	29	39.2	13	7	ADP45270	Adp45270 G alpha c
36	29	39.2	13	7	ADL83494	Adl83494 Drosophila
37	29	39.2	13	8	ADR03214	Adr03214 G-protein
38	29	39.2	15	4	AAK78238	AAK78238 Human hex
39	29	39.2	15	6	ABR31310	Abri31310 Human can
40	29	39.2	15	6	ABR31106	Abri31106 Human can
41	29	39.2	15	6	ABR30735	Abri30735 Human can
42	29	39.2	15	6	ABR30664	Abri30664 Human can
43	29	39.2	15	6	ABR31569	Abri31569 Human can
44	29	39.2	15	6	ABR30379	Abri30379 Human can
45	29	39.2	15	6	ABR30870	Abri30870 Human can

ALIGNMENTS

RESULT 1
ADG46077
ID ADG46077 standard; peptide; 15 AA.
XX
AC
XX
ADG46077;
XX
DT 25-MAR-2004 (first entry)
XX
DE Human CDT peptide fragment #3.
XX
KW antibody; carbohydrate-deficient transferrin; CDT;
KM non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.
XX
OS Homo sapiens.
XX
PN EP1378521-A1.
XX
PD 07-JUN-2004.
XX
PF 19-MAY-2003; 2003EP-00011334.
XX
PR 05-JUL-2002; 2002DE-01030550.
XX
PA (DADE-) DADE BEHRING MAREBURG GMBH.
XX
PI Althaus H;
XX
DR WPI; 2004-073743/08.
XX
PT New antibody specific for carbohydrate-deficient transferrin, useful for
PT diagnosis of alcoholism, can bind its target in solution, eliminating
PT need for immobilization.
XX
PS Claim 4; SEQ ID NO 3; 21bp; German.
XX
CC This invention describes a novel antibody that, in aqueous solution,
CC binds selectively to carbohydrate-deficient transferrin (CDT) without
CC having to bind CDT to a solid phase. The invention also describes an
CC antibody that binds selectively to CDT at regions containing the
CC sequences VVARMSGKEDLIWEL, TTEDSYAKIMGEADAMSIDGAF, SKLMSGGLNLEPN and
CC YEKYGEYEVAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
CC using the antibodies of the invention. The antibodies of the invention
CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
CC antibodies are obtained by immunisation with non-glycosylated
CC transferrin, or a fragment, then generation of hybridomas by standard
CC fusion of spleen and myeloma cells. Hybridomas are then selected for
CC production of antibodies that specifically bind CDT from the aqueous
CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which

CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
 CC alcohols. The antibodies allow direct detection of CDT in solution,
 CC eliminating the need for immobilizing it on a solid phase (as required
 CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
 CC fragments used in the method of the invention.

XX Sequence 15 AA;

Query Match 100.0%; Score 74; DB 8; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.3e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SKLSMGSGNLSEPN 15
 |||||
 DB 1 SKLSMGSGNLSEPN 15

RESULT 2
 ADG46094
 ID ADG46094 standard; peptide; 13 AA.

XX ADG46094;

XX 25-MAR-2004 (first entry)

XX Human CDT peptide fragment #20.

XX antibody; carbohydrate-deficient transferrin; CDT;
 XX non-glycosylated transferrin; alcoholism; alcoholic; diagnosis; human.

XX Homo sapiens.

XX EP1378521-A1.

XX 07-JAN-2004.

XX 19-MAY-2003; 2003EP-00011334.

XX 05-JUL-2002; 2002DE-01030550.

XX (DADE-) DADE BEHRING MARBURG GMBH.

XX Althaus H;

XX WPI: 2004-073743/08.

XX New antibody specific for carbohydrate-deficient transferrin, useful for
 PT diagnosis of alcoholism, can bind its target in solution, eliminating
 PT need for immobilization.

XX Example 7; Page 15; 21pp; German.

XX This invention describes a novel antibody that, in aqueous solution,
 CC binds selectively to carbohydrate-deficient transferrin (CDT) without
 CC having to bind CDT to a solid phase. The invention also describes an
 CC antibody that binds selectively to CDT at regions containing the
 CC sequences VVANSMGSGKEDLIMEL, TTEDSIRAKINMGADAMSIDGGF, SKLSMGSGNLSEPN and
 CC YEKLGEEYKAV (ADG46075-ADG46078) and an immunoassay for detecting CDT
 CC using the antibodies of the invention. The antibodies of the invention
 CC are monoclonal, specifically from hybridomas DSM ACC2540 or 2541. The
 CC antibodies are obtained by immunisation with non-glycosylated
 CC transferrin, or a fragment, then generation of hybridomas by standard
 CC fusion of spleen and myeloma cells. Hybridomas are then selected for
 CC production of antibodies that specifically bind CDT from the aqueous
 CC phase. The antibodies are useful for diagnosis of alcoholism, CDT, which
 CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
 CC alcohols. The antibodies allow direct detection of CDT in solution,
 CC eliminating the need for immobilizing it on a solid phase (as required
 CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
 CC fragments used in the method of the invention.

XX Sequence 13 AA;

Query Match 87.8%; Score 65; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 LSMGSGNLSEPN 15
 |||||
 DB 1 LSMGSGNLSEPN 13

RESULT 3
 ADR15909
 ID ADR15909 standard; peptide; 15 AA.

XX ADR15909;

XX 04-NOV-2004 (first entry)

XX Transferrin peptide fragment #67.

XX glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.

XX Synthetic.

XX WO2004070389-A1.

XX 19-AUG-2004.

XX 06-FEB-2004; 2004WO-GB000480.

XX 06-FEB-2003; 2003GB-00002740.

XX (AXIS-) AXIS-SHIELD ASA.

XX Rye PD;

XX WPI: 2004-625547/60.

XX Assay for differentiating protein isoforms to determine their
 PT concentrations in sample e.g. blood, involves contacting the sample with
 PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
 PT detecting.

XX Disclosure; Page 15; 30pp; English.

XX The present invention describes an assay for a protein having at least
 CC two isoforms with different glycosylation patterns. The assay involves
 CC contacting a sample containing the protein with a proteolytic enzyme,
 CC followed by detecting the content or relative content of at least one
 CC peptide fragment produced by proteolysis. Also described is a kit for the
 CC assay method comprising the proteolytic enzyme and a substrate bound
 CC specific binding partner (S1) for at least 2 of the isoforms of the
 CC proteins. The method can be used for assaying isoforms of proteins
 CC according to their glycosylation pattern to determine their concentration
 CC or relative concentration in the sample or material (e.g. blood). The
 CC method avoids use of antibodies for distinguishing between glycosylated
 CC isoforms of the proteins. The present sequence represents a transferrin
 CC peptide fragment which is used in the exemplification of the present
 CC invention.

XX Sequence 15 AA;

Query Match 74.3%; Score 55; DB 8; Length 15;
 Best Local Similarity 84.6%; Pred. No. 0.0087;
 Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 LSMGSGNLSEPN 15
 |||||
 DB 1 LSMGSGNLSEPN 13

RESULT 4
 ADR15970
 ID ADR15970 standard; peptide; 15 AA.

XX AC ADR15970;
XX
XX 04-NOV-2004 (first entry)
XX
XX Transferrin peptide fragment #128.
DE
XX glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.
XX
XX Synthetic.
OS
XX WO2004070389-A1.
XX
XX 19-AUG-2004.
PD
XX 06-FEB-2004; 2004WO-GB000480.
XX
XX 06-FEB-2003; 2003GB-00002740.
PR
XX (AXIS-) AXIS-SHIELD ASA.
PA
XX Rye PD;
PI
XX WPI; 2004-62547/60.
DR
XX Assay for differentiating protein isoforms to determine their
PT concentrations in sample e.g. blood, involves contacting the sample with
PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
PT detecting.
XX
XX Disclosure; Page 17; 30pp; English.
PS
XX The present invention describes an assay for a protein having at least
CC two isoforms with different glycosylation patterns. The assay involves
CC contacting a sample containing the protein with a proteolytic enzyme,
CC followed by detecting the content or relative content of at least one
CC peptide fragment produced by proteolysis. Also described is a kit for the
CC assay method comprising the proteolytic enzyme and a substrate bound
CC specific binding partner (S1) for at least 2 of the isoforms of the
CC proteins. The method can be used for assaying isoforms of proteins
CC according to their glycosylation pattern to determine their concentration
CC or relative concentration in the sample or material (e.g. blood). The
CC method avoids use of antibodies for distinguishing between glycosylated
CC isoforms of the proteins. The present sequence represents a transferrin
CC peptide fragment which is used in the exemplification of the present
CC invention.
XX
XX Sequence 15 AA;
SQ
Query Match 74.3%; Score 55; DB 8; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0087; Mismatches 0; Gaps 0;
Matches 11; Conservative 0; Indels 2;
OY 3 LSWGSGLNISEPN 15
| | | | | | | | | | | | | | | | | |
Db 1 LCMGSGLNICEPN 13

RESULT 5
ADSI3393
ID ADSI3393 standard; peptide; 15 AA.
XX
XX ADSI3393;
AC
XX 16-DEC-2004 (first entry)
XX
XX Human rheumatoid arthritis marker peptide - SEQ ID 184.
DE
XX rheumatoid arthritis; marker; antiinflammatory; antiarthritic.
XX
XX Homo sapiens.
OS
XX WPI; 2004-69029/67.
PN

XX PD 30-SEP-2004.
XX
XX 15-MAR-2004; 2004WO-US007880.
XX
XX 14-MAR-2003; 2003US-0455037P.
PR
XX (SURR-) SURROMED INC.
PA
XX Kantor AB, Becker CH, Schulman H;
PI
XX WPI; 2004-69029/67.
DR
XX New isolated marker for rheumatoid arthritis, useful in preparing a
PT composition for diagnosing or treating rheumatoid arthritis.
PT
XX Claim 1; SEQ ID NO 184; 184pp; English.
PS
XX The invention relates to a novel isolated marker for rheumatoid arthritis
CC selected from one of many (around 400) markers defined in the
CC specification. Rheumatoid arthritis is a chronic inflammatory disorder of
CC the small joints which is estimated to affect 2.1 million people in the
CC United States alone. Current approaches to treat the disease include the
CC use of non-steroidal antiinflammatory drugs (NSAIDs), which may reduce
CC pain, swelling and inflammation, and disease-modifying anti-rheumatic
CC drugs (DMARDs), which act to slow the progression of the disease and
CC avoid further joint injury. These drugs are associated with a number of
CC serious side effects and the search for improved therapeutics is a
CC subject of active research. The marker of the invention demonstrates
CC antiarthritic activity and may be useful in preparing a composition for
CC diagnosing or treating rheumatoid arthritis. The current sequence is that
CC of a human rheumatoid arthritis marker peptide of the invention.
XX
XX Sequence 15 AA;
SQ
Query Match 74.3%; Score 55; DB 8; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0087; Mismatches 0; Gaps 0;
Matches 11; Conservative 0; Indels 2;
OY 3 LSWGSGLNISEPN 15
| | | | | | | | | | | | | | | | | |
Db 1 LCMGSGLNICEPN 13

RESULT 6
ADSI3389
ID ADSI3389 standard; peptide; 15 AA.
XX
XX ADSI3389;
AC
XX 16-DEC-2004 (first entry)
XX
XX Human rheumatoid arthritis marker peptide - SEQ ID 180.
DE
XX rheumatoid arthritis; marker; antiinflammatory; antiarthritic.
XX
XX Homo sapiens.
OS
XX WO2004082617-A2.
PN
XX 30-SEP-2004.
XX
XX 15-MAR-2004; 2004WO-US007880.
XX
XX 14-MAR-2003; 2003US-0455037P.
PR
XX (SURR-) SURROMED INC.
PA
XX Kantor AB, Becker CH, Schulman H;
PI
XX WPI; 2004-69029/67.
DR
XX New isolated marker for rheumatoid arthritis, useful in preparing a
PT

PT composition for diagnosing or treating rheumatoid arthritis.
XX
PS Claim 1; SEQ ID NO 180; 184bp; English.
XX
CC The invention relates to a novel isolated marker for rheumatoid arthritis
CC selected from one of many (around 400) markers defined in the
CC specification. Rheumatoid arthritis is a chronic inflammatory disorder of
CC the small joints which is estimated to affect 2.1 million people in the
CC United States alone. Current approaches to treat the disease include the
CC use of non-steroidal antiinflammatory drugs (NSAIDs), which may reduce
CC pain, swelling and inflammation, and disease-modifying anti-rheumatic
CC drugs (DMARDs), which act to slow the progression of the disease and
CC avoid further joint injury. These drugs are associated with a number of
CC serious side effects and the search for improved therapeutics is a
CC subject of active research. The marker of the invention demonstrates
CC antiarthritis activity and may be useful in preparing a composition for
CC diagnosing or treating rheumatoid arthritis. The current sequence is that
CC of a human rheumatoid arthritis marker peptide of the invention.
XX
SQ Sequence 15 AA;
XX
Query Match 74.3%; Score 55; DB 8; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0087;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 3 LSMGSLNLSPPN 15
DB 1 LCMGSLNLCERN 13
XX
RESULT 7
AAV70486
ID AAV70486 standard; protein; 15 AA.
XX
AC AAV70486;
XX
DT 04-JUL-2000 (first entry)
XX
DE Synthesised peptide-1 from human prothrombin kringle-2 protein.
XX
XX Human prothrombin kringle-2; prothrombin; kringle domain; cancer therapy;
KM anti-endothelial cell proliferation; anti-tumour; angiogenesis; cancer;
KM skin; laryngeal; uterine; colon; lung; bone marrow; cytostatic;
KM anti-angiogenic.
XX
OS Homo sapiens.
XX
XX WO200014209-A1.
XX
XX 16-MAR-2000.
XX
PD 07-SEP-1999; 99WO-KR000525.
XX
PF 07-SEP-1998; 98KR-00036786.
XX
PR 07-SEP-1998;
XX
XX (KIMS/) KIM S. S.
XX (GENO-) GENOTECH CORP.
XX
XX Rhim TY, Park CS, Kim EK;
XX
XX WPI; 2000-256965/22.
XX
XX Human prothrombin kringle-1 and kringle-2 polypeptides that inhibit
XX angiogenesis, useful for treating cancer.
XX
XX Example 7, Page 19; 43bp; English.
XX
XX The present sequence is a synthesised peptide of human prothrombin
XX kringle-2 protein which is derived from human plasma prothrombin.
XX Peptides were synthesised having amino acid sequences in order from N-
XX terminal sequence of prothrombin kringle-2 by overlapping 2-5 amino acids
XX of both N-terminal and C-terminal of peptides. These peptides were
XX purified by high performance liquid chromatography (HPLC). Kringle

CC domains from prothrombin have anti-endothelial cell proliferation and
CC anti-tumour activities. These inhibit angiogenesis which is involved in
CC tumour growth. They are also useful for the treatment of cancer, e.g.
CC skin, laryngeal, uterine, colon, lung and bone marrow cancer. The human
CC prothrombin kringle-2 significantly suppresses tumour growth in vivo
XX
SQ Sequence 15 AA;
XX
Query Match 44.6%; Score 33; DB 3; Length 15;
Best Local Similarity 63.6%; Pred. No. 78;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 4 SMGSLNLSPPN 14
DB 1 SEGSSVNLSPN 11
XX
RESULT 8
ABJ08867
ID ABJ08867 standard; peptide; 9 AA.
XX
AC ABJ08867;
XX
DT 14-NOV-2002 (first entry)
XX
DE Hepatitis B virus epitope #3085.
XX
XX Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
KM virucide; hepatotropic; antiinflammatory.
XX
XX Hepatitis B virus.
XX
OS WO200219986-A1.
XX
XX 14-MAR-2002.
XX
PD 08-SEP-2000; 2000WO-US024802.
XX
PF 08-SEP-2000; 2000WO-US024802.
XX
PR 08-SEP-2000; 2000WO-US024802.
XX
XX (EPIM-) EPIMUNE INC.
XX (SETT/) SETT A.
XX
XX Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD,
PI Cells B, Kubo RT, Grey HM, Chesnut RW,
XX
XX WPI; 2002-643192/69.
XX
XX Vaccine composition for treating or preventing hepatitis B virus (HBV)
XX infection, and/or for stimulating an immune response to HBV, comprises a
XX HBV peptide epitope.
XX
XX Disclosure; Page 178; 228bp; English.
XX
XX The present invention relates to a composition comprising at least one
XX hepatitis B virus epitope. This can be used in the production of a
XX vaccine for use in preventing or treating hepatitis B virus infection.
XX The present sequence is a peptide described in the exemplification of the
XX invention
XX
SQ Sequence 9 AA;
XX
Query Match 40.5%; Score 30; DB 5; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 8 GLNLSPPN 15
DB 2 GTNLSVPPN 9
XX
RESULT 9
ABJ09159

ID ABJ09159 standard; peptide; 9 AA.
 XX
 AC ABJ09159;
 XX
 DT 14-NOV-2002 (first entry)
 XX
 DE Hepatitis B virus epitope #3377.
 XX
 KM Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
 KW virulence; hepatocarcinoma; antiinflammatory.
 XX
 OS Hepatitis B virus.
 XX
 PN MO200219986-A1.
 PD 14-MAR-2002.
 XX
 PF 08-SEP-2000; 2000MO-US024802.
 XX
 PR 08-SEP-2000; 2000MO-US024802.
 XX
 PA (EPIM-) EPIMUNE INC.
 PA (SETT/) SETTLE A.
 XX
 PI Settle A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
 PI Cells E, Kubo RT, Grey HM, Chesnut RW;
 XX
 DR WPI; 2002-643192/69.
 XX
 PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
 PT infection, and/or for stimulating an immune response to HBV, comprises a
 PT HBV peptide epitope.
 XX
 PS Disclosure; Page 181; 228pp; English.
 XX
 CC The present invention relates to a composition comprising at least one
 CC hepatitis B virus epitope. This can be used in the production of a
 CC vaccine for use in preventing or treating hepatitis B virus infection.
 CC The present sequence is a peptide described in the exemplification of the
 CC invention
 XX
 SQ Sequence 9 AA;
 XX
 Query Match 40.5%; Score 30; DB 5; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 8 GUNLSEPN 15
 | | | | |
 Db 2 GTNLSTVFN 9
 XX
 RESULT 10
 ADQ12374
 ID ADQ12374 standard; peptide; 9 AA.
 XX
 AC ADQ12374;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Hepatitis B virus MHC class I restricted T-cell stimulating peptide 173.
 XX
 KM HBV, MHC class I restricted T-cell stimulating peptide; surface peptide;
 KW core peptide; polymerase peptide; immunogenic composition; vaccine;
 KW cytotoxic T-lymphocyte response; CTL response.
 XX
 OS Hepatitis B virus.
 XX
 PN MO2004058807-A2.
 PD 15-JUL-2004.
 XX
 PF 09-DEC-2003; 2003MO-EP013948.
 XX

XX
 PR 24-DEC-2002; 2002EP-00447276.
 XX
 PA (ALGO-) ALGONOMICS NV.
 XX
 PI Lasters I, Desmet J, Stegmann T, Castelein B;
 XX
 DR WPI; 2004-525861/50.
 XX
 PT New peptide comprising a major histocompatibility complex class I
 PT restricted T-cell stimulating epitope of the hepatitis B virus (HBV)
 PT surface, core and/or polymerase polypeptide, for preparation of an HBV
 PT immunogenic composition.
 XX
 PS Example 7; SEQ ID NO 173; 108pp; English.
 XX
 CC The invention comprises major histocompatibility complex (MHC) class I
 CC restricted T-cell stimulating epitopes of the hepatitis B virus (HBV)
 CC surface, core and polymerase proteins. The peptides of the invention are
 CC useful for generating an HBV immunogenic composition (e.g. vaccine) that
 CC induces a cytotoxic T-lymphocyte (CTL) response. The present amino acid
 CC sequence represents an MHC class I restricted T-cell stimulating HBV
 CC peptide of the invention.
 XX
 SQ Sequence 9 AA;
 XX
 Query Match 40.5%; Score 30; DB 8; Length 9;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 8 GUNLSEPN 15
 | | | | |
 Db 2 GTNLSTVFN 9
 XX
 RESULT 11
 ADQ12375
 ID ADQ12375 standard; peptide; 9 AA.
 XX
 AC ADQ12375;
 XX
 DT 07-OCT-2004 (first entry)
 XX
 DE Hepatitis B virus MHC class I restricted T-cell stimulating peptide 174.
 XX
 KM HBV, MHC class I restricted T-cell stimulating peptide; surface peptide;
 KW core peptide; polymerase peptide; immunogenic composition; vaccine;
 KW cytotoxic T-lymphocyte response; CTL response.
 XX
 OS Hepatitis B virus.
 XX
 PN MO2004058807-A2.
 PD 15-JUL-2004.
 XX
 PF 09-DEC-2003; 2003MO-EP013948.
 XX
 PR 24-DEC-2002; 2002EP-00447276.
 XX
 PA (ALGO-) ALGONOMICS NV.
 XX
 PI Lasters I, Desmet J, Stegmann T, Castelein B;
 XX
 DR WPI; 2004-525861/50.
 XX
 PT New peptide comprising a major histocompatibility complex class I
 PT restricted T-cell stimulating epitope of the hepatitis B virus (HBV)
 PT surface, core and/or polymerase polypeptide, for preparation of an HBV
 PT immunogenic composition.
 XX
 PS Example 7; SEQ ID NO 174; 108pp; English.
 XX
 CC The invention comprises major histocompatibility complex (MHC) class I

CC restricted T-cell stimulating epitopes of the hepatitis B virus (HBV)
CC surface, core and polymerase proteins. The peptides of the invention are
CC useful for generating an HBV immunogenic composition (e.g. vaccine) that
CC induces a cytotoxic T-lymphocyte (CTL) response. The present amino acid
CC sequence represents an MHC class I restricted T-cell stimulating HBV
CC peptide of the invention.

XX Sequence 9 AA;

Query Match 40.5%; Score 30; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 8 GINLSEPN 15
| | | | |
Db 1 GTNLSPN 8

RESULT 12

AA38384
ID AA38384 standard; peptide; 10 AA.

AC AA38384;

DT 25-MAR-2003 (revised)

DT 21-OCT-1993 (first entry)

DE T-cell epitope from HBsAg/p43 pre-S(1).

KM Hybrid; immunogen; T-cell; epitope; antigen; HIV; cyclic;

KM principal neutralising determinant; CPND; hepatitis-B pre-S(1); antibody;

XX immunity.

XX OS Synthetic.

FN EP547689-A2.

PD 23-JUN-1993.

PF 10-DEC-1992; 92EP-00203855.

PR 18-DEC-1991; 91US-00811041.

PA (MERI) MERCK & CO INC.

PI Hannah J, Tolman RL;

DR WPI; 1993-198695/25.

PS Claim 3; Page 23; 24pp; English.

XX A hybrid immunogen comprises a T-cell stimulatory epitope from HBsAg/p43
XX pre-S(1) (AA38384) and a cyclic HIV principal neutralising determinant,
XX CPND (AA38385). The two components may be linked via an intervening
XX sequence of 1-4 amino acids which may include a marker amino acid. The
XX hybrid immunogen is used to induce anti-HIV PND, anti-HIV or HIV-
XX neutralising immune response. (Updated on 25-MAR-2003 to correct PN
XX field.)

SQ Sequence 10 AA;

Query Match 40.5%; Score 30; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 8 GINLSEPN 15
| | | | |
Db 2 GTNLSPN 9

RESULT 13
AB06595
ID AB06595 standard; peptide; 10 AA.

AC AB06595;

DT 14-NOV-2002 (first entry)

DE Hepatitis B virus epitope #813.

KM Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;

KM virucide; hepatotropic; antiinflammatory.

OS Hepatitis B virus.

FN WO200219986-A1.

PD 14-MAR-2002.

PF 08-SEP-2000; 2000WO-US024802.

PR 08-SEP-2000; 2000WO-US024802.

PA (EPIM-) EPIMMUNE INC.

PA (SETT/) SETTE A.

PI Sette A, Sidney J, Southwood S, Vitello MA, Livingstone BD;

PI Cells E, Kudo RT, Grey HM, Chesnut RW;

DR WPI; 2002-643192/69.

PS Disclosure; Page 128; 228pp; English.

XX The present invention relates to a composition comprising at least one
XX hepatitis B virus epitope. This can be used in the production of a
XX vaccine for use in preventing or treating hepatitis B virus infection.
XX The present sequence is a peptide described in the exemplification of the
XX invention

SQ Sequence 10 AA;

Query Match 40.5%; Score 30; DB 5; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 8 GINLSEPN 15
| | | | |
Db 1 GTNLSPN 8

RESULT 14
AB07286
ID AB07286 standard; peptide; 10 AA.

AC AB07286;

DT 14-NOV-2002 (first entry)

DE Hepatitis B virus epitope #1504.

KM Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;

KM virucide; hepatotropic; antiinflammatory.

OS Hepatitis B virus.

FN WO200219986-A1.

PD 14-MAR-2002.

XX 08-SEP-2000; 2000WO-US024802.
PF 08-SEP-2000; 2000WO-US024802.
XX
XX (EPIM-) EPIMMUNE INC.
PA (SETT/) SETTE A.
XX
PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
PI Cells E, Kubo RT, Grey HM, Chesnut RW;
XX
DR WPI; 2002-643192/59.
XX
PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
PT infection, and/or for stimulating an immune response to HBV, comprises a
PT HBV peptide epitope.
XX
PS Disclosure; Page 140; 228pp; English.
XX
XX The present invention relates to a composition comprising at least one
CC hepatitis B virus epitope. This can be used in the production of a
CC vaccine for use in preventing or treating hepatitis B virus infection.
CC The present sequence is a peptide described in the exemplification of the
CC invention
XX
SQ Sequence 10 AA;

Query Match 40.5%; Score 30; DB 5; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GNTLSEPN 15
| | | | |
DB 1 GNTLSVFN 8

RESULT 15
ABJ06082
ID ABJ06082 standard; peptide; 10 AA.
XX
AC ABJ06082;
XX
DT .14-NOV-2002 (first entry)
XX
DE Hepatitis B virus epitope #300.
XX
KM Hepatitis B virus; HBV; epitope; vaccine; HBV infection; hepatitis;
KM virucide; hepatotropic; antiinflammatory.
XX
OS Hepatitis B virus.
XX
PN WO200219986-A1.
XX
PD 14-MAR-2002.
XX
PF 08-SEP-2000; 2000WO-US024802.
XX
PR 08-SEP-2000; 2000WO-US024802.
XX
PA (EPIM-) EPIMMUNE INC.
PA (SETT/) SETTE A.
XX
PI Sette A, Sidney J, Southwood S, Vitiello MA, Livingstone BD;
PI Cells E, Kubo RT, Grey HM, Chesnut RW;
XX
DR WPI; 2002-643192/59.
XX
PT Vaccine composition for treating or preventing hepatitis B virus (HBV)
PT infection, and/or for stimulating an immune response to HBV, comprises a
PT HBV peptide epitope.
XX
PS Disclosure; Page 115; 228pp; English.
XX

CC The present invention relates to a composition comprising at least one
CC hepatitis B virus epitope. This can be used in the production of a
CC vaccine for use in preventing or treating hepatitis B virus infection.
CC The present sequence is a peptide described in the exemplification of the
CC invention
XX
SQ Sequence 10 AA;

Query Match 40.5%; Score 30; DB 5; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 GNTLSEPN 15
| | | | |
DB 1 GNTLSVFN 8

Search completed: November 1, 2005, 14:11:44
Job time : 163 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 14:06:05 ; Search time 42 Seconds
(without alignments)
26.660 Million cell updates/sec

Title: US-10-612-162a-3

Perfect score: 74

Sequence: 1 SKLSMSGSLSEPN 15

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 164526

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A COMB. pep.*
2: /cgn2_6/prodata/1/1aa/5B COMB. pep.*
3: /cgn2_6/prodata/1/1aa/6A COMB. pep.*
4: /cgn2_6/prodata/1/1aa/6B COMB. pep.*
5: /cgn2_6/prodata/1/1aa/PCTUS COMB. pep.*
6: /cgn2_6/prodata/1/1aa/backfile1.pcp.*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	40.5	10	4	US-09-239-043D-257
2	30	40.5	10	4	US-09-239-043D-743
3	30	40.5	10	4	US-09-239-043D-1374
4	30	40.5	15	4	US-09-239-043D-2101
5	29	39.2	13	4	US-09-489-156-22
6	29	39.2	13	4	US-09-489-156-23
7	29	39.2	13	4	US-09-693-746-124
8	28	37.8	10	1	US-08-462-949-11
9	28	37.8	10	1	US-08-023-764B-11
10	27	36.5	13	1	US-08-200-900A-23
11	27	36.5	13	4	US-09-489-156-25
12	27	36.5	13	4	US-08-794-042-23
13	27	36.5	13	5	PCT-US94-00616-23
14	27	36.5	15	4	US-09-255-501-96
15	27	36.5	15	4	US-09-255-501-97
16	27	36.5	15	4	US-09-060-872A-96
17	27	36.5	15	4	US-09-060-872A-97
18	27	36.5	15	4	US-09-500-135C-96
19	27	36.5	15	4	US-09-500-135C-97
20	26	35.1	10	5	PCT-US94-01234-39
21	26	35.1	11	4	US-09-239-043D-44
22	26	35.1	11	4	US-09-239-043D-796
23	26	35.1	12	3	US-09-239-043D-1585
24	26	35.1	12	3	US-09-248-588-113
25	26	35.1	12	3	US-09-261-368-35
26	26	35.1	12	4	US-09-106-568E-66
27	26	35.1	12	4	US-09-106-568E-82

28	26	35.1	12	4	US-10-114-176-35	Sequence 35, Appl
29	26	35.1	12	6	5178861-10	Patent No. 5178861
30	26	35.1	12	6	5178861-10	Patent No. 5178861
31	26	35.1	15	2	US-08-572-951-6	Sequence 6, Appl
32	26	35.1	15	2	US-08-572-951-23	Sequence 23, Appl
33	26	35.1	15	4	US-09-255-501-98	Sequence 98, Appl
34	26	35.1	15	4	US-09-239-043D-2113	Sequence 2113, Ap
35	26	35.1	15	4	US-09-239-043D-2120	Sequence 2120, Ap
36	26	35.1	15	4	US-09-060-872A-98	Sequence 98, Appl
37	26	35.1	15	4	US-09-500-135C-98	Sequence 98, Appl
38	25	33.8	8	4	US-09-239-043D-298	Sequence 298, App
39	25	33.8	8	4	US-09-239-043D-372	Sequence 372, App
40	25	33.8	8	4	US-09-239-043D-795	Sequence 795, App
41	25	33.8	8	4	US-09-239-043D-897	Sequence 897, App
42	25	33.8	8	4	US-10-152-158-8	Sequence 8, Appl
43	25	33.8	9	4	US-09-239-043D-1221	Sequence 1221, Ap
44	25	33.8	10	1	US-08-462-949-23	Sequence 23, Appl
45	25	33.8	10	1	US-08-023-764B-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-09-239-043D-257
Sequence 257, Application US/09239043D
Patent No. 6689363
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Vitellio, Maria A.
APPLICANT: Livingston, Brian D.
APPLICANT: Celis, Esteban
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Cheenut, Robert
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0060007
CURRENT FILING DATE: 1999-01-27
CURRENT FILING DATE: 1999-01-27
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1998-11-10
PRIOR FILING DATE: 1997-11-25
PRIOR FILING DATE: 1997-11-25
PRIOR FILING DATE: 1997-03-12
PRIOR FILING DATE: 1997-03-12
PRIOR FILING DATE: 1996-03-13
PRIOR FILING DATE: 1995-06-05
PRIOR FILING DATE: 1995-06-05
PRIOR FILING DATE: 1994-12-01
PRIOR FILING DATE: 1994-12-01
PRIOR FILING DATE: 1994-11-23
PRIOR FILING DATE: 1994-07-21
PRIOR FILING DATE: 1994-07-21
PRIOR FILING DATE: 1994-03-04
PRIOR FILING DATE: 1994-03-04
PRIOR FILING DATE: 1994-02-16
PRIOR FILING DATE: 1994-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 2579
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 257
LENGTH: 10
TYPE: PRT
ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-257
Query Match 40.5%; Score 30; DB 4; Length 10;

Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 GNLSEPN 15
| | | | |
Db 1 GTNLSTVPN 8

RESULT 2

US-09-239-043D-743
; Sequence 743, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 743
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus

US-09-239-043D-743

Query Match 40.5%; Score 30; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 GNLSEPN 15
| | | | |
Db 1 GTNLSTVPN 8

RESULT 3

US-09-239-043D-1374
; Sequence 1374, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John

; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: EpiImmune Inc.

; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1374
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus

US-09-239-043D-1374

Query Match 40.5%; Score 30; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 GNLSEPN 15
| | | | |
Db 1 GTNLSTVPN 8

RESULT 4

US-09-239-043D-2101
; Sequence 2101, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10

```

; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/197,484
; PRIOR FILING DATE: 1994-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: PaeSeq for Windows Version 4.0
; SEQ ID NO 2101
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-2101
```

```

Query Match          40.5%; Score 30; DB 4; Length 15;
Best Local Similarity 75.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      8 GNLSEPN 15
        |||||
Db       1 GTNLVYPN 8
```

```

RESULT 5
US-09-489-156-22
; Sequence 22, Application US/09489156
; Patent No. 6559128
; GENERAL INFORMATION:
; APPLICANT: HAMM, Heidi
; APPLICANT: GILCHRIST, Annette
; TITLE OF INVENTION: INHIBITORS OF G PROTEIN-MEDIATED SIGNALING, METHODS OF MAKING THE
; FILE REFERENCE: 0290-29 (NU 99037)
; CURRENT APPLICATION NUMBER: US/09/489,156
; CURRENT FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: G alpha 11 peptide
US-09-489-156-22
```

```

Query Match          39.2%; Score 29; DB 4; Length 13;
Best Local Similarity 63.6%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      5 MSGNLSEPN 15
        |||||
Db       1 MGQLNLKEYN 11
```

```

RESULT 6
US-09-489-156-23
; Sequence 23, Application US/09489156
; Patent No. 6559128
; GENERAL INFORMATION:
; APPLICANT: HAMM, Heidi
```

```

; APPLICANT: GILCHRIST, Annette
; TITLE OF INVENTION: INHIBITORS OF G PROTEIN-MEDIATED SIGNALING, METHODS OF MAKING THE
; FILE REFERENCE: 0290-29 (NU 99037)
; CURRENT APPLICATION NUMBER: US/09/489,156
; CURRENT FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 23
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: G alpha q peptide
US-09-489-156-23
```

```

Query Match          39.2%; Score 29; DB 4; Length 13;
Best Local Similarity 63.6%; Pred. No. 72;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      5 MSGNLSEPN 15
        |||||
Db       1 MGQLNLKEYN 11
```

```

RESULT 7
US-09-693-746-124
; Sequence 124, Application US/09693746
; Patent No. 6835546
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Metho
; FILE REFERENCE: 6297,1CD
; CURRENT APPLICATION NUMBER: US/09/693,746
; CURRENT FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/425,676
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6835546e1 Sequence
US-09-693-746-124
```

```

Query Match          39.2%; Score 29; DB 4; Length 13;
Best Local Similarity 55.6%; Pred. No. 72;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      7 SGLNSEPN 15
        |||||
Db       1 SDIGISEPN 9
```

```

RESULT 8
US-08-462-949-11
; Sequence 11, Application US/08462949
; Patent No. 5606022
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Beth Ann
; TITLE OF INVENTION: Cloning and Identification of a Two
; TITLE OF INVENTION: Component Signal Transducing Regulatory System from
; TITLE OF INVENTION: Bacteroiodes Fragilis
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby P.C.
; STREET: 805 Third Avenue
```

CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,949
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/023,764
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Robinson, Joseph R.
REGISTRATION NUMBER: 33,448
REFERENCE/DOCKET NUMBER: 0646/1B024-US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEFAX: 201-753-6237
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-462-949-11

Query Match 37.8%; Score 28; DB 1; Length 10;
Best Local Similarity 85.7%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GSGJLNS 12
Db 2 GSGJGLS 8

RESULT 9
US-08-023-764B-11
Sequence 11, Application US/08023764B
Patent No. 5679540
GENERAL INFORMATION:
APPLICANT: Rasmussen, Beth Ann
TITLE OF INVENTION: Cloning and Identification of a Two
TITLE OF INVENTION: Component Signal Transducing Regulatory System from
TITLE OF INVENTION: Bacterioides Fragilis
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: United States
ZIP: 07470-8426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/023,764B
FILING DATE: 26-FEB-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Barnhard, Elizabeth M.
REGISTRATION NUMBER: 31,088
REFERENCE/DOCKET NUMBER: 31,658-00

TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 831-3246
TELEFAX: (201) 831-3305
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-023-764B-11

Query Match 37.8%; Score 28; DB 1; Length 10;
Best Local Similarity 85.7%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GSGJLNS 12
Db 2 GSGJGLS 8

RESULT 10
US-08-200-900A-23
Sequence 23, Application US/08200900A
Patent No. 5665566
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc. - Legal Affairs
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/200,900A
FILING DATE: 23-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weinert, Maureen C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI 5201-FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170 X8574
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-200-900A-23

Query Match 36.5%; Score 27; DB 1; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GSGJLNS 14
Db 5 GYGJGPEP 13

RESULT 11

US-09-489-156-25
; Sequence 25, Application US/09489156
; Patent No. 6559128
; GENERAL INFORMATION:
; APPLICANT: HAMM, Heidi
; APPLICANT: GILCHRIST, Anneette
; TITLE OF INVENTION: INHIBITORS OF G PROTEIN-MEDIATED SIGNALING, METHODS OF MAKING THE
; FILE REFERENCE: 0290-29 (NU 99037)
; CURRENT APPLICATION NUMBER: US/09/489,156
; CURRENT FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 25
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: G alpha 14 peptide
US-09-489-156-25

Query Match 36.5%; Score 27; DB 4; Length 13;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 MSGSLNLRPN 15
DB 1 MGLQJLNLRPN 11

RESULT 12

US-08-794-042-23
; Sequence 23, Application US/08794042
; Patent No. 6746859

; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. - Legal Affairs
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,042
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/200,900
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weinert, Maureen C.
; REGISTRATION NUMBER: 31,544
; REFERENCE/DOCKET NUMBER: GI 5201-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 876-1170 X8574
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-794-042-23

Query Match 36.5%; Score 27; DB 4; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 GSGJLNLRPN 14
DB 5 GYGJLGRPN 13

RESULT 13

PCT-US94-00616-23
; Sequence 23, Application PC/TUS9400616
; GENERAL INFORMATION:

; APPLICANT:
; TITLE OF INVENTION: CLONING OF ENTEROKINASE AND METHOD OF USE
; NUMBER OF SEQUENCES: 33
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/00616
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-00616-23

Query Match 36.5%; Score 27; DB 5; Length 13;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 GSGJLNLRPN 14
DB 5 GYGJLGRPN 13

RESULT 14

US-09-255-501-96
; Sequence 96, Application US/09255501
; Patent No. 6596525

; GENERAL INFORMATION:
; APPLICANT: Batell, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN
; TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND
; FILE REFERENCE: GCS27
; PRODUCING SUCH PROTEINS
; CURRENT APPLICATION NUMBER: US/09/255,501
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 96
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-255-501-96

Query Match 36.5%; Score 27; DB 4; Length 15;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLSMGSG 8
DB 5 ASLSLGSG 12

RESULT 15

US-09-255-501-97
; Sequence 97, Application US/09255501
; Patent No. 6596525
; GENERAL INFORMATION:
; APPLICANT: Esteil, David
; APPLICANT: Harding, Fiona
; TITLE OF INVENTION: MUTANT PROTEINS HAVING LOWER ALLERGENIC RESPONSE IN
; TITLE OF INVENTION: HUMANS AND METHODS FOR CONSTRUCTING, IDENTIFYING AND
; TITLE OF INVENTION: PRODUCING SUCH PROTEINS
; FILE REFERENCE: GC527
; CURRENT APPLICATION NUMBER: US/09/255,501
; CURRENT FILING DATE: 1999-02-23
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 97
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-255-501-97

Query Match 36.5%; Score 27; DB 4; Length 15;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SKLSMSG 8
: ||: ||
Db 2 ASLSLGS 9

Search completed: November 1, 2005, 14:21:31
Job time : 47 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 14:12:03 ; Search time 170 Seconds

(without alignments)
36.886 Million cell updates/sec

Title: US-10-612-162a-3

Perfect score: 74

Sequence: 1 SKLSMGSGLNSEPN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 323103

Minimum DB seq length: 0
Maximum DB seq length: 15Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	15	US-10-612-162-3	Sequence 3, Appli
2	55	74.3	15	US-10-769-514-10	Sequence 10, Appli
3	55	74.3	15	US-10-769-514-42	Sequence 42, Appli
4	55	74.3	15	US-10-801-990-180	Sequence 180, Appli
5	55	74.3	15	US-10-801-990-184	Sequence 184, Appli
6	33	44.6	14	US-10-059-271-37	Sequence 37, Appli
7	31	41.9	13	US-10-993-351-3	Sequence 3, Appli
8	30	40.5	10	US-10-654-601-257	Sequence 257, Appli
9	30	40.5	10	US-10-654-601-743	Sequence 743, Appli
10	30	40.5	10	US-10-654-601-1374	Sequence 1374, Appli
11	30	40.5	15	US-10-654-601-2101	Sequence 2101, Appli

12	29	39.2	10	US-10-930-300-93	Sequence 93, Appli
13	29	39.2	13	US-09-882-910-114	Sequence 114, Appli
14	29	39.2	13	US-09-882-910-115	Sequence 115, Appli
15	29	39.2	13	US-10-283-423-124	Sequence 124, Appli
16	29	39.2	13	US-10-373-540-22	Sequence 22, Appli
17	29	39.2	13	US-10-373-540-23	Sequence 23, Appli
18	29	39.2	13	US-10-213-821-124	Sequence 124, Appli
19	29	39.2	13	US-10-411-364-114	Sequence 114, Appli
20	29	39.2	13	US-10-411-364-115	Sequence 115, Appli
21	29	39.2	13	US-10-736-048-124	Sequence 124, Appli
22	29	39.2	11	US-10-795-676-58	Sequence 58, Appli
23	28	37.8	11	US-10-970-242-15	Sequence 15, Appli
24	28	37.8	12	US-10-785-819-43	Sequence 43, Appli
25	28	37.8	14	US-10-153-244-95	Sequence 95, Appli
26	28	37.8	14	US-10-153-244-157	Sequence 157, Appli
27	28	37.8	14	US-10-153-244-206	Sequence 206, Appli
28	28	37.8	14	US-10-153-244-258	Sequence 258, Appli
29	28	37.8	15	US-10-769-514-16	Sequence 16, Appli
30	27	36.5	9	US-10-296-317-46	Sequence 46, Appli
31	27	36.5	12	US-10-356-257-98	Sequence 98, Appli
32	27	36.5	13	US-10-375-540-85	Sequence 85, Appli
33	27	36.5	14	US-10-327-558-595	Sequence 595, Appli
34	27	36.5	14	US-10-769-514-17	Sequence 17, Appli
35	27	36.5	14	US-10-862-195-89	Sequence 89, Appli
36	27	36.5	15	US-10-769-514-15	Sequence 15, Appli
37	27	36.5	15	US-10-924-092A-96	Sequence 96, Appli
38	27	36.5	15	US-10-924-092A-97	Sequence 97, Appli
39	27	36.5	15	US-11-020-628-96	Sequence 96, Appli
40	26	35.1	15	US-11-020-628-97	Sequence 97, Appli
41	26	35.1	9	US-10-062-109A-390	Sequence 390, Appli
42	26	35.1	9	US-10-062-109A-484	Sequence 484, Appli
43	26	35.1	9	US-10-062-109A-578	Sequence 578, Appli
44	26	35.1	9	US-10-005-460A-390	Sequence 390, Appli
45	26	35.1	9	US-10-005-460A-484	Sequence 484, Appli

ALIGNMENTS

RESULT 1
US-10-612-162-3
; Sequence 3, Application US/10612162
; Publication No. US20040014145A1
GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
; FILE REFERENCE: 2002/B001
; CURRENT APPLICATION NUMBER: US/10/612,162
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; PRIOR FILING DATE: 2003-05-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 15
; TYPE: PR
; ORGANISM: Homo sapiens
US-10-612-162-3

Query Match 100.0%; Score 74; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SKLSMGSGLNSEPN 15
Db 1 SKLSMGSGLNSEPN 15
RESULT 2
US-10-769-514-10

```
; Sequence 10, Application US/10769514
; Publication No. US20040258695A1
; GENERAL INFORMATION:
; APPLICANT: Schryvers, Anthony
; TITLE OF INVENTION: Transferrin Binding Peptides and Uses Thereof
; FILE REFERENCE: 028722-001
; CURRENT APPLICATION NUMBER: US/10/769,514
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,113
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-769-514-10
```

```
Query Match          74.3%; Score 55; DB 16; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0082;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      3 LMSGGLNLSEPN 15
      |||||
Db      1 LCMGSGNLCEPN 13
```

```
RESULT 3
US-10-769-514-42
; Sequence 42, Application US/10769514
; Publication No. US20040258695A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Schryvers, Anthony
; TITLE OF INVENTION: Transferrin Binding Peptides and Uses Thereof
; FILE REFERENCE: 028722-001
; CURRENT APPLICATION NUMBER: US/10/769,514
; PRIOR FILING DATE: 2004-01-30
; PRIOR APPLICATION NUMBER: US 60/444,113
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: TdpB-binding peptides
US-10-769-514-42
```

```
Query Match          74.3%; Score 55; DB 16; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0082;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      3 LMSGGLNLSEPN 15
      |||||
Db      1 LCMGSGNLCEPN 13
```

```
RESULT 4
US-10-801-990-180
; Sequence 180, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
; APPLICANT: Kantor, Aaron B.
; APPLICANT: Schulman, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121
; CURRENT APPLICATION NUMBER: US/10/801,990
; PRIOR FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; NUMBER OF SEQ ID NOS: 395
```

```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 180
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-180
```

```
Query Match          74.3%; Score 55; DB 17; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0082;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      3 LMSGGLNLSEPN 15
      |||||
Db      1 LCMGSGNLCEPN 13
```

```
RESULT 5
US-10-801-990-184
```

```
; Sequence 184, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Kantor, Aaron B.
; APPLICANT: Schulman, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121
; CURRENT APPLICATION NUMBER: US/10/801,990
; PRIOR FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 184
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-184
```

```
Query Match          74.3%; Score 55; DB 17; Length 15;
Best Local Similarity 84.6%; Pred. No. 0.0082;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      3 LMSGGLNLSEPN 15
      |||||
Db      1 LCMGSGNLCEPN 13
```

```
RESULT 6
US-10-059-271-37
```

```
; Sequence 37, Application US/10059271
; Publication No. US20030082208A1
; GENERAL INFORMATION:
```

```
; APPLICANT: REPPE, HEINRICH
; APPLICANT: BUDDÉ, ECKHARD
; APPLICANT: NICOLAUS, STEFAN
; TITLE OF INVENTION: PROTEIN HAVING MULTIPLE ANTIGEN/EPITOPE SEQUENCES AND
; FILE REFERENCE: ALBRE-22
; CURRENT APPLICATION NUMBER: US/10/059,271
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: DE 101 06 295
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-059-271-37
```

Query Match 44.6%; Score 33; DB 14; Length 14;
Best Local Similarity 41.7%; Pred. No. 70;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 4 SMGGLNLEPN 15
:|:|:|:|:
DB 1 AVGIGINCTRN 12

RESULT 7
US-10-992-351-3
; Sequence 3, Application US/10992351
; Publication No. US2005013562A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Antibodies directed against prothrombin fragment F1+2, the prepar
; FILE REFERENCE: 05552.1454
; CURRENT APPLICATION NUMBER: US/10/992,351
; CURRENT FILING DATE: 2004-11-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-992-351-3

Query Match 41.9%; Score 31; DB 17; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSGGLNLEPN 14
:|:|:|:|:
DB 1 GSSVNLSP 9

RESULT 8
US-10-654-601-257
; Sequence 257, Application US/10654601
; Publication No. US20050063983A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Cheenut, Robert
; APPLICANT: Eptimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/10/654,601
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/239,043
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23

; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 257
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-10-654-601-257

Query Match 40.5%; Score 30; DB 17; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 8 GNLNLEPN 15
:|:|:|:|:
DB 1 GNLNLEPN 8

RESULT 9
US-10-654-601-743
; Sequence 743, Application US/10654601
; Publication No. US20050063983A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Cheenut, Robert
; APPLICANT: Eptimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/10/654,601
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/09/239,043
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 743
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-10-654-601-743

Query Match 40.5%; Score 30; DB 17; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;

```
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 8 GINLSEPN 15
Db 1 GTNLSEPN 8

RESULT 10
US-10-654-601-1374
; Sequence 1374, Application US/10654601
; Publication No. US20050063983A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT FILING DATE: 2003-09-04
; PRIOR APPLICATION NUMBER: US/10/654,601
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1374
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-10-654-601-1374

Query Match 40.5%; Score 30; DB 17; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 GINLSEPN 15
Db 1 GTNLSEPN 8

RESULT 11
US-10-654-601-2101
; Sequence 2101, Application US/10654601
; Publication No. US20050063983A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
```

```
; APPLICANT: Vitiello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; FILE REFERENCE: 2060.0060007
; CURRENT FILING DATE: US/10/654,601
; PRIOR APPLICATION NUMBER: US/09/239,043
; PRIOR FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
; PRIOR FILING DATE: 1994-11-23
; PRIOR APPLICATION NUMBER: US 08/278,634
; PRIOR FILING DATE: 1994-07-21
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2579
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2101
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Orthohepadnaviridae hepatitis B virus
US-10-654-601-2101

Query Match 40.5%; Score 30; DB 17; Length 15;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 GINLSEPN 15
Db 1 GTNLSEPN 8

RESULT 12
US-10-930-300-93
; Sequence 93, Application US/10930300
; Publication No. US20050014138A1
; GENERAL INFORMATION:
; APPLICANT: Rath, Matthias
; TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL
; OLIGOPEPTIDES
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: INHOUSE IP MANAGEMENT
; STREET: 280 Colorado Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk, 3.50 inch, 1.44MB Storage
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: MS WORD 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/930,300
```

```

; FILING DATE: 30-Aug-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/182,248
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: ALI KAMAREI
; REGISTRATION NUMBER: 37000
; REFERENCE/DOCKET NUMBER: 10262-10US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-322-7371
; TELEFAX: 650-322-7389
; INFORMATION FOR SEQ ID NO: 93:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 93:
US-10-930-300-93
```

```

Query Match          39.2%; Score 29; DB 17; Length 10;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      6 GSGGLNS 12
      |||||
Db      4 GSGGLNS 10
```

```

RESULT 13
US-09-852-910-114
; Sequence 114, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 114
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(13)
; OTHER INFORMATION: G alpha q minigene peptide
US-09-852-910-114
```

```

Query Match          39.2%; Score 29; DB 10; Length 13;
Best Local Similarity 63.6%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      5 MSGGLNLSEPN 15
      |||||
Db      1 MGLQLNLKEYN 11
```

```

RESULT 14
US-09-852-910-115
; Sequence 115, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor
; FILE REFERENCE: 2661-101
```

```

; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 115
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(13)
; OTHER INFORMATION: G alpha q** minigene peptide
US-09-852-910-115
```

```

Query Match          39.2%; Score 29; DB 10; Length 13;
Best Local Similarity 63.6%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      5 MSGGLNLSEPN 15
      |||||
Db      1 MGLQLNLKEYN 11
```

```

RESULT 15
US-10-283-423-124
; Sequence 124, Application US/10283423
; Publication No. US2003016223A1
; GENERAL INFORMATION:
; APPLICANT: Lowery, David E.
; APPLICANT: Smith, Valdin G.
; APPLICANT: Kubiak, Teresa M.
; APPLICANT: Larsen, Martha J.
; TITLE OF INVENTION: Drosophila G Protein Coupled Receptors, Nucleic Acids, And Metho
; FILE REFERENCE: PHRM0002-102
; Application Project
; -----
; CURRENT APPLICATION NUMBER: US/10/283,423
; CURRENT FILING DATE: 2002-10-30
; Earlier Applications
; -----
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/693,746
; PRIOR FILING DATE: PriorFilingDate : 2000-10-20
; PRIOR APPLICATION NUMBER: PriorAppNumber : 09/425,676
; PRIOR FILING DATE: PriorFilingDate : 1999-10-22
; NUMBER OF SEQ ID NOS: 187
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. US2003016223A1el Sequence
US-10-283-423-124
```

```

Query Match          39.2%; Score 29; DB 14; Length 13;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      7 SGLNLSEPN 15
      |||||
Db      1 SDIGISEPN 9
```

```

Search completed: November 1, 2005, 14:26:03
Job time : 171 secs
```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 14:01:36 ; Search time 39 Seconds
(without alignments)
37.006 Million cell updates/sec

Title: US-10-612-162a-3

Perfect score: 74

Sequence: 1 SKUSMSGSLNLEPN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 2523

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	32.4	13	2 E47630	Ig kappa chain J r
2	23	31.1	10	2 PT0289	Ig heavy chain CRD
3	23	31.1	14	2 PH0801	T-cell receptor al
4	21	28.4	9	2 A44873	caldesmon - rabbit
5	21	28.4	12	2 D20907	Ig kappa-1 chain J
6	21	28.4	13	2 H33932	Ig kappa chain J r
7	21	28.4	15	2 S21238	hydrogen sulfite re
8	21	28.4	15	2 C36198	T-cell receptor be
9	21	28.4	15	2 A36315	recycling receptor
10	21	28.4	15	2 PH1455	T-cell receptor al
11	20	27.0	10	2 F60589	sperm-activating p
12	20	27.0	10	2 H60588	sperm-activating p
13	20	27.0	12	2 A37933	Ig lambda chain J
14	20	27.0	13	2 B25448	Ig kappa chain J r
15	20	27.0	13	2 D47630	Ig kappa chain J r
16	20	27.0	15	2 S49409	H+-transporting tw
17	20	27.0	15	2 A56049	urinary tract ston
18	19	25.7	12	2 PT0319	Ig heavy chain CRD
19	19	25.7	12	2 PH1183	T-cell receptor al
20	19	25.7	12	2 S29830	dimethylamylamine
21	19	25.7	13	2 PH0445	urotensin II - lau
22	19	25.7	14	2 PH0795	T-cell receptor al
23	19	25.7	15	2 S26527	T-cell receptor al
24	19	25.7	15	2 S43634	cytochrome-c oxida
25	19	25.7	15	2 PH0775	T-cell receptor al
26	18	24.3	5	2 D44823	synaptoosomal-assoc
27	18	24.3	7	2 PT0579	T-cell receptor be
28	18	24.3	9	2 S70345	amine oxidase (cop
29	18	24.3	10	2 A47364	placental lactogen

30	18	24.3	10	2 E60787	sperm-activating p
31	18	24.3	10	2 C60588	sperm-activating p
32	18	24.3	10	2 E60527	sperm-activating p
33	18	24.3	12	2 A20907	Ig kappa chain J1
34	18	24.3	12	2 F20907	Ig kappa-2 chain J
35	18	24.3	12	2 E58502	43.2K bile stone p
36	18	24.3	13	2 PH0783	T-cell receptor al
37	18	24.3	13	2 S03879	6-phosphofructokin
38	18	24.3	14	2 B29743	translation initia
39	18	24.3	14	2 PH0776	T-cell receptor al
40	18	24.3	14	2 B56819	PS I complex subun
41	18	24.3	15	2 PH0784	T-cell receptor al
42	18	24.3	15	2 PH0751	T-cell receptor be
43	18	24.3	15	2 S05699	insulin-like growt
44	18	24.3	15	2 G24417	interphotoreceptor
45	17	23.0	6	2 A44916	mosquitocidal toxi

ALIGNMENTS

```

RESULT 1
E47630
Ig kappa chain J region J4 - southeastern Australian rat
C/Species: Rattus sordidus villosissimus (southeastern Australian rat)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Nov-1999
C/Accession: E47630
R/Gutman, G.A.; Beeta, R.M.; Frank, M.B.; Baverstock, P.R.
Immunogenetics 26, 14-20, 1987
J>Title: Duplication of J-kappa genes within genus Rattus.
A/Reference number: A47630; MUID:87278355; PMID:3111993
A/Accession: E47630
A/Status: preliminary; not compared with conceptual translation
A/Residues: 1-13 <GUT>
A/Molecule type: DNA
A/Keywords: heterotrimer; immunoglobulin

Query Match
Best Local Similarity 32.4%; Score 24; DB 2; Length 13;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 LSMGSLN 11
DB 1 LTFGSGTKL 9

RESULT 2
PT0289
Ig heavy chain CRD3 region (clone 4-109) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0289
R/Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A/Reference number: PT0222; MUID:91108337; PMID:1899102
A/Accession: PT0289
A/Molecule type: DNA
A/Residues: 1-10 <YAM>
A/Experimental source: B lymphocyte
C/Keywords: heterotrimer; immunoglobulin

Query Match
Best Local Similarity 31.1%; Score 23; DB 2; Length 10;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LSMGSG 8
DB 5 LSMGG 10

RESULT 3

```

PH0801
T-cell receptor alpha chain (J5) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C:Accession: PH0801
R:Caanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-T
allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; PMID:92078846; PMID:1636010
A:Accession: PH0801
A:Molecule type: mRNA
A:Residues: 1-14 <CAS>
A:Cross-references: EMBL:X60909
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 31.1%; Score 23; DB 2; Length 14;
Best Local Similarity 83.3%; Pred. No. 7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 1 SKLSWG 6
Db 9 SKLSFG 14

RESULT 4
A44873
caldesmon - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A44873
R:Rebe, M.; Hornick, T.
Arch. Biochem. Biophys. 288, 538-542, 1991
A:Title: Determination of the phosphorylation sites of smooth muscle caldesmon by protei
A:Reference number: A44873; PMID:91378498; PMID:1898046
A:Accession: A44873
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <IKE>
A:Cross-references: UNIPROT:Q9TRW2
A:Experimental source: skeletal myosin
A:Note: sequence extracted from NCBI Backbone (NCBI:63199)
C:Superfamily: caldesmon

Query Match 28.4%; Score 21; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 6 GSGNLSE 13
Db 1 GSSLKIEE 8

RESULT 5
D20907
I9 kappa-1 chain J4 segment (b95 allele) - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 05-Nov-1999
C:Accession: D20907; D53275
R:Emorine, L.; Max, E.E.
Nucleic Acids Res. 11, 8877-8890, 1983
A:Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multipl
A:Reference number: A20907; PMID:84169523; PMID:6324107
A:Accession: D20907
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <EMO>
A:Cross-references: GB:X00231; NID:G1577; PIDN:CAA25049.1; PID:e8275; PID:G1364234
R:Avadl, H.; Marche, P.N.; Cazenave, P.A.
Immunogenetics 34, 201-207, 1991
A:Title: Evolution of the rabbit immunoglobulin kappa chain genes.
A:Reference number: A53275; PMID:91372868; PMID:190995

A:Accession: D53275
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-12 <ATA>
A:Note: sequence extracted from NCBI backbone (NCBI:56069, NCBI:56166)
C:Comment: This J4 segment may not be functional because of a short space between the 7
C:Keywords: heterotetramer; immunoglobulin

Query Match 28.4%; Score 21; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 3 LSMGSG 8
Db 1 LTFSGG 6

RESULT 6
H33932
I9 kappa chain J region (D23) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C:Accession: H33932
R:Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A:Title: Two murine natural polyclonal antibodies are encoded by nonmutated germ-1
A:Reference number: A33932; PMID:69282823; PMID:2499887
A:Accession: H33932
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-13 <BAC>
A:Cross-references: UNIPROT:Q8K1F2; UNIPROT:Q8R028
C:Keywords: heterotetramer; immunoglobulin

Query Match 28.4%; Score 21; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 3 LSMGGLNL 11
Db 1 LTFGAGTKL 9

RESULT 7
S21238
hydrogensulfite reductase (BC 1.8.99.3) beta chain - Desulfovibrio vulgaris (fragment)
N:Alternate names: bsulfite reductase; desulfotubidin; desulfotubidin; desulfovibridin;
C:Species: Desulfovibrio vulgaris
C:Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C:Accession: S21238
R:Pierik, A.J.; Duyvis, M.G.; van Helvoort, J.M.L.M.; Wolbert, R.B.G.; Hagen, W.R.
Eur. J. Biochem. 205, 111-115, 1992
A:Title: The third subunit of desulfovibridin-type dissimilatory sulfite reductases.
A:Reference number: S21197; PMID:92209491; PMID:1555572
A:Accession: S21238
A:Molecule type: protein
A:Residues: 1-15 <PIE>
A:Experimental source: strain Hildenborough
C:Genetics:
A:Gene: dsyB
C:Complex: heterohexamer; two alpha, two beta and two gamma chains
C:Function:
A:Description: catalyzes the six-electron reduction of sulfite to sulfide
A:Pathway: the terminal oxidase in the sulfate-reduction pathway
C:Keywords: heterohexamer; oxidoreductase

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Oy 5 MGSGNLSEP 14
Db 3 ISSGVNPKP 12

RESULT 8

C36198
T-cell receptor beta chain J region - chicken (fragment)
C/Species: Gallus gallus (chicken)
C/Date: 26-Mar-1991 #sequence_rev1sion 26-Mar-1991 #text_change 21-Jul-2000
C/Accession: C36198
R/Toolset: L.W.; Carlson, L.M.; Lee, K.; Lahti, J.; McCormack, W.T.; Leiden, J.M.; Chen
Proc. Natl. Acad. Sci. U.S.A. 87, 7856-7860, 1990
A/Title: Evolutionary conservation of antigen recognition: the chicken T-cell receptor B
A/Reference number: A36198; PMID:91045896; PMID:2236002
A/Accession: C36198
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-15 <TIO>
A/Cross-references: EMBL:M37799; NID:9212737; PIDN:AAA62754.1; PID:9555475
C/Keywords: T-cell receptor

Query Match

Best Local Similarity 28.4%; Score 21; DB 2; Length 15;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 LSMGSGTLLS 12
| | | | |
DB 4 LNRGQCTRLT 13

RESULT 9

A36315
recycling receptor p180 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 25-Jan-1991 #sequence_rev1sion 25-Jan-1991 #text_change 30-Sep-1993
C/Accession: A36315
R/Isaac: C.M.; van der Geer, P.; Hunter, T.; Trowbridge, I.S.
Mol. Cell. Biol. 10, 2606-2618, 1990
A/Title: p180, a novel recycling transmembrane glycoprotein with restricted cell type ex
A/Reference number: A36315; PMID:90288846; PMID:2188094
A/Accession: A36315
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-15 <ISA>

Query Match

Best Local Similarity 28.4%; Score 21; DB 2; Length 15;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 LSEPN 15
| | | | |
DB 7 LPEPN 11

RESULT 10

PH1455
T-cell receptor alpha chain (clone A24/PEF4) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 10-Mar-1994 #sequence_rev1sion 10-Mar-1994 #text_change 15-Mar-2004
C/Accession: PH1455
R/Casanova, J.L.; Martinou, F.; Gournier, H.; Barra, C.; Panetier, C.; Regnault, A.; Ko
J. Exp. Med. 177, 811-820, 1993
A/Title: T cell receptor selection by and recognition of two class I major histocompatib
A/Reference number: PH1430; PMID:93171821; PMID:8436911
A/Accession: PH1455
A/Molecule type: mRNA
A/Residues: 1-15 <CAS>
A/Experimental source: cytolytic T-lymphocyte
C/Keywords: receptor; T-cell

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.8e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 LSMGSGT 9

DB 3 LSMGSGT 9
| | | | |

RESULT 11

F60589
sperm-activating peptide (Asn-3, Ser-5 SAP-I) - Echinosmetra mathaei (type A)
C/Species: Echinosmetra mathaei
C/Date: 17-Apr-1993 #sequence_rev1sion 17-Apr-1993 #text_change 16-Aug-2004
C/Accession: F60589
R/Yoshino, K.I.; Kajitani, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamagu
Comp. Biochem. Physiol. B 94, 739-751, 1989
A/Title: A halogenated amino acid-containing sperm activating peptide and its related p
otus nudus, Echinosmetra mathaei and Heterocentrotus mammillatus.
A/Reference number: A60527
A/Accession: F60589
A/Molecule type: protein
A/Residues: 1-10 <YOS>
A/Cross-references: UNIPROT:Q7M4C5

Query Match

Best Local Similarity 27.0%; Score 20; DB 2; Length 10;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 GLNTLS 12
| | | | |
DB 1 GPNLS 5

RESULT 12

H60588
sperm-activating peptide (Thr-2,5, Leu-3, Pro-4, Ser-7,10 SAP-I) - slate-pencil urchin
C/Species: Heterocentrotus mammillatus
C/Date: 17-Apr-1993 #sequence_rev1sion 17-Apr-1993 #text_change 16-Aug-2004
C/Accession: H60588
R/Yoshino, K.I.; Kajitani, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamagu
Comp. Biochem. Physiol. B 94, 739-751, 1989
A/Title: A halogenated amino acid-containing sperm activating peptide and its related p
otus nudus, Echinosmetra mathaei and Heterocentrotus mammillatus.
A/Reference number: A60527
A/Accession: H60588
A/Molecule type: protein
A/Residues: 1-10 <YOS>
A/Cross-references: UNIPROT:Q7M4B8

Query Match

Best Local Similarity 27.0%; Score 20; DB 2; Length 10;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 LSMGSGT 10
| | | | |
DB 3 LPTGSGVS 10

RESULT 13

A37933
Ig lambda chain J region - sheep (fragment)
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 26-Jul-1991 #sequence_rev1sion 26-Jul-1991 #text_change 05-Nov-1999
C/Accession: A37933
R/Reynaud, C.A.; Mackay, C.R.; Mueller, R.G.; Wells, J.C.
Cell 64, 995-1005, 1991
A/Title: Somatic generation of diversity in a mammalian primary lymphoid organ: the shee
A/Reference number: A37933; PMID:91160063; PMID:1900459
A/Accession: A37933
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-12 <REV>
A/Cross-references: GB:M60440; NID:9165946; PIDN:AAA31550.1; PID:9552425
C/Keywords: heterotrimer; Immunoglobulin

Query Match 27.0%; Score 20; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 6 GSGGLNLS 12
: ||| :
Db 4 GSGTRLT 10

RESULT 14

B25448
I;Kappa-1 chain, 69 allotype, J-K1.1 segment - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
C;Accession: B25448
R;Arkmenko, M.A.; Mariame, B.; Rougeon, F.
Proc. Natl. Acad. Sci. U.S.A. 83, 5180-5183, 1986
A;Title: Evolution of the immunoglobulin kappa light chain locus in the rabbit: evidence
A;Reference number: A94110; MUID:86259753; PMID:3088570
A;Accession: B25448
A;Molecule type: DNA
A;Residues: 1-13 <AK1>
A;Cross-references: GB:M14067; GB:M14062; GB:M14063; GB:M14064; GB:M14065; GB:M14066; NT
C;Keywords: heterotetramer; immunoglobulin

Query Match 27.0%; Score 20; DB 2; Length 13;
Best Local Similarity 37.5%; Pred. No. 2.3e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 SMGSGNL 11
: ||| :
Db 2 AFGAGTNV 9

RESULT 15

D47630
I;Kappa chain J region J3 - southeastern Australian rat
C;Species: Rattus norvegicus villosissimus (southeastern Australian rat)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Nov-1999
C;Accession: D47630
R;Gutman, G.A.; Beeta, R.M.; Frank, M.B.; Baverstock, P.R.
Immunogenetics 26, 14-20, 1987
A;Title: Duplication of J-kappa genes within genus Rattus.
A;Reference number: A47630; MUID:87278355; PMID:3111993
A;Accession: D47630
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-13 <GUT>
A;Cross-references: GB:M17319; NID:9204788; PIDN:AAA41400.1; PID:9204792
C;Keywords: heterotetramer; immunoglobulin

Query Match 27.0%; Score 20; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 SMGSGNL 11
: ||| :
Db 2 TFGSCTL 9

Search completed: November 1, 2005, 14:12:30
Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 13:52:29 ; Search time 172 Seconds
(without alignments)
44.658 Million cell updates/sec

Title: US-10-612-162A-3
Perfect score: 74
Sequence: 1 SKLMSGSGUNLSEPN 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 6622

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	39.2	13	1	P43173 ascaris suu
2	26	35.1	11	2	Q80B26 hepatic b
3	24	32.4	13	1	P82064 limodynaet
4	24	32.4	13	2	Q8JUG5 asbha goss
5	23	31.1	8	2	P83531 lactobacill
6	22	29.7	10	1	P80699 bacillus su
7	22	29.7	11	2	Q77913 oreochromis
8	22	29.7	13	2	Q6R272 lactococcus
9	22	29.7	14	2	Q73591 gallus gall
10	21	28.4	9	2	Q9TRW2 oryctolagus
11	21	28.4	14	2	Q7SAV2 neurospora
12	21	28.4	14	2	Q9QVM9 rattus sp.
13	21	28.4	15	2	Q65177 mesembryant
14	20	27.0	10	1	DY82 LIMDU
15	20	27.0	10	2	Q7M4B8 heterocent
16	20	27.0	11	2	Q7M4C5 echinometra
17	20	27.0	11	2	Q16217 homo sapien
18	20	27.0	11	2	Q7RH33 plasmodium
19	20	27.0	11	2	Q6LA95 rattus norv
20	20	27.0	11	2	Q9Z1H5 mus musculu
21	20	27.0	13	2	Q7BD41 streptococ
22	20	27.0	14	2	Q78023 neurospora
23	20	27.0	15	1	FIBA_SYNCA
24	20	27.0	15	2	Q78362 neurospora
25	20	27.0	15	2	Q9UC83 homo sapien
26	20	27.0	15	2	Q9TMB6 tritaneutes
27	20	27.0	15	2	Q798U8 streptococ
28	20	27.0	15	2	Q84332 simian viru
29	19.5	26.4	13	2	Q13377
30	19.5	26.4	15	1	GTER_PSEUD
31	19	25.7	8	1	P41872 panagrellus

32	19	25.7	8	2	Q83349	Q83349 murine hepa
33	19	25.7	9	2	Q78E72	Q78E72 rattus norv
34	19	25.7	10	2	Q9UJ48	Q9UJ48 homo sapien
35	19	25.7	12	2	Q7M2Q0	Q7M2Q0 macaca fasc
36	19	25.7	14	1	TEMB_RANLU	P82831 rana luteiv
37	19	25.7	14	2	Q50845	Q50845 methanococ
38	19	25.7	14	2	Q95179	Q95179 homo sapien
39	19	25.7	14	2	P82326	P82326 pibum saliv
40	19	25.7	14	2	Q61864	Q61864 mus musculu
41	19	25.7	15	2	Q86WB2	Q86WB2 homo sapien
42	19	25.7	15	2	Q9WTA3	Q9WTA3 amoropholal
43	19	25.0	15	2	Q8USK4	Q8USK4 human immun
44	18.5	25.0	15	2	Q9GV76	Q9GV76 mus sp. . P
45	18	24.3	8	1	DY81_LIMIN	P82079 limodynaet

ALIGNMENTS

RESULT 1
FARB_ASCSU STANDARD; PRT; 13 AA.
AC P43173;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-UTL-2004 (Rel. 44, Last annotation update)
DE FMRFamide-like neuropeptide Af11.
OS Ascaris suum (pig roundworm) (Ascaris lumbricoidea).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RP SEQUENCE.
RX MEDLINE=95380362; PubMed=7651904; DOI=10.1016/0196-9781(94)00211-N;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARB (FMRFamide related peptide)
family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 13 13 Phenylalanine amide.
SQ SEQUENCE 13 AA; 1495 MM; 9CAEC650D6886B05 CRC64;
Query Match 39.2%; Score 29; DB 1; Length 13;
Best Local Similarity 55.6%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 7 SGLNLSEPN 15
Db 1 SDIGISEPN 9
RESULT 2
Q80B26 PRELIMINARY; PRT; 11 AA.
ID Q80B26;
AC Q80B26;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Pre-S1 protein (Fragment).
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95011308; PubMed=7926515;
RA Chen C.H., Chen P.J., Chu J.S., Yeh K.H., Lai M.Y., Chen D.S.;
RT "Ribosving cholestastic hepatitis in a hepatitis B surface antigen
carrier after renal transplantation.";
RL Gastroenterology 107:1514-1518(1994).
DR EMBL; S74182; AAP21092.1; -.

```

FT  NON TER      11      11
SQ  SEQUENCE     11 AA; 1161 MW; 1535A06CA1B5B724 CRC64;

Query Match
Best Local Similarity 35.1%; Score 26; DB 2; Length 11;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY  5 MSGSGLNSEP 14
    |||:|:|
    1 MGNLSTSNP 10

RESULT 3
FLET LIMFT      STANDARD;      PRT;      13 AA.
AC  P82064;
DT  29-MAR-2004 (Rel. 43, Created)
DT  29-MAR-2004 (Rel. 43, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Fletcherin.
OS  Limnodynastes fletcheri (Barking marsh frog).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
OC  Limnodynastidae; Limnodynastes.
OX  NCBI_TaxID=39403;
RN  [1]
RP  SEQUENCE, AND MASS SPECTROMETRY.
RC  TISSUE=Skin secretion.
RA  Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT  "Peptides from Australian frogs. The structure of the dynastins from
RT  Limnodynastes salmali and fletcheri from Limnodynastes fletcheri.";
RL  Aust. J. Chem. 46:1235-1244(1993).
CC  -I- SUBCELLULAR LOCATION: Secreted.
CC  -I- TISSUE SPECIFICITY: Secreted by the skin dorsal glands.
CC  -I- MASS SPECTROMETRY: MW=1197; METHOD=PM; RANGE=4-13; NOTE=Ref.1.
KW  Direct protein sequencing.
SQ  SEQUENCE 13 AA; 1197 MW; 56B5B1FAEA7C723 CRC64;

Query Match
Best Local Similarity 32.4%; Score 24; DB 1; Length 13;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY  1 SKLSMSGSL 9
    |||:|:|
    5 SKLVSGIGL 13

RESULT 4
O8JIG5      PRELIMINARY;      PRT;      14 AA.
AC  O8JIG5;
DT  01-MAR-2003 (TREMBlrel. 23, Created)
DT  01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT  01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE  YLR191 (Fragment).
GN  Name=YLR191;
OS  Asbya gossypii (Yeast) (Eremothecium gossypii).
OC  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC  Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX  NCBI_TaxID=33169;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Alberti-Segui C., Dietrich F., Philippen P.;
RL  Submitted (May-2001) to the EMBL/Genbank/DBJ databases.
DR  EMBL; AF378569; AAN87136.1; -.
FT  NON TER      1
SQ  SEQUENCE 14 AA; 1205 MW; 36967F5A00467868 CRC64;

Query Match
Best Local Similarity 32.4%; Score 24; DB 2; Length 14;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY  4 SMGSGLNISE 13

```

```

DB  1 SAGSGTGPSE 10
    |||:|:|

RESULT 5
P83531      PRELIMINARY;      PRT;      8 AA.
AC  P83531;
DT  01-JUN-2003 (TREMBlrel. 24, Created)
DT  01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT  01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE  Unknown protein from 2D-page (Fragment).
OS  Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).
OC  Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC  Lactobacillus.
OX  NCBI_TaxID=1625;
RN  [1]
RP  SEQUENCE.
RC  STRAIN=DSM 20451;
RX  PubMed=12112860;
RX  DOI=10.1002/1615-9861(200206)2:6<765::AID-PROT765>3.0.CO;2-V;
RA  Draws O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;
RT  "High pressure effects step-wise altered protein expression in
RT  Lactobacillus sanfranciscensis.";
RL  Proteomics 2:765-774(2002).
CC  -I- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
CC  protein is: 15 kDa.
FT  NON TER      1
FT  NON TER      8
SQ  SEQUENCE 8 AA; 677 MW; C835B87865B87735 CRC64;

Query Match
Best Local Similarity 31.1%; Score 23; DB 2; Length 8;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY  4 SMGSGLNISE 11
    |||:|:|
    1 SLGSGSL 8

RESULT 6
VEG6_BACSU      STANDARD;      PRT;      10 AA.
AC  P80699;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  05-JUL-2004 (Rel. 44, Last annotation update)
DE  Vegetative protein 6 (VEG6) (Fragment).
OS  Bacillus subtilis.
OC  Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX  NCBI_TaxID=1423;
RN  [1]
RP  SEQUENCE.
RC  STRAIN=168 / 1S58;
RX  MEDLINE=97237728; PubMed=9084183;
RA  Schmid R., Bernhardt J., Antelmann H., Voelker U., Mach H.,
RA  Voelker A., Hecker M.;
RT  "Identification of vegetative proteins for a two-dimensional protein
RT  index of Bacillus subtilis.";
RL  Microbiology 143:991-998(1997).
CC  -I- CAUTION: Could not be found in the genome of B.subtilis 168.
KW  Direct protein sequencing.
FT  NON TER      10
FT  NON TER      10
SQ  SEQUENCE 10 AA; 973 MW; 8793A6B2C8772861 CRC64;

Query Match
Best Local Similarity 29.7%; Score 22; DB 1; Length 10;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY  5 MSGSGLNSE 13
    |||:|:|
    1 LGTGLVDQ 9

```

```

RESULT 7
077913 PRELIMINARY; PRT; 11 AA.
AC 077913;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
MHC class II B locus 4 (Fragment).
OC Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
NCBI_TaxID=8128;
OX NCBI
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
RA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among cichlid MHC
RT class II B loci."
RL Genetics 149:1527-1537(1998).
DR EMBL; AF050024; AAC4363.1; -.
FT NON_TER 1 1
FT SEQUENCE 11 AA; 1181 MW; 723258737EASB72B CRC64;

Query Match
Best Local Similarity 29.7%; Score 22; DB 2; Length 11;
Pred. No. 5.1e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SKLSMCS 7
DB 3 SELSCGS 9

RESULT 8
06R272 PRELIMINARY; PRT; 13 AA.
AC 06R272;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Arca (Fragment).
GN Name=arca;
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MG1363;
RA Pubmed=14762010; DOI=10.1128/JB.186.4.1147-1157.2004;
RA Larsen R., Bulst G., Kuipers O.P., Kok J.;
RT "ArgR and ArgC are both required for regulation of arginine metabolism
RT in Lactococcus lactis."
RL J. Bacteriol. 186:1147-1157(2004).
DR EMBL; AF518515; AAR9646.1; -.
FT NON_TER 13 13
FT SEQUENCE 13 AA; 1390 MW; 0F42B7F1AC8D52C4 CRC64;

Query Match
Best Local Similarity 29.7%; Score 22; DB 2; Length 13;
Pred. No. 6.2e+03;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 MSGGLNLS 12
DB 1 MNINGINVN 8

RESULT 9
073591 PRELIMINARY; PRT; 14 AA.
ID 073591

```

```

AC 073591;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hox C10 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phaethidae; Phaethinae;
OC Gallus.
NCBI_TaxID=9031;
OX NCBI
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=White Leghorn;
RA MEDLINE=98141813; PubMed=9473273; DOI=10.1006/abio.1997.2500;
RA Reale F.V. Jr., Mason K., Hunter A.W., Bothwell M.;
RT "Multiplex display polymerase chain reaction amplifies and resolves
RT related sequences sharing a single moderately conserved domain."
RL Anal. Biochem. 256:158-168(1998).
DR EMBL; U34614; AAC36452.1; -.
FT NON_TER 1 1
FT SEQUENCE 14 AA; 1673 MW; 81258FCE81FDA5 CRC64;

Query Match
Best Local Similarity 29.7%; Score 22; DB 2; Length 14;
Pred. No. 6.7e+03;
Matches 3; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 KLSMSGGLNLS 13
DB 1 RLHISKSLTLD 12

RESULT 10
09TRW2 PRELIMINARY; PRT; 9 AA.
AC 09TRW2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE CALDESNON=PHOSPHORYLATION site (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=91378498; PubMed=1898046;
RA Ikebe M., Hornick T.;
RT "Determination of the phosphorylation sites of smooth muscle caldesmon
RT by protein kinase C."
RL Arch. Biochem. Biophys. 288:538-542(1991).
DR PIR; A44873; A44873.
FT NON_TER 1 1
FT SEQUENCE 9 AA; 1018 MW; 8C901B10533735A5 CRC64;

Query Match
Best Local Similarity 28.4%; Score 21; DB 2; Length 9;
Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 GSGGLNLS 13
DB 1 GSSLKIEE 8

RESULT 11
07SAV2 PRELIMINARY; PRT; 14 AA.
ID 07SAV2
AC 07SAV2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.

```

```

GN Name=NCU05682.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCB1_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=0874A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Valte D., Fitzhugh W., Ma L.-U., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Mashburne M.,
RA Seitzemikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Koche G.O., Jedd G., Mewes W., Steben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kanai M., Kamysheva M., Mauceli E., Bielke C., Rudd S., Fishman D.,
RA Kyrstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
RA Desouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Nativig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -! CAUTION: The sequence shown here is derived from an
CC preliminary data.
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000180; EAAJ3560.1; -
SQ SEQUENCE 14 AA; 1354 MW; 90BC62C653BB8CBE CRC64;

Query Match 28.4%; Score 21; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 1e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 MSGSLINSE 13
DB 1 MGLGVGCS 9

RESULT 12
OYQVW9 PRELIMINARY; PRT; 14 AA.
ID 09QVW9
AC 09QVW9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Gila-derived nexin, GDN, protease nexin-1 (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCB1_TaxID=10116;
RN [1]
RP SEQUENCE.
RC MEDLINE=92207980; PubMed=1554734;
RA Rowell G., Stone S.R., Guidolin A., Sommer J., Monard D.;
RT "Characterization of the heparin-binding site of gila-derived
RT nexin/protease nexin-1.";
RL Biochemistry 31:3542-3549(1992).
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 14 AA; 1498 MW; 21ACE79A02590957 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 10 NLSEPN 15
DB 3 NLSPN 8

RESULT 13
O65177

```

```

ID 065177 PRELIMINARY; PRT; 15 AA.
AC 065177;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Turgor responsive protein homolog (Fragment).
OS Mesembryanthemum crystallinum (Common ice plant).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Alzooceae; Mesembryanthemum.
OX NCB1_TaxID=3544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root;
RA Michalowski C.B., Bohnert H.J.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF054444; AAC14178.1; -.
FT NON_TER 1
SQ SEQUENCE 15 AA; 1607 MW; 4137ED0DF9B3FC21 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 15;
Best Local Similarity 30.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 SKLSMSGSLN 10
DB 4 NELPLAQGIN 13

RESULT 14
DYS2 LIMDU STANDARD; PRT; 10 AA.
ID DYS2 LIMDU
AC P82080;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUN-2004 (Rel. 44, Last annotation update)
DE Dynastin 2.
OS Limodysnaetes dumerilii (Eastern banjo frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Myobatrachidae;
OC Limnodynastinae; Limnodynastes.
OX NCB1_TaxID=104065;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Tibial gland;
RA Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT "Peptides from Australian frogs. The structure of the dynastin from
RT the banjo frogs Limodysnaetes interiorae, Limodysnaetes dumerilii and
RT Limodysnaetes terraereginae.";
RL Aust. J. Chem. 46:833-842(1993).
CC -! SUBCELLULAR LOCATION: Secreted.
CC -! TISSUE SPECIFICITY: Skin.
CC -! MASS SPECTROMETRY: MW=986; METHOD=FAB; RANGE=1-10; NOTE=Ref. 1.
KW Direct protein sequencing.
SQ SEQUENCE 10 AA; 986 MW; 550FDC287735A5B7 CRC64;

Query Match 27.0%; Score 20; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 GLNL 11
DB 7 GLNL 10

RESULT 15
O7M4B8 PRELIMINARY; PRT; 10 AA.
ID O7M4B8
AC O7M4B8;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Sperm-activating peptide (Thr-2,5, Leu-3, Pro-4, Ser-7,10 SAP-I).

```

OS Heterocentrotus mammillatus (Slate-pencil urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinodermata; Echinodermata; Echinodermata;
 OC Heterocentrotus.
 OK NCBI_TaxID=31180;
 RN (1)
 RP SEQUENCE.
 RA Yoshino K.I., Kajitani H., Nomura K., Takao T., Shimonishi Y.,
 RA Kurita M., Yamaguchi M., Suzuki N.;
 RT "A halogenated amino acid-containing sperm activating peptide and its
 RT related peptides isolated from the egg jelly of sea urchins,
 RT Tripteneutes gracillia, Pseudobolita maculata, Strongylocentrotus
 RT nudus, Echinometra mathaei and Heterocentrotus mammillatus.";
 RL Comp. Biochem. Physiol. 94:739-751(1989).
 DR PIR: H60588; H60588;
 SQ SEQUENCE 10 AA; 875 MW; 59F15365B861B767 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 3 LSMGSGLN 10
 | | | | |
 Db 3 LPTGSGVS 10

Search completed: November 1, 2005, 14:09:02
 Job time : 183 secs

THIS PAGE BLANK (USPTO)

CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcoholic. The antibodies allow direct detection of CDT in solution,
CC eliminating the need for immobilising it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
CC fragments used in the method of the invention.

XX Sequence 13 AA;

Query March 100.0%; Score 68; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00038; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

QY 1 YEKYLGESEYVAV 13
| | | | | | | | | | | | | |
Db 1 YEKYLGESEYVAV 13

RESULT 2
ABP72836
ID ABP72836 standard; peptide; 49 AA.

XX AC ABP72836;

DT 11-AUG-2003 (first entry)

XX Human transferrin peptide insertion region.

XX Transferrin; neuroprotective; cerebroprotective; vasotropic;
XX antiparkinsonian; nootropic; anti-HIV; antileukemic; antiallergic;
XX cytostatic; immunosuppressive; antithrombotic; cardiac;
XX gynaecological; immunostimulant; antineoplastic; haemostatic;
XX antinflammatory; dermatological; antibacterial; virucide; antiparasitic;
XX fungicide; hepatotropic; antihypertensive; antidiabetic; antipruritic;
XX transglutinin; vulnery; antidiabetic; nephroprotective; antipruritic;
XX gastrointestinal; gene therapy; transgenic animal.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Modified-site 1..3 /note= "Asn is N-glycosylated"

FT Misc-difference 15..16 /note= "peptide insertion site"

FT W02003020746-A1.

XX PN 13-MAR-2003.

XX PD 30-AUG-2002; 2002MO-US027637.

XX PR 30-AUG-2001; 2001US-0315745P.

XX PR 30-NOV-2001; 2001US-0334059P.

XX PA (BIOR-) BIOREXIS PHARM CORP.

XX PI Prior CP;

XX WPI; 2003-332916/31.

XX New fusion protein, useful in the diagnosis and treatment of diseases or
XX disorders relating to the respiratory, cardiovascular and digestive
XX systems, comprises a transferrin protein fused to a therapeutic protein.

XX Example 3; Page 249; 298pp; English.

XX The present sequence is a portion of the human transferrin (Tf) C domain,
XX comprising amino acids 611-659 of the Tf sequence given in ABP72820. The
XX invention relates to novel fusion proteins of Tf and a therapeutic
XX protein or peptide. The therapeutic protein or peptide, e.g. an
XX erythropoietin mimetic (see ABP72834), can be fused to the N- or C-
XX terminus of Tf, or inserted into Tf especially between residues Glu-625
XX and Thr-626 of the Tf N domain. Modified Tf fusion proteins of the
XX invention can be used in the diagnosis, prognosis, prevention and/or

CC treatment of diseases and/or disorders of the endocrine, nervous, immune,
CC respiratory, cardiovascular, reproductive and digestive systems, diseases
CC and/or disorders relating to the blood or to cell proliferation,
CC inflammatory conditions and infectious diseases, or to deliver a
CC therapeutic agent to a cell or across the blood-brain barrier

XX Sequence 49 AA;

Query March 100.0%; Score 68; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.0015; Indels 0; Gaps 0;
Matches 13; Conservative 0; Mismatches 0;

QY 1 YEKYLGESEYVAV 13
| | | | | | | | | | | | | |
Db 37 YEKYLGESEYVAV 49

RESULT 3
ADH89394
ID ADH89394 standard; protein; 49 AA.

XX AC ADH89394;

DT 15-APR-2004 (first entry)

XX Human transferrin protein domain SegID38.

XX fusion protein; transferrin protein; glycosylation;
XX antibody variable region; cytostatic; antibacterial; virucide;
XX antiparasitic; immunosuppressive; antileukemic; gene therapy;
XX septic shock; endotoxic shock; cachexia syndrome; bacterial infection;
XX viral infection; parasitic infection; neoplasm; autoimmune disease;
XX arthritis; graft rejection; human.

XX Homo sapiens.

XX US2003226155-A1.

XX PD 04-DEC-2003.

XX PR 10-MAR-2003; 2003US-00384060.

XX PR 30-AUG-2001; 2001US-0315745P.

XX PR 30-NOV-2001; 2001US-0334059P.

XX PR 30-AUG-2002; 2002US-00231494.

XX PR 30-AUG-2002; 2002US-0406977P.

XX PA (BIOR-) BIOREXIS PHARM CORP.

XX PI Sadeghi H, Prior CP, Turner A;

XX WPI; 2004-022093/02.

XX Example 2; SEQ ID NO 38; 82pp; English.

XX This invention relates to a novel fusion protein which comprises a
XX transferrin protein exhibiting reduced glycosylation fused to at least
XX one antibody variable region. The invention may be useful for the
XX development of compounds with cytostatic, antibacterial, virucide,
XX antiparasitic, immunosuppressive or antileukemic activity. In addition,
XX the sequences disclosed may be useful for gene therapy. The fusion
XX protein is useful for preparing a composition for treating a disease or
XX disease symptom in a patient for example septic shock, endotoxic shock,
XX cachexia syndromes associated with bacterial, viral or parasitic
XX infections, neoplasm, autoimmune disease, arthritis or adverse effects
XX associated with treatment for preventing graft rejection. The present
XX sequence is that of a domain of the human transferrin protein which was
XX used in the exemplification of the invention.

```
XX SQ Sequence 49 AA;
XX
XX Query Match 100.0%; Score 68; DB 8; Length 49;
XX Best Local Similarity 100.0%; Pred. No. 0.0015;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEKYLGEERYKAV 13
XX |||||||
XX 37 YEKYLGEERYKAV 49
DB

RESULT 4
ADK15882
ID ADK15882 standard; protein; 49 AA.
XX
XX ADK15882;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Human transferrin (Tf) protein fragment #4.
XX
XX KW fusion protein; transferrin; Tf; beta-interferon; beta-IFN;
XX KW glucosylated peptide; GLP-1; erythropoietin mimetic peptide; EMP1;
XX KW T-20; soluble toxin receptor; epitope tagging; human.
XX
XX OS Homo sapiens.
XX
XX PN US2003221201-A1.
XX
XX PD 27-NOV-2003.
XX
XX PF 04-MAR-2003; 2003US-00378094.
XX
XX PR 30-AUG-2001; 2001US-0315745P.
XX PR 30-NOV-2001; 2001US-0334059P.
XX PR 30-AUG-2002; 2002US-00231494.
XX PR 30-AUG-2002; 2002US-0406977P.
XX
XX PA (BIOREXIS PHARM CORP.
XX
XX PI Prior CP, Lai C, Sadeghi H, Turner A;
XX
XX DR WPI; 2004-010899/01.
XX
XX PT New fusion protein comprising a modified transferrin (Tf) protein fused
XX to a therapeutic protein or peptide, useful for epitope tagging.
XX
XX PS Example 5; SEQ ID NO 16; 70pp; English.
XX
XX CC The invention comprises a fusion protein that contains a modified
XX transferrin (Tf) protein fused to a therapeutic protein/peptide (e.g.
XX beta-interferon - IFN, glucosylated peptide - GLP-1, erythropoietin
XX mimetic peptide - EMP1, T-20 and soluble toxin receptor). The fusion
XX protein of the invention is useful for epitope tagging. The present amino
XX acid sequence represents a fragment of the human Tf protein.
XX
XX SQ Sequence 49 AA;
XX
XX Query Match 100.0%; Score 68; DB 8; Length 49;
XX Best Local Similarity 100.0%; Pred. No. 0.0015;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEKYLGEERYKAV 13
XX |||||||
XX 37 YEKYLGEERYKAV 49
DB

RESULT 5
ADL70756
ID ADL70756 standard; peptide; 49 AA.
XX
XX AC ADL70756;
```

```
XX DT 03-JUN-2004 (first entry)
XX
XX DE Human transferrin, Tf, insertion region SEQ ID 27.
XX
XX KW Immunosuppressive; Haemostatic; Anti-allergic; Antiasthmatic;
XX Dermatological; Anti-inflammatory; Antibacterial; Vasotropic;
XX Nephrotoxic; Neuroprotective; Cytostatic; Cerbroprotective; Vulnerary;
XX Antiparkinsonian; Nootropic; Cardiant; Antianemic; Antithrombotic;
XX Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;
XX Tf; transferrin fusion protein; Tf fusion protein; human.
XX
XX OS Homo sapiens.
XX
XX PN WO2004020588-A2.
XX
XX PD 11-MAR-2004.
XX
XX PF 28-AUG-2003; 2003WO-US026779.
XX
XX PR 30-AUG-2002; 2002US-0406977P.
XX PR 10-MAR-2003; 2003US-00384060.
XX PR 09-JUL-2003; 2003US-0485404P.
XX
XX PA (BIOREXIS PHARM CORP.
XX
XX PI Prior CP, Turner AJ, Sadeghi H;
XX
XX DR WPI; 2004-239175/22.
XX
XX PT Novel library containing several fusion proteins each of which comprises
XX first transferrin polypeptide fused to at least one second peptide,
XX useful for screening for transferrin fusion protein having the particular
XX activity.
XX
XX PS Example 3; SEQ ID NO 27; 243pp; English.
XX
XX CC The present invention relates to a library (1) of modified fusion
XX proteins of transferrin (Tf) and therapeutic proteins with increased
XX serum half-life or serum stability. Preferred fusion proteins include
XX those modified so that the Tf moiety exhibits no or reduced
XX glycosylation, iron binding and/or Tf receptor binding. The transferrin
XX fusion proteins are useful for treating, preventing or ameliorating
XX disorders or diseases of endocrine system, nervous system, immune system,
XX respiratory system, cardiovascular system, diseases and/or disorders
XX relating to cell proliferation, and/or diseases or disorders relating to
XX blood. The modified fusion proteins are useful in diagnosis, prognosis,
XX prevention and/or treatment of autoimmune disorders; diseases and
XX disorders of haematopoietic cells (e.g., leukopenia, neutropenia, anaemia
XX and thrombocytopenia); allergic reactions such as allergic asthma,
XX anaphylaxis, ige-mediated allergic reactions such as asthma, rhinitis and
XX eczema; inflammatory conditions e.g., inflammation associated with
XX infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,
XX nephritis, Crohn's disease, multiple sclerosis, respiratory disorders
XX (asthma and allergy), gastrointestinal disorders (inflammatory bowel
XX disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders
XX (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative
XX disorders such as Parkinson's disease, Alzheimer's disease), etc. The
XX fusion protein is also useful as an adjuvant to enhance antibacterial or
XX antifungal immune responses, antiparasitic immune responses, etc. The
XX fusion protein is also useful for treating monoclonal gammopathy of
XX undetermined significance (MGUS), Waldenstrom's disease, plasmacytomas,
XX adult respiratory distress syndrome, for stimulating wound repair, for
XX preventing or treating infections of joints, bones, skin, etc. The fusion
XX protein is also useful for treating or preventing thrombosis, myocardial
XX infarction, cancers, thrombocytopenia, sickle cell anaemia,
XX glomerulonephritis, cardiac arrest, edema, pulmonary embolism,
XX atherosclerosis, etc. The present sequence is a DNA sequence for a
XX peptide fragment of Tf(611-659) illustrating an insertion site
XX (Glu625/Thr626) for producing the Tf fusion proteins.
XX
XX SQ Sequence 49 AA;
```

Query Match	Similarity	100.0%	Score 68	DB 8	Length 49
Best Local	Similarity	100.0%	Pred. No. 0.0015		
Matches 13	Conservative	0	Mismatches 0	Indels 0	Gaps 0
Qy	1 YEKYLGEYVKAV 13				
Db	37 YEKYLGEYVKAV 49				
RESULT 6					
ID	ADP74798				
XX	ADP74798 standard; protein; 137 AA.				
XX	ADP74798;				
AC					
XX	26-FEB-2004 (first entry)				
XX					
DE					
XX	Human NOVX protein to treat human pathological conditions (SeqID 12).				
KM	human; NOVX; metabolic disorder; diabetes; anorexia; cancer;				
KM	cardiovascular; infectious; neurodegenerative; immune;				
KM	haematopoietic disease; dyslipidaemia; anorectic; virucide; nootropic;				
KM	antiinflammatory; neuroprotective; antilipemic; anabolic; cardiac;				
KM	neurogenesis; wound healing; angiogenesis; chromosome mapping;				
KM	tissue typing; preventive medicine; pharmacogenomic.				
XX					
OS	Homo sapiens.				
PN	WO2003076578-A2.				
XX					
PD	18-SEP-2003.				
XX					
PF	06-MAR-2003; 2003WO-US006794.				
XX					
PR	06-MAR-2002; 2002US-0361974P.				
PR	08-MAR-2002; 2002US-00093463.				
PR	08-MAR-2002; 2002WO-US007288.				
PR	15-MAR-2002; 2002US-0365034P.				
PR	19-MAR-2002; 2002US-0365477P.				
PR	20-MAR-2002; 2002US-0365884P.				
PR	20-MAR-2002; 2002US-0365984P.				
PR	20-MAR-2002; 2002US-0365985P.				
PR	22-MAR-2002; 2002US-0366928P.				
PR	12-APR-2002; 2002US-0372018P.				
PR	12-APR-2002; 2002US-0372022P.				
PR	23-APR-2002; 2002US-0374682P.				
PR	12-JUN-2002; 2002US-0388096P.				
PR	14-JUN-2002; 2002US-0389143P.				
PR	26-JUN-2002; 2002US-0391779P.				
PR	15-AUG-2002; 2002US-0403743P.				
PR	13-SEP-2002; 2002US-0410755P.				
PR	23-SEP-2002; 2002US-0412957P.				
PR	22-OCT-2002; 2002US-0420382P.				
PR	05-MAR-2003; 2003US-00420382.				
XX					
PA	(CURA-) CURAGEN CORP.				
PI	Alsebrook JP, Anderson DW, Boldog FL, Burgess CE, Chaudhuri A;				
PI	Colman SD, Estinger SR, Etenberg S, Gangoli EA, Gerlach VL;				
PI	Gorman L, Guo X, Kekuda R, Li L, MacLachlan T, Malayanar UW;				
PI	Meres PS, Miller CE, Millet I, Padigar M, Paturajan M, Peyman J;				
PI	Qian X, Rastelli L, Rieger DK, Smithson G, Spyrek KA, Stone DJ;				
PI	Sukumaran S, Vermet CAM, Voss EZ, Zhong M;				
XX					
DR	WPI; 2003-697890/66.				
DR	N-PSDB; ADP74797.				
XX					
PT	New isolated NOVX polypeptides and polynucleotides, useful for				
PT	preventing, diagnosing or treating NOVX-associated disorders, e.g.				
PT	osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,				
PT	asthma, or infections.				
XX					
95	Claim 1; SEQ ID NO 12; 282pp; English.				

XX	CC	XX	This invention relates to a novel nucleic acid, and encoded polypeptides
XX	CC	CC	thereof, which have properties related to the stimulation of biochemical
XX	CC	or physiological responses in a cell, tissue, organ or organism.	
XX	CC	Specifically, it refers to the use of biologically active fragments for	
CC	diagnostic and prognostic assays and furthermore in the treatment of		
CC	diverse pathological conditions. The present invention describes novel		
CC	human and murine NOX proteins, as well as methods to modulate their		
CC	expression using antisense oligos, ribozymes and peptide nucleic acids.		
CC	The polypeptides, nucleic acid molecules and antibodies are useful in the		
CC	manufacture of a medicament for treating metabolic disorders, diabetes,		
CC	anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune		
CC	and haematopoietic diseases as well as various dyslipidaemias.		
CC	Accordingly, these molecules have many activities including anorectic,		
CC	virucide, neurotropic, antiinflammatory, neuroprotective, antilipemic,		
CC	anabolic and cardiatic. Furthermore, they are useful in screening assays		
CC	to identify small molecules that modulate or inhibit, for example,		
CC	neogenesis, wound healing and angiogenesis. The nucleic acids are also		
CC	used as in chromosome mapping, tissue typing, preventive medicine and		
CC	pharmacogenomics. This polypeptide is a human NOX protein of the		
CC	invention.		
XX	XX	XX	
SQ	Sequence 137 AA;		
	Query Match	100.0%;	Score 68; DB 7; Length 137;
	Best Local Similarity	100.0%;	Pred. No. 0.0043;
	Matches 13; Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1 YEKYIGERYKAV 13		
Db	105 YEKYIGERYKAV 117		
RESULT 7			
AAAB84371			
ID	AAAB84371 standard; protein; 328 AA.		
XX	AAAB84371;		
XX	22-AUG-2001 (first entry)		
DT			
XX			
DE	Amino acid sequence of a human transferrin.		
XX			
XX	Human; transferrin; autoimmune disease; rheumatoid arthritis;		
KW	hyperproliferative disorder; neoplasm; cardiovascular disorder;		
KW	cardiac arrest; cerebrovascular disorder; cerebral ischemia;		
KW	angiogenesis; nervous system disorder; Alzheimer's disease; infection;		
KW	ocular disorder; corneal infection; wound healing;		
KW	epithelial cell proliferation; aging; organ transplant.		
XX			
OS	Homo sapiens.		
XX			
XX	WO200146254-A1.		
XX	28-JUN-2001.		
PD			
XX	21-DEC-2000; 2000WO-US034769.		
PF			
XX	23-DEC-1999; 99US-0171595P.		
PR			
XX	(HUMA-) HUMAN GENOME SCI INC.		
PA			
XX			
XX	Ruben SM, Shi Y, Choi GH;		
XX			
PI			
DR	WPI, 2001-381910/40.		
XX			
XX	N-PSDB; AAH25190.		
PT	Isolated nucleic acid molecule encoding a human tranferrin protein is		
XX	used in preventing, treating or ameliorating a medical condition.		
PS	Claim 11, Page 286-287; 290pp; English.		
XX			
CC	The present sequence represents human transferrin polypeptide.		

CC Transferrin polypeptides and polynucleotides are used to prevent, treat
CC or ameliorate a medical condition in e.g. humans, mice, rabbits, goats,
CC horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or
CC treated include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
CC ocular disorders e.g. corneal infection. The polypeptides can also be
CC used to aid wound healing and epithelial cell proliferation, to prevent
CC skin aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis. The polypeptides can also be used as a food additive or
CC preservative to increase or decrease storage capabilities

SQ Sequence 328 AA;

Query Match 100.0%; Score 68; DB 4; Length 328;

Best Local Similarity 100.0%; Pred. No. 0.01; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEYVKAV 13
| | | | | | | | | | | | | | |
DB 296 YEKYLGEYVKAV 308

RESULT 8

AAU02980 AAU02980 standard; protein; 539 AA.

AC AAU02980;

DT 12-SEP-2001 (first entry)

DE Angiotensin converting enzyme (ACEV) splice variant protein #80.

XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C;
KW vasorelaxant intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW noncardiotoxic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; asbestosis.

OS Homo sapiens.

PN WO200136632-A2.

PD 25-MAY-2001.

PF 17-NOV-2000; 2000WO-IL000766.

PR 17-NOV-1999; 99IL-00132978.

PR 10-DEC-1999; 99IL-00133455.

PA (COMP-) COMPUGEN LTD.

PI Levine Z, David A, Azar I, Khosravi R, Bernstein U;

DR WPI; 2001-336004/35.

DR N-PSDB; AAS06080.

PT Novel alternative splicing variants e.g. variant of angiotensin
PT converting enzyme (ACEV), useful in identifying candidate compounds
PT capable of binding to the variant and to detect anti-variant antibodies.

PS Claim 4; Fig 80; 519pp; English.

CC The sequence represents an angiotensin converting enzyme splice variant
CC (ACEV) polypeptide. The polypeptides of the invention include variants of

CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
CC inhibitor 1C, cellular tumour antigen P53, and vasorelaxant intestinal
CC polypeptide receptor 2. The polypeptides and their associated nucleic
CC acids are useful for identification of variant sequences and detection of
CC candidate compounds capable of binding the molecules. The sequences of
CC the invention can be used in the treatment and diagnosis of various
CC disorders including cardiovascular diseases such as arteriosclerosis,
CC myocardial infarction and coronary arterial thrombosis, renal diseases
CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
CC immune disorders such as immune complex nephritis, multiple sclerosis,
CC cancer, sarcoidosis, noncardiotoxic pulmonary granulomatous diseases such
CC as asbestosis and vascular pathologies involving an endothelial
CC abnormality such as deep vein thrombosis

SQ Sequence 539 AA;

Query Match 100.0%; Score 68; DB 4; Length 539;

Best Local Similarity 100.0%; Pred. No. 0.017; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEYVKAV 13
| | | | | | | | | | | | | | |
DB 507 YEKYLGEYVKAV 519

RESULT 9

ABR82321 ABR82321 standard; protein; 575 AA.

AC ABR82321;

DT 06-NOV-2003 (first entry)

DE Human metalloprotein (MEPR) polypeptide (Id-7509328CD1).

XX MEPR; metalloprotein; anti-HIV; anti-allergic; anti-inflammatory; human;
KW antianemic; antiparkinsonian; nootropic; anticonvulsant; cytostatic;
KW antiatherosclerotic; antiaesthetic; immunosuppressive; antichytoid;
KW hepatotropic; dermatological; antidiabetic; nephrotoxic; antigout;
KW thymostimetic; neuroprotective; osteopathic; antiarthritic; uteropathic;
KW antiparasitic; antihelminthic; antiparasitic; ophthalmological; virucide;
KW antitumoric; haemostatic; antibacterial; protozoacide; fungicide;
KW gene therapy; transgenic.

OS Homo sapiens.

PN WO2003060089-A2.

PD 24-JUL-2003.

PF 14-JAN-2003; 2003WO-US001485.

PR 14-JAN-2002; 2002US-0348769P.

PR 18-JAN-2002; 2002US-0350701P.

PR 19-MAR-2002; 2002US-0366059P.

PR 10-MAY-2002; 2002US-0379907P.

PA (INCY-) INCYTE GENOMICS INC.

PI Kable AE, Griffin JA, Gorrad AE, Becha SD, Richardson TW;

DR Emerling BW, Chien D, Jin P, Chawla NK, Yue H, Khare R, Marquis JP;

DR Tang YT;

DR WPI; 2003-598523/56.

DR N-PSDB; ACP35812.

PT New human metalloproteins and polynucleotides, useful for diagnosing,
PT treating or preventing autoimmune or inflammatory disorders (e.g. AIDS,
PT allergy or anemia), multiple sclerosis, osteoarthritis, cancer or
PT hepatitis.

PS Claim 1; Page 146-148; 153pp; English.

XX The invention relates to novel human metalloproteins (MEPR) and encoding
CC polynucleotides. The human MEPR polypeptides, polynucleotides and
CC modulators are useful for diagnosing, treating or preventing disorders
CC associated with aberrant expression of MEPR, particularly cell
CC proliferative disorders (e.g. arteriosclerosis, atherosclerosis,
CC cirrhosis, hepatitis, paroxysmal nocturnal hemoglobinuria, polycythemia
CC vera, psoriasis, primary thrombocytopenia or cancer), developmental
CC disorders (e.g. renal tubular acidosis, anemia or mental retardation),
CC neurological disorders (e.g. Alzheimer's disease, Parkinson's disease or
CC epilepsy), autoimmune/inflammatory disorders (e.g. AIDS, allergies,
CC asthma, autoimmune thyroiditis, contact dermatitis, Crohn's disease,
CC diabetes mellitus, glomerulonephritis, Goodpasture's syndrome, gout,
CC Graves' disease, Hashimoto's thyroiditis, irritable bowel syndrome,
CC multiple sclerosis, osteoarthritis, osteoporosis, pancreatitis, Reiter's
CC syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis), or viral,
CC bacterial, fungal, parasitic, protozoan or helminthic infections. The
CC polynucleotides encoding MEPR are useful for creating transgenic animals
CC to model human disease. Sequences ABR82316-323 represent the human MEPR
CC polypeptides of the invention
XX

SO Sequence 575 AA;

Query Match 100.0%; Score 68; DB 6; Length 575;
Best Local Similarity 100.0%; Pred. No. 0.018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVAV 13
|||||
Db 543 YEKYLGEYVAV 555

RESULT 10
ABM83782
ID ABM83782 standard; protein; 609 AA.
XX
AC ABM83782;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4031.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dtbp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Hartsbhorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstlin EH;
PI Petralia CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
DR N-PSDB; ACN42434.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX Claim 27; Page; 190pp; English.
PS
XX The invention relates to novel diagnostic and therapeutic polynucleotides
XX selected from one of the 2722 sequences defined in the specification. A
XX polynucleotide of the invention may have a use in gene therapy. The human
XX diagnostic and therapeutic polynucleotides (dtbp) or polypeptides may be
XX used to diagnose a particular condition, disease or disorder associated
XX with human molecules, e.g. cell proliferative disorders,
XX autoimmune/inflammatory disorder, developmental disorder, endocrine
XX disorder, neurological disorders, gastrointestinal disorders, or
XX infections caused by virus, bacteria, fungi or parasite. The dtbp
XX molecules may also be used in genetic mapping, in identifying individuals
XX from minute biological samples, in detecting single nucleotide
XX polymorphisms, as molecular weight markers, and for somatic or germline
XX gene therapy. The present sequence represents a dtbp protein of the
XX invention. Note: The sequence data for this patent is not represented in
XX the printed specification, but was obtained in electronic format directly
XX from WIPO at www.wipo.int/pct/en/sequences/listing.htm
XX

SO Sequence 609 AA;

Query Match 100.0%; Score 68; DB 8; Length 609;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVAV 13
|||||
Db 577 YEKYLGEYVAV 589

RESULT 11
ABM83781
ID ABM83781 standard; protein; 627 AA.
XX
AC ABM83781;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4030.
XX
KW gene therapy; human diagnostic and therapeutic polynucleotide; dtbp.
XX
OS Homo sapiens.
XX
PN WO2004023973-A2.
XX
PD 25-MAR-2004.
XX
PF 12-SEP-2003; 2003WO-US028227.
XX
PR 12-SEP-2002; 2002US-0410259P.
XX
PR 12-SEP-2002; 2002US-0410260P.
XX
PA (INCY-) INCYTE CORP.
XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Hartsbhorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstlin EH;
PI Petralia CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
DR N-PSDB; ACN42433.
XX
PT New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

PS Claim 27, Page: 190pp; English.

XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dthp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dthp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

SO Sequence 627 AA:

Query Match 100.0%; Score 68; DB 8; Length 627;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
|||
DB 595 YEKYLGEERYKAV 607

RESULT 12
ABM83779
ID ABM83779 standard; protein; 628 AA.

AC ABM83779;
XX
XX 18-NOV-2004 (first entry)

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4028.

XX
XX gene therapy; human diagnostic and therapeutic polynucleotide; dthp.

OS Homo sapiens.

XX
XX WO2004023973-A2.

PN 25-MAR-2004.

XX
XX 12-SEP-2003; 2003WO-US028227.

PF 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

XX
XX (INCY-) INCYTE CORP.

XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Hartschorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV,
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH,
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kilton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;

XX
PI MPI; 2004-329368/30.

DR N-PSDB; ACN42431.

XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX
PS Claim 27, Page: 190pp; English.

XX
CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dthp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or
CC infections caused by virus, bacteria, fungi or parasite. The dthp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dthp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

SO Sequence 628 AA:

Query Match 100.0%; Score 68; DB 8; Length 628;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
|||
DB 596 YEKYLGEERYKAV 608

RESULT 13
ABM83778
ID ABM83778 standard; protein; 643 AA.

AC ABM83778;
XX
XX 18-NOV-2004 (first entry)

DT 18-NOV-2004 (first entry)

DE Human diagnostic and therapeutic pprotein SEQ ID NO:4027.

XX
XX gene therapy; human diagnostic and therapeutic polynucleotide; dthp.

OS Homo sapiens.

XX
XX WO2004023973-A2.

PN 25-MAR-2004.

XX
XX 12-SEP-2003; 2003WO-US028227.

PF 12-SEP-2002; 2002US-0410259P.

PR 12-SEP-2002; 2002US-0410260P.

XX
XX (INCY-) INCYTE CORP.

XX
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F,
PI Hartschorne TA, Suchorolski MT, Altus CM, Plets SJ, Elder LV,
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP,
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH,
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kilton ES;
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;

XX
PI MPI; 2004-329368/30.

DR N-PSDB; ACN42431.

XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX
PS Claim 27, Page: 190pp; English.

CC The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorder, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
CC
SQ Sequence 643 AA;
Query Match 100.0%; Score 68; DB 8; Length 643;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YEKYLGESEYKAV 13
|||
Db 611 YEKYLGESEYKAV 623
RESULT 14
ABM83783
ID ABM83783 standard; protein; 645 AA.
XX
XX ABM83783;
AC
XX 18-NOV-2004 (first entry)
DT
XX Human diagnostic and therapeutic protein SEQ ID NO:4032.
DE
XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
XX
XX Homo sapiens.
OS
XX WO2004023973-A2.
PN
XX 25-MAR-2004.
PD
XX 12-SEP-2003; 2003WO-US028227.
PF
XX 12-SEP-2002; 2002US-0410259P.
PR
XX 12-SEP-2002; 2002US-0410260P.
XX
XX (INCY-) INCYTE CORP.
PA
XX Schmidt JF, Wright RJ, Bruna CM, Marjanovic MM, Shen F,
PI Hartsbhorne TA, Suchotolski MT, Alcus CM, Plets SJ, Elder LV,
PI Mooney EM, Deleagane AM, Panesar IS, Banville SC, Reddy TP,
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH,
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL,
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vilt UA, Kitron ES,
PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D,
PI Patry S, Shi X, Suarez CJ;
XX
XX WPI; 2004-329368/30.
DR N-PSDB; ACN42435.
XX
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.
XX
XX Claim 27; Page; 190pp; English.
XX
XX The invention relates to novel diagnostic and therapeutic polynucleotides

CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorder, or
CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
CC
SQ Sequence 645 AA;
Query Match 100.0%; Score 68; DB 8; Length 645;
Best Local Similarity 100.0%; Pred. No. 0.021;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YEKYLGESEYKAV 13
|||
Db 613 YEKYLGESEYKAV 625
RESULT 15
AAU02938
ID AAU02938 standard; protein; 646 AA.
XX
XX AAU02938;
AC
XX 12-SEP-2001 (first entry)
DT
XX Angiotensin converting enzyme (ACEV) splice variant protein #38.
DE
XX
XX Angiotensin converting enzyme splice variant; ACEV; interleukin 6;
KW granulocyte colony stimulating factor receptor; glucagon; hypertrophy;
KW platelet-derived endothelial cell growth factor; cardiovascular disease;
KW cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C;
KW vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer;
KW myocardial infarction; coronary arterial thrombosis; renal disease;
KW diabetic nephropathy; muscular disease; immune disorder; sarcoidosis;
KW multiple sclerosis; immune complex nephritis; deep vein thrombosis;
KW nonaroidotic pulmonary granulomatous disease; endothelial abnormality;
KW vascular disorder; atherosclerosis.
XX
XX Homo sapiens.
OS
XX WO200136632-A2.
PN
XX 25-MAY-2001.
PD
XX 17-NOV-2000; 2000WO-IL000766.
PF
XX 17-NOV-1999; 99IL-00132978.
PR
XX 10-DEC-1999; 99IL-00133455.
XX
XX (COMP-) COMPUGEN LTD.
PA
XX Levine Z, David A, Azar I, Khosravi R, Bernstein J;
PI
XX WPI; 2001-336004/35.
DR N-PSDB; AAS06038.
XX
XX Novel alternative splicing variants e.g. variant of angiotensin
PT converting enzyme (ACEV), useful in identifying candidate compounds
PT capable of binding to the variant and to detect anti-variant antibodies.
XX
XX Claim 4; Fig 38; 519pp; English.
XX
XX The sequence represents an angiotensin converting enzyme splice variant

CC (ACEV) polypeptide. The polypeptides of the invention include variants of
 CC granulocyte colony stimulating factor receptor, glucagon, interleukin 6,
 CC platelet-derived endothelial cell growth factor, cyclin-dependent kinase
 CC inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal
 CC polypeptide receptor 2. The polypeptides and their associated nucleic
 CC acids are useful for identification of variant sequences and detection of
 CC candidate compounds capable of binding the molecules. The sequences of
 CC the invention can be used in the treatment and diagnosis of various
 CC disorders including cardiovascular diseases such as arteriosclerosis,
 CC myocardial infarction and coronary arterial thrombosis, renal diseases
 CC such as diabetic nephropathy, muscular diseases such as hypertrophy,
 CC immune disorders such as immune complex nephritis, multiple sclerosis,
 CC cancer, sarcoidosis, nonrheumatic pulmonary granulomatous diseases such
 CC as asbestosis and vascular pathologies involving an endothelial
 CC abnormality such as deep vein thrombosis
 XX

SQ Sequence 646 AA;

Query Match 100.0%; Score 68; DB 4; Length 646;

Best Local Similarity 100.0%; Pred. No. 0.021; Mismatches 0; Indels 0; Gaps 0;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 YEKYLGEYVKAV 13

Db 614 YEKYLGEYVKAV 626

Search completed: November 1, 2005, 12:48:53
 Job time : 74.3676 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:37:09 ; Search time 19.1176 Seconds
(without alignments)
50.761 Million cell updates/sec

Title: US-10-612-162a-4

Perfect score: 68
Sequence: 1 YEKYLGEYVKAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/prodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/prodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/prodata/1/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	696	6 5262177-4	Patent No. 5262177
2	68	100.0	696	6 5262177-4	Sequence 2, Appl1
3	68	100.0	698	2 US-08-175-158A-2	Sequence 2, Appl1
4	68	100.0	698	4 US-09-439-740-2	Sequence 2, Appl1
5	68	100.0	1074	2 US-08-470-058-2	Sequence 2, Appl1
6	68	100.0	1074	3 US-09-037-188-2	Sequence 2, Appl1
7	68	100.0	1074	3 US-09-285-310-2	Sequence 2, Appl1
8	68	100.0	1410	2 US-08-470-058-4	Sequence 4, Appl1
9	68	100.0	1410	3 US-09-037-188-4	Sequence 4, Appl1
10	68	100.0	1410	3 US-09-285-310-4	Sequence 4, Appl1
11	56	82.4	703	1 US-08-145-681-6	Sequence 6, Appl1
12	56	82.4	703	1 US-08-453-703-6	Sequence 6, Appl1
13	56	82.4	703	1 US-08-456-106-6	Sequence 6, Appl1
14	56	82.4	703	3 US-08-456-108-6	Sequence 6, Appl1
15	56	82.4	703	3 US-09-265-577-6	Sequence 6, Appl1
16	56	82.4	703	4 US-09-633-739-6	Sequence 6, Appl1
17	51	75.0	708	1 US-08-145-681-4	Sequence 4, Appl1
18	51	75.0	708	1 US-08-453-703-4	Sequence 4, Appl1
19	51	75.0	708	2 US-08-456-106-4	Sequence 4, Appl1
20	51	75.0	708	3 US-08-456-108-4	Sequence 4, Appl1
21	51	75.0	708	3 US-09-265-577-4	Sequence 4, Appl1
22	51	75.0	708	4 US-09-633-739-4	Sequence 4, Appl1
23	48	70.6	694	3 US-08-724-586-2	Sequence 2, Appl1
24	48	70.6	694	3 US-09-421-632-2	Sequence 2, Appl1
25	48	70.6	694	4 US-09-932-190-2	Sequence 2, Appl1
26	48	70.6	705	4 US-08-655-640-2	Sequence 2, Appl1
27	48	70.6	708	2 US-08-655-640-4	Sequence 4, Appl1

28	48	70.6	709	1 US-08-154-019-2	Sequence 2, Appl1
29	48	70.6	709	1 US-08-461-333-2	Sequence 2, Appl1
30	48	70.6	709	3 US-08-464-167-2	Sequence 2, Appl1
31	48	70.6	709	3 US-09-158-313-2	Sequence 2, Appl1
32	48	70.6	709	3 US-08-476-798-2	Sequence 2, Appl1
33	48	70.6	711	1 US-08-145-681-2	Sequence 2, Appl1
34	48	70.6	711	1 US-08-250-308-2	Sequence 2, Appl1
35	48	70.6	711	1 US-08-154-019-4	Sequence 4, Appl1
36	48	70.6	711	1 US-08-461-333-4	Sequence 4, Appl1
37	48	70.6	711	1 US-08-453-703-2	Sequence 2, Appl1
38	48	70.6	711	2 US-08-456-106-2	Sequence 2, Appl1
39	48	70.6	711	3 US-08-464-167-4	Sequence 4, Appl1
40	48	70.6	711	3 US-09-158-313-4	Sequence 4, Appl1
41	48	70.6	711	3 US-08-456-108-2	Sequence 2, Appl1
42	48	70.6	711	3 US-08-476-798-4	Sequence 2, Appl1
43	48	70.6	711	3 US-09-265-577-2	Sequence 2, Appl1
44	48	70.6	711	4 US-09-633-739-2	Sequence 2, Appl1
45	48	70.6	711	5 PCT-US93-03614-2	Sequence 2, Appl1

ALIGNMENTS

```
RESULT 1
5262177-4
; Patent No. 5262177
; APPLICANT: BROWN, J. JOSEPH P.; ESTIN, CHARLES D.; PLOWMAN, GREGORY
; D.; HELSTROM, KARL E.; ROSE, TIMOTHY M.; HELSTROM, INEGERD;
; PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 827,313
; FILING DATE: 07-FEB-1986
; SEQ ID NO:4:
; LENGTH: 696

Query Match          100.0%; Score 68; DB 6; Length 696;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 YEKYLGEYVKAV 13
Db      664 YEKYLGEYVKAV 676

RESULT 2
5262177-4
; Patent No. 5262177
; APPLICANT: BROWN, J. JOSEPH P.; ESTIN, CHARLES D.; PLOWMAN, GREGORY
; D.; HELSTROM, KARL E.; ROSE, TIMOTHY M.; HELSTROM, INEGERD;
; PURCHIO, ANTHONY F.; HU, SHU-LOK; PENNATHUR, SRIDHAR
; TITLE OF INVENTION: RECOMBINANT VIRUSES ENCODING THE HHUMAN
; MELANOMA-ASSOCIATED ANTIGEN
; NUMBER OF SEQUENCES: 6
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/7230
; FILING DATE: 27-JAN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 827,313
; FILING DATE: 07-FEB-1986
; SEQ ID NO:4:
; LENGTH: 696

Query Match          100.0%; Score 68; DB 6; Length 696;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

OY 1 YEKYLGEERYKAV 13
Db 664 YEKYLGEERYKAV 676

RESULT 3
US-08-175-158A-2

; Sequence 2, Application US/08175158A
; Patent No. 5986067
; GENERAL INFORMATION:
; APPLICANT: FUNK, Walter D.
; APPLICANT: MACGILLIVRAY, Rose T.A.
; APPLICANT: MASON, Anne B.
; APPLICANT: WOODWORTH, Robert C.
; TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
; TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/175,158A
; FILING DATE: 26-DEC-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/832,029
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: UVI-005CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 698 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-175-158A-2

Query Match 100.0%; Score 68; DB 2; Length 698;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEERYKAV 13
Db 666 YEKYLGEERYKAV 678

RESULT 4
US-09-439-740-2
; Sequence 2, Application US/09439740
; Patent No. 6825037
; GENERAL INFORMATION:
; APPLICANT: FUNK, Walter D.
; APPLICANT: MACGILLIVRAY, Rose T.A.
; APPLICANT: MASON, Anne B.
; APPLICANT: WOODWORTH, Robert C.
; TITLE OF INVENTION: RECOMBINANT TRANSFERRINS, TRANSFERRIN HALF-
; TITLE OF INVENTION: MOLECULES AND MUTANTS THEREOF
; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/439,740
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/175,158
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: UVI-005CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 698 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-439-740-2

Query Match 100.0%; Score 68; DB 4; Length 698;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEERYKAV 13
Db 666 YEKYLGEERYKAV 678

RESULT 5
US-08-470-058-2
; Sequence 2, Application US/08470058
; Patent No. 5817789
; GENERAL INFORMATION:
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Lemont, Jeffrey F.
; TITLE OF INVENTION: Chimeric Proteins For Use in Transport
; TITLE OF INVENTION: of a Selected Substance Into Cells
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Millitia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227

REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-2

Query Match 100.0%; Score 68; DB 2; Length 1074;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
|||||
Db 1042 YEKYLGEYVKAV 1054

RESULT 6
US-09-037-188-2
Sequence 2, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-2

Query Match 100.0%; Score 68; DB 3; Length 1074;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEKYLGEYVKAV 13
|||||

Db 1042 YEKYLGEYVKAV 1054

RESULT 7
US-09-285-310-2
Sequence 2, Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1074 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-2

Query Match 100.0%; Score 68; DB 3; Length 1074;
Best Local Similarity 100.0%; Pred. No. 0.0016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
|||||
Db 1042 YEKYLGEYVKAV 1054

RESULT 8
US-08-470-058-4
Sequence 4, Application US/08470058
Patent No. 5817789
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
TITLE OF INVENTION: Chimeric Proteins For Use in Transport
TITLE OF INVENTION: of a Selected Substance into Cells
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Millitia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA

ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,058
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: TKT93-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
TELEFAX: 617-861-9540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-058-4

Query Match 100.0%; Score 68; DB 2; Length 1410;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 YEKYLGEERYKAV 13
Db 1378 YEKYLGEERYKAV 1390

RESULT 9
US-09-037-188-4
Sequence 4, Application US/09037188
Patent No. 6027921
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/037,188
FILING DATE: 02-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Frazer, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-037-188-4

Query Match 100.0%; Score 68; DB 3; Length 1410;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEKYLGEERYKAV 13
Db 1378 YEKYLGEERYKAV 1390

RESULT 10
US-09-285-310-4
Sequence 4, Application US/09285310
Patent No. 6262026
GENERAL INFORMATION:
APPLICANT: Heartlein, Michael W.
APPLICANT: Lemont, Jeffrey F.
APPLICANT: Concino, Michael F.
TITLE OF INVENTION: CHIMERIC PROTEINS FOR USE
TITLE OF INVENTION: IN TRANSPORT OF A SELECTED SUBSTANCE INTO CELLS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,310
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/037,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Frazer, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 07236/009002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-285-310-4

Query Match 100.0%; Score 68; DB 3; Length 1410;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEKYLGEERYKAV 13
Db 1378 YEKYLGEERYKAV 1390

RESULT 11
US-08-145-681-6
Sequence 6, Application US/08145681

```
/ Patent No. 5571691
/ GENERAL INFORMATION:
/ APPLICANT: Conneely, Orla M.
/ APPLICANT: Heaton, Denis R.
/ APPLICANT: O'Malley, Bert W.
/ APPLICANT: May, Gregory S.
/ TITLE OF INVENTION: Production of Recombinant Lactoferrin
/ TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
/ VARIOUS ORGANISMS
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Baker & Botts, L.L.P.
/ STREET: 910 Louisiana St
/ CITY: Houston
/ STATE: Texas
/ COUNTRY: USA
/ ZIP: 77002
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/145,681
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mcgregor, Martin L.
/ REGISTRATION NUMBER: 29,329
/ REFERENCE/DOCKET NUMBER: 19928-0125
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 713/229/1874
/ TELEFAX: 713/229/1522
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 703 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: YES
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Sus scrofa
/ US-08-145-681-6

Query Match      82.4%; Score 56; DB 1; Length 703;
Best Local Similarity 76.9%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 YEKYLGEYVKAV 13
DB      671 YEKYLGEYVKAV 683

RESULT 12
US-08-453-703-6
/ Sequence 6, Application US/08453703
/ Patent No. 576939
/ GENERAL INFORMATION:
/ APPLICANT: Conneely, Orla M.
/ APPLICANT: Heaton, Denis R.
/ APPLICANT: O'Malley, Bert W.
/ APPLICANT: May, Gregory S.
/ TITLE OF INVENTION: Production of Recombinant Lactoferrin
/ TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
/ VARIOUS ORGANISMS
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Penile & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
```

```
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/453,703
/ FILING DATE: Concurrently herewith
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/145,681
/ FILING DATE: October 28, 1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Albert P. Halluin
/ REGISTRATION NUMBER: 25,227
/ REFERENCE/DOCKET NUMBER: 8206-024
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-854-3660
/ TELEFAX: 415-854-3694
/ INFORMATION FOR SEQ ID NO: 6:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 703 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: YES
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Sus scrofa
/ US-08-453-703-6

Query Match      82.4%; Score 56; DB 1; Length 703;
Best Local Similarity 76.9%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 YEKYLGEYVKAV 13
DB      671 YEKYLGEYVKAV 683

RESULT 13
US-08-456-106-6
/ Sequence 6, Application US/08456106
/ Patent No. 5849881
/ GENERAL INFORMATION:
/ APPLICANT: Conneely, Orla M.
/ APPLICANT: Heaton, Denis R.
/ APPLICANT: O'Malley, Bert W.
/ APPLICANT: May, Gregory S.
/ TITLE OF INVENTION: Production of Recombinant Lactoferrin
/ TITLE OF INVENTION: and Lactoferrin Polypeptides Using cDNA Sequences in
/ VARIOUS ORGANISMS
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Penile & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: IBM PC compatible
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/456,106
/ FILING DATE: Concurrently herewith
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/145,681
/ FILING DATE: October 28, 1993
```

ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-025
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sus scrofa
US-08-456-106-6

Query Match 82.4%; Score 56; DB 2; Length 703;
Best Local Similarity 76.9%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13
|||||
Db 671 YEKYLGEYVAVI 683

RESULT 14
US-08-456-108-6
Sequence 6, Application US/08456108
Patent No. 6100054
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: O'Malley, Bert W.
TITLE OF INVENTION: Production of Recombinant Lactoferrin
TITLE OF INVENTION: and Lactoferrin Polypeptides Using CDNA Sequences in
TITLE OF INVENTION: Various Organisms
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,108
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/145,681
FILING DATE: October 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8206-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 703 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

HYPOTHETICAL: YES
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Sus scrofa
US-08-456-108-6

Query Match 82.4%; Score 56; DB 3; Length 703;
Best Local Similarity 76.9%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13
|||||
Db 671 YEKYLGEYVAVI 683

RESULT 15
US-09-265-577-6
Sequence 6, Application US/09265577
Patent No. 6228614
GENERAL INFORMATION:
APPLICANT: Conneely, Orla M.
APPLICANT: Headon, Denis R.
APPLICANT: O'Malley, Bert W.
TITLE OF INVENTION: PRODUCTION OF RECOMBINANT LACTOFERRIN
TITLE OF INVENTION: AND LACTOFERRIN POLYPEPTIDES USING CDNA SEQUENCES IN VARIOUS
FILE REFERENCE: 01380023US01
CURRENT APPLICATION NUMBER: US/09/265,577
CURRENT FILING DATE: 1999-03-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 703
TYPE: PRT
ORGANISM: Sus scrofa
US-09-265-577-6

Query Match 82.4%; Score 56; DB 3; Length 703;
Best Local Similarity 76.9%; Pred. No. 0.13;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13
|||||
Db 671 YEKYLGEYVAVI 683

Search completed: November 1, 2005, 12:57:31
Job time : 19.1176 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:54:52 ; Search time 65.7647 Seconds
(without alignments)
82.636 Million cell updates/sec

Title: US-10-612-162a-4

Perfect score: 68

Sequence: 1 YEKYLGEERYKAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 1865214

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubppaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	13	US-10-612-162-4	Sequence 4, Appli
2	68	100.0	49	US-10-378-094-16	Sequence 16, Appli
3	68	100.0	49	US-10-384-060-38	Sequence 38, Appli
4	68	100.0	49	US-10-231-494-27	Sequence 27, Appli
5	68	100.0	137	US-10-383-201-12	Sequence 12, Appli
6	68	100.0	328	US-09-891-126-5	Sequence 5, Appli
7	68	100.0	328	US-10-266-745-5	Sequence 5, Appli
8	68	100.0	679	US-10-378-094-3	Sequence 3, Appli
9	68	100.0	679	US-10-384-060-3	Sequence 3, Appli
10	68	100.0	679	US-10-231-494-3	Sequence 3, Appli
11	68	100.0	679	US-10-429-482-4	Sequence 4, Appli

12	68	100.0	679	16	US-10-429-497-4	Sequence 4, Appli
13	68	100.0	679	16	US-10-429-515-4	Sequence 4, Appli
14	68	100.0	679	16	US-10-429-598-4	Sequence 4, Appli
15	68	100.0	679	16	US-10-429-635-4	Sequence 4, Appli
16	68	100.0	679	16	US-10-429-653-4	Sequence 4, Appli
17	68	100.0	679	16	US-10-429-659-4	Sequence 4, Appli
18	68	100.0	679	16	US-10-429-661-4	Sequence 4, Appli
19	68	100.0	679	16	US-10-429-660-4	Sequence 4, Appli
20	68	100.0	679	16	US-10-429-662-4	Sequence 4, Appli
21	68	100.0	679	16	US-10-429-655-4	Sequence 4, Appli
22	68	100.0	679	16	US-10-429-654-4	Sequence 4, Appli
23	68	100.0	698	10	US-09-935-642-6	Sequence 6, Appli
24	68	100.0	698	15	US-10-378-094-2	Sequence 2, Appli
25	68	100.0	698	15	US-10-384-060-2	Sequence 2, Appli
26	68	100.0	698	15	US-10-231-494-2	Sequence 2, Appli
27	68	100.0	698	15	US-10-383-201-10	Sequence 10, Appli
28	68	100.0	698	15	US-10-383-201-14	Sequence 14, Appli
29	68	100.0	698	17	US-10-887-711-2	Sequence 2, Appli
30	68	100.0	698	18	US-10-513-523-3	Sequence 3, Appli
31	68	100.0	1074	9	US-09-753-385-2	Sequence 2, Appli
32	68	100.0	1410	9	US-09-753-385-4	Sequence 4, Appli
33	68	100.0	1410	16	US-10-473-127-805	Sequence 805, App
34	68	100.0	1418	16	US-10-473-127-804	Sequence 804, App
35	56	82.4	15	16	US-10-769-514-14	Sequence 14, Appli
36	56	82.4	15	16	US-10-769-514-47	Sequence 47, Appli
37	56	82.4	703	17	US-10-620-256-6	Sequence 6, Appli
38	51	75.0	698	14	US-10-316-253-273	Sequence 273, App
39	51	75.0	698	14	US-10-316-253-275	Sequence 275, App
40	51	75.0	698	15	US-10-205-331-55	Sequence 35, Appli
41	51	75.0	708	14	US-10-169-297-8	Sequence 8, Appli
42	51	75.0	708	17	US-10-620-256-4	Sequence 4, Appli
43	51	75.0	708	18	US-10-513-523-2	Sequence 2, Appli
44	48	70.6	99	17	US-10-487-556-116	Sequence 116, App
45	48	70.6	323	9	US-09-891-126-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-612-162-4
; Sequence 4, Application US/10612162
; Publication No. US20040014145A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT)-specific
; FILE REFERENCE: 2002/B001
; CURRENT APPLICATION NUMBER: US/10/612,162
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-162-4

Query Match 100.0%; Score 68; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YQ 1 YEKYLGEERYKAV 13
Db 1 YEKYLGEERYKAV 13
RESULT 2
US-10-378-094-16

Sequence 16, Application US/10378094
Publication No. US20030221201A1
GENERAL INFORMATION:
APPLICANT: PRIOR, Christopher P.
APPLICANT: LAI, Chai-Huei
APPLICANT: SADEGH, Homayoun
APPLICANT: TURNER, Andrew
TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
FILE REFERENCE: 54710-5001-01-US
CURRENT APPLICATION NUMBER: US/10/378,094
CURRENT FILING DATE: 2003-03-04
PRIOR APPLICATION NUMBER: US 10/231,494
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/334,059
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/315,745
PRIOR FILING DATE: 2001-08-30
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.2
SEQ ID NO 16
LENGTH: 49
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
OTHER INFORMATION: C2 subdomain of transferrin
US-10-378-094-16

Query Match 100.0%; Score 68; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEERYKAV 13
|||||
Db 37 YEKYLGEERYKAV 49

RESULT 3
US-10-384-060-38
Sequence 38, Application US/10384060
Publication No. US20030226155A1
GENERAL INFORMATION:
APPLICANT: SADEGH, Homayoun
APPLICANT: PRIOR, Christopher P.
APPLICANT: TURNER, Andrew
TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
FILE REFERENCE: 54710-5004-US
CURRENT APPLICATION NUMBER: US/10/384,060
CURRENT FILING DATE: 2003-03-10
PRIOR APPLICATION NUMBER: US 10/231,494
PRIOR FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/334,059
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/315,745
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/406,977
PRIOR FILING DATE: 2002-08-30
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.2
SEQ ID NO 38
LENGTH: 49
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: C2 domain of huma Tf
US-10-384-060-38

Query Match 100.0%; Score 68; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 YEKYLGEERYKAV 13
|||||

Db 37 YEKYLGEERYKAV 49

RESULT 4
US-10-231-494-27
Sequence 27, Application US/10231494
Publication No. US20040023334A1
GENERAL INFORMATION:
APPLICANT: Prior, Christopher P.
TITLE OF INVENTION: Modified Transferrin Fusion Proteins
FILE REFERENCE: 54710-5001-US
CURRENT APPLICATION NUMBER: US/10/231,494
CURRENT FILING DATE: 2002-08-30
PRIOR APPLICATION NUMBER: US 60/315,745
PRIOR FILING DATE: 2001-08-30
PRIOR APPLICATION NUMBER: US 60/334,059
PRIOR FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 27
LENGTH: 49
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Transferrin
US-10-231-494-27

Query Match 100.0%; Score 68; DB 15; Length 49;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEERYKAV 13
|||||
Db 37 YEKYLGEERYKAV 49

RESULT 5
US-10-383-201-12
Sequence 12, Application US/10383201
Publication No. US20040029226A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
FILE REFERENCE: 21402-568A
CURRENT APPLICATION NUMBER: US/10/383,201
CURRENT FILING DATE: 2003-03-06
PRIOR APPLICATION NUMBER: 10/029020
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/365,984
PRIOR FILING DATE: 2002-03-20
PRIOR APPLICATION NUMBER: 60/372,022
PRIOR FILING DATE: 2002-04-12
PRIOR APPLICATION NUMBER: 60/389,143
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/391,779
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/410,755
PRIOR FILING DATE: 2002-09-13
PRIOR APPLICATION NUMBER: 60/412,957
PRIOR FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 10/051,874
PRIOR FILING DATE: 2002-01-16
PRIOR APPLICATION NUMBER: 60/366,928
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 10/055,877
PRIOR FILING DATE: 2002-01-22
NUMBER OF SEQ ID NOS: 155
SOFTWARE: Curaseq1st version 0.1
SEQ ID NO 12
LENGTH: 137
TYPE: PRT
ORGANISM: Homo sapiens

US-10-383-201-12

Query Match 100.0%; Score 68; DB 15; Length 137;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
|||||
DB 105 YEKYLGEERYKAV 117

RESULT 6
US-09-891-126-5
; Sequence 5, Application US/09891126
; Patent No. US20020072596A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT035P1
; CURRENT APPLICATION NUMBER: US/09/891,126
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: PCT/US00/34769
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/171,595
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-891-126-5

Query Match 100.0%; Score 68; DB 9; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
|||||
DB 296 YEKYLGEERYKAV 308

RESULT 7
US-10-266-745-5
; Sequence 5, Application US/10266745
; Publication No. US20030149256A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Transferrin Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT035P1
; CURRENT APPLICATION NUMBER: US/10/266,745
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/891,126
; PRIOR FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: PCT/US00/34769
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: 60/171,595
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-266-745-5

Query Match 100.0%; Score 68; DB 14; Length 328;
Best Local Similarity 100.0%; Pred. No. 0.0057;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
|||||
DB 296 YEKYLGEERYKAV 308

RESULT 8
US-10-378-094-3
; Sequence 3, Application US/10378094
; Publication No. US20030221201A1
; GENERAL INFORMATION:
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: LAI, Char-Huei
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN FUSION PROTEINS
; FILE REFERENCE: 54710-5001-01-US
; CURRENT APPLICATION NUMBER: US/10/378,094
; CURRENT FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: MISC FEATURE
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Mature Transferrin Protein
US-10-378-094-3

Query Match 100.0%; Score 68; DB 15; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
|||||
DB 647 YEKYLGEERYKAV 659

RESULT 9
US-10-384-060-3
; Sequence 3, Application US/10384060
; Publication No. US20030226155A1
; GENERAL INFORMATION:
; APPLICANT: SADEGHI, Homayoun
; APPLICANT: PRIOR, Christopher P.
; APPLICANT: TURNER, Andrew
; TITLE OF INVENTION: MODIFIED TRANSFERRIN-ANTIBODY FUSION PROTEINS
; FILE REFERENCE: 54710-5004-US
; CURRENT APPLICATION NUMBER: US/10/384,060
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: US 10/231,494
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/406,977
; PRIOR FILING DATE: 2002-08-30
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: MISC FEATURE
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: Mature Transferrin Protein
US-10-384-060-3

Query Match 100.0%; Score 68; DB 15; Length 679;

Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEYKAV 13
|||||

Db 647 YEKYLGEYKAV 659

RESULT 10
US-10-231-494-3

; Sequence 3, Application US/10231494
; Publication No. US2004002334A1

; GENERAL INFORMATION:

; APPLICANT: Prior, Christopher P.

; TITLE OF INVENTION: Modified Transferrin Fusion Proteins

; FILE REFERENCE: 54710-5001-US

; CURRENT APPLICATION NUMBER: US/10/231,494

; CURRENT FILING DATE: 2002-08-30

; PRIOR APPLICATION NUMBER: US 60/315,745

; PRIOR FILING DATE: 2001-08-30

; PRIOR APPLICATION NUMBER: US 60/334,059

; PRIOR FILING DATE: 2001-11-30

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 679

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE: Mature transferrin protein

; OTHER INFORMATION: Mature transferrin protein

US-10-231-494-3

Query Match 100.0%; Score 68; DB 15; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEYKAV 13
|||||

Db 647 YEKYLGEYKAV 659

RESULT 11
US-10-429-482-4

; Sequence 4, Application US/10429482

; Publication No. US20040219097A1

; GENERAL INFORMATION:

; APPLICANT: Sandhu, Jasbir

; TITLE OF INVENTION: Composition Useful For The Diagnosis, Imaging and Treatment Of T

; FILE REFERENCE: 2537.000001

; CURRENT APPLICATION NUMBER: US/10/429,482

; CURRENT FILING DATE: 2003-05-02

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 679

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-429-482-4

Query Match 100.0%; Score 68; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEYKAV 13
|||||

Db 647 YEKYLGEYKAV 659

RESULT 12

US-10-429-497-4

; Sequence 4, Application US/10429497

; Publication No. US20040219098A1

; GENERAL INFORMATION:

; APPLICANT: Sandhu, Jasbir

; TITLE OF INVENTION: Methods For The Treatment of Tumors

; FILE REFERENCE: 2537.000006

; CURRENT APPLICATION NUMBER: US/10/429,497

; CURRENT FILING DATE: 2003-05-02

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 679

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-429-497-4

Query Match 100.0%; Score 68; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEYKAV 13
|||||

Db 647 YEKYLGEYKAV 659

RESULT 13

US-10-429-515-4

; Sequence 4, Application US/10429515

; Publication No. US20040219099A1

; GENERAL INFORMATION:

; APPLICANT: Sandhu, Jasbir

; TITLE OF INVENTION: Methods For The Treatment Of Tumors

; FILE REFERENCE: 2537.000005

; CURRENT APPLICATION NUMBER: US/10/429,515

; CURRENT FILING DATE: 2003-05-02

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 679

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-429-515-4

Query Match 100.0%; Score 68; DB 16; Length 679;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEYKAV 13
|||||

Db 647 YEKYLGEYKAV 659

RESULT 14

US-10-429-598-4

; Sequence 4, Application US/10429598

; Publication No. US20040219100A1

; GENERAL INFORMATION:

; APPLICANT: Sandhu, Jasbir

; TITLE OF INVENTION: Composition Useful For The Treatment of Tumors

; FILE REFERENCE: 2537.000003

; CURRENT APPLICATION NUMBER: US/10/429,598

; CURRENT FILING DATE: 2003-05-02

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 679

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-429-598-4

Query Match 100.0%; Score 68; DB 16; Length 679;

Best Local Similarity 100.0%; Pred. No. 0.012;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYLGEYKAV 13
|||||

DB 647 YEKYLGEYVKAV 659

RESULT 15
 US-10-429-635-4
 ; Sequence 4, Application US/10429635
 ; Publication No. US20040219101A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sandhu, Jasbir
 ; TITLE OF INVENTION: Composition Useful For Treatment Of Tumors
 ; FILE REFERENCE: 2537.000007
 ; CURRENT APPLICATION NUMBER: US/10/429,635
 ; CURRENT FILING DATE: 2003-05-02
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 679
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-429-635-4

Query Match 100.0%; Score 68; DB 16; Length 679;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
 |||||
 DB 647 YEKYLGEYVKAV 659

Search completed: November 1, 2005, 13:26:07
 Job time : 65.7647 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:35:39 ; Search time 13.1912 Seconds
(without alignment)
94,822 Million cell updates/sec

Title: US-10-612-162A-4

Perfect score: 68
Sequence: 1 YEKIIGERYKAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	698	1	TFHUP
2	58	83.3	694	1	TFRBP
3	56	82.4	703	2	A45543
4	55	80.9	708	2	JC2323
5	51	75.0	695	2	S49163
6	51	75.0	704	2	I47228
7	51	75.0	708	1	TFBOL
8	48	70.6	215	2	A60166
9	48	70.6	216	1	A39684
10	48	70.6	711	1	TFHUL
11	47	69.1	696	1	S01384
12	45	66.2	705	2	S33761
13	45	66.2	707	1	A28438
14	44	66.7	305	2	D64326
15	43	63.2	334	2	E75153
16	43	63.2	614	2	B83818
17	43	63.2	692	2	H70362
18	42	61.8	115	2	T50390
19	42	61.8	188	2	D64017
20	41	60.3	408	2	H97236
21	41	60.3	431	2	C86812
22	41	60.3	500	2	E89852
23	41	60.3	711	2	S37025
24	40	58.8	203	2	T39117
25	40	58.8	425	2	A99939
26	40	58.8	466	1	STECNT
27	40	58.8	466	2	AF0616
28	40	58.8	466	2	C85619
29	40	58.8	466	2	E90755

30	40	58.8	467	2	B96829	probable sugar tra
31	40	58.8	518	1	X11MHA	homoserine O-acety
32	40	58.8	635	2	A42988	dnak-type molecule
33	40	58.8	738	1	TFHUM	melanotransferrin
34	39.5	58.1	328	1	B64478	hypothetical prote
35	39	57.4	311	2	A28446	transferrin - mous
36	39	57.4	334	1	D80YG	glyceroldehyde-3-P
37	39	57.4	407	2	E70309	hypothetical prote
38	39	57.4	600	2	A49230	dnak-type molecula
39	39	57.4	605	2	I39837	dnak-type molecula
40	39	57.4	607	2	B95060	dnak protein limpo
41	39	57.4	607	2	G97928	hypothetical prote
42	39	57.4	661	2	A69252	3-hydroxyacyl-CoA
43	39	57.4	728	2	S59964	procollagen-lysine
44	39	57.4	731	2	D71332	probable DNA topoi
45	39	57.4	883	2	T06848	phycobillosome link

ALIGNMENTS

RESULT 1

TFHUP

transferrin precursor [validated] - human

N.Alternate names: siderophilin

C.Species: Homo sapiens (man)

C.Date: 15-Oct-1982 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C.Accession: A20981; A92417; A94044; A29090; A32739; I51959; I63133; I54011; I68160; A03

R.Yang, F.; Lum, J.B.; McGill, J.R.; Moore, C.M.; Naylor, S.L.; van Bragt, P.H.; Baldwin

Proc. Natl. Acad. Sci. U.S.A. 81, 2752-2756, 1984

A.Title: Human transferrin: CDNA characterization and chromosomal localization.

A.Reference number: A20981; MUID:84194084; PMID:6585826

A.Contents: variant C

A.Accession: A20981

A.Molecule type: mRNA

A.Residues: 1-698 <YAN>

A.Cross-references: UNIPROT:P02787; EMBL:M12530; NID:G339452; PIDN:AAA61140.1; PID:G3394

A.Note: the authors translated the codon CAA for residue 203 as Glu

R.MacGillivray, R.T.A.; Mendez, E.; Shewale, J.G.; Sinha, S.K.; Lineback-Zins, J.; Brew,

J. Biol. Chem. 258, 3543-3553, 1983

A>Title: The primary structure of human serum transferrin. The structures of seven cyano

A.Reference number: A92417; MUID:83160878; PMID:6833213

A.Accession: A92417

A.Molecule type: protein

A.Residues: 20-263, 'E', 265-328, 'N', 330-379, 'SD', 382-435, 'D', 437-557, 'T', 559-560, 'P', 562-

A.Note: the sequence shown is the predominant electrophoretic genetic variant (C or TIC)

R.Park, I.; Schaeffer, E.; Sidoli, A.; Baralle, F.E.; Cohen, G.N.; Zakim, M.M.

Proc. Natl. Acad. Sci. U.S.A. 82, 3149-3153, 1985

A>Title: Organization of the human transferrin gene: direct evidence that it originated

A.Reference number: A94044; MUID:85216459; PMID:3858812

A.Accession: A94044

A.Molecule type: DNA

A.Residues: 73-263, 'E', 265-328, 'N', 330-562 <PAR>

A.Cross-references: EMBL:M11361

R.Adrjan, G.S.; Korinek, B.W.; Bowman, B.H.; Yang, F.

Gene 49, 167-175, 1986

A>Title: The human transferrin gene: 5' region contains conserved sequences which match

A.Reference number: A29090; MUID:87192006; PMID:3106157

A.Accession: A29090

A.Molecule type: DNA

A.Residues: 1-72;291-300 <ADR>

A.Cross-references: EMBL:M15673

R.Uzan, G.; Frahn, M.; Park, I.; Beaumont, C.; Maessen, G.; Trepat, J.S.; Zakim, M.M.; Kah

Biochem. Biophys. Res. Commun. 119, 273-281, 1984

A>Title: Molecular cloning and sequence analysis of cDNA for human transferrin.

A.Reference number: A32739; MUID:84153910; PMID:6322780

A.Accession: A32739

A.Molecule type: mRNA

A.Residues: 422-690, 'G', 692-698 <UZA>

A.Cross-references: EMBL:M12525; NID:G339468; PIDN:AAA61142.1; PID:G339469

R.MacGillivray, R.T.A.; Mendez, E.; Sinha, S.K.; Sutton, M.R.; Lineback-Zins, J.; Brew, I

Proc. Natl. Acad. Sci. U.S.A. 79, 2504-2508, 1982

R.Lydon, J.P., O'Malley, B.R.; Saucedo, O.; Lee, T.; Headon, D.R.; Conneely, O.M.
Biochim. Biophys. Acta 1132, 97-99, 1992
A>Title: Nucleotide and primary amino acid sequence of porcine lactoferrin.
A'Reference number: S24173; MUID:92379101; PMID:1511016
A'Accession: S24173
A'Molecule type: mRNA
A'Residuals: 1-11, 'W', 13-50, 'I', 52-84, 'G', 86-120, 'L', 121-130, 'I', 132-282, 'S', 284-571, 'Q',
A'Cross-references: EMBL:M92089; NID:g164613; PIDN:AAA31102.1; PID:g164614
A'Experimental source: mammary gland
C'Superfamily: transferrin; transferrin repeat homology
C'Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
F.1.19/Domain: signal sequence #status predicted <Sig>
F.20-703/Product: lactoferrin #status predicted <MAT>
F.20-350/Domain: transferrin repeat homology <TRH1>
F.36-48/Region: antimicrobial
F.354-691/Domain: transferrin repeat homology <TRH2>
F.28-62, 38-53, 129-212, 171-187, 184-195, 245-259, 362-394, 372-385, 419-698, 439-661, 471-546, 49
F.177, 107, 206, 267/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
F.103/Binding site: carbonate (Arg) #status predicted
F.409, 447, 540, 609/Binding site: iron (Asp, Tyr, Tyr, His) #status predicted
F.477/Binding site: carbonate (Arg) #status predicted
F.490/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 82.4%; Score 56; DB 2; Length 703;
Best Local Similarity 76.9%; Pred. No. 0.14;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEKYLGESEYKAV 13
Db 671 YEKYLGESEYKAV 683
RESULT 4
JC2323
Lactoferrin - goat
C'Species: Capra aegagrus hircus (domestic goat)
C'Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #ext_change 07-May-1999
C'Accession: JC2323
R'Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A>Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
A'Reference number: JC2323; MUID:94380047; PMID:8093048
A'Accession: JC2323
A'Molecule type: mRNA
A'Residuals: 1-708 <LEP>
C'Superfamily: transferrin; transferrin repeat homology
C'Keywords: duplication; glycoprotein
F.359-696/Domain: transferrin repeat homology <TRH2>
F.252, 300, 387, 495, 564/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 80.9%; Score 55; DB 2; Length 708;
Best Local Similarity 76.9%; Pred. No. 0.21;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 YEKYLGESEYKAV 13
Db 676 YEKYLGESEYKAV 688
RESULT 5
S49163
transferrin precursor - rat
N'Alternate names: lung-derived growth factor; siderophilin
C'Species: Rattus norvegicus (Norway rat)
C'Date: 16-Feb-1995 #sequence_revision 12-May-1995 #ext_change 09-Jul-2004
C'Accession: S49163; S54980; A30014; A14679; A53289; A30512; I52203
R'Eschbacher, H.; Pierce, A.; Codderville, B.; Gonzalez, F.; Benabasa, M.; Leger, D.; Wierus
submitted to the EMBL Data Library, January 1994
A'Description: Rat mammary gland transferrin: glycan structure, nucleotide sequence and
A'Reference number: S49163
A'Accession: S49163
A'Status: preliminary
A'Molecule type: mRNA

A'Residuals: 1-695 <ESC>
A'Cross-references: UNIPROT:P12346; UNIPROT:Q63602; EMBL:X77158; NID:9510195; PIDN:CAAS-
R'Eschbacher, H.; Pierce, A.; Codderville, B.; Gonzalez, F.; Benabasa, M.; Leger, D.; Wierus
Biochem. J. 307, 47-55, 1995
A>Title: Rat mammary-gland transferrin: nucleotide sequence, phylogenetic analysis and
A'Reference number: S54980; MUID:95234054; PMID:7717992
A'Accession: S54980
A'Status: preliminary
A'Molecule type: mRNA
A'Residuals: 1-695 <ES2>
A'Cross-references: EMBL:X77158; NID:9510195; PIDN:CAAS4403.1; PID:9510196
R'Huguenyik, J.I.; Idzerdt, R.L.; Haywood, L.; Lee, D.C.; McKnight, G.S.; Griswold, M.D.
Endocrinology 120, 332-340, 1987
A>Title: Transferrin messenger ribonucleic acid: molecular cloning and hormonal regulation
A'Reference number: A30014; MUID:87053639; PMID:3023031
A'Accession: A30014
A'Molecule type: mRNA
A'Residuals: 518-687, 'D', 689-692, 'TA', 695 <HUG>
A'Cross-references: GB:M27966; NID:9207439; PIDN:AAA42267.1; PID:9207440
R'Schreiber, G.; Dryburgh, H.; Millership, A.; Matsuda, Y.; Inglier, A.; Phillips, J.; Ek
J. Biol. Chem. 254, 12013-12019, 1979
A>Title: The synthesis and secretion of rat transferrin.
A'Reference number: A14679; MUID:80049855; PMID:500689
A'Accession: A14679
A'Molecule type: protein
A'Residuals: 20-47 <SCH>
R'Cavanaugh, P.G.; Nicolson, G.L.
J. Cell. Biochem. 47, 261-271, 1991
A>Title: Lung-derived growth factor that stimulates the growth of lung-metastasizing tun
A'Reference number: A53289; MUID:92165927; PMID:1791188
A'Accession: A53289
A'Status: preliminary
A'Molecule type: protein
A'Residuals: 89, 'Y', 91, 'A', 93-99, 'V', 101-102, 'N', 233, 'AN', 236-243, 401-406, 'N', 408 <CAV>
A'Experimental source: lung
A>Note: sequence modified after extraction from NCBI backbone
A'Note: sequence extracted from NCBI backbone (NCBIP:86115, NCBIP:86114)
R'Putres, L.R.; Putres, M.; Linton, N.; Brandt, W.; Johnson, G.; Jacobs, P.
Biochim. Biophys. Acta 966, 318-327, 1998
A>Title: Properties of the transferrin associated with rat intestinal mucosa.
A'Reference number: A30512; MUID:88327006; PMID:304665
A'Accession: A30512
A'Molecule type: protein
A'Residuals: 20-30, 639-643, 'KD', 646, 'LXACD', <PUR>
R'Alfred, A.R.; Howlett, G.J.; Schreiber, G.
Biochem. Biophys. Res. Commun. 122, 960-965, 1984
A>Title: Synthesis of rat transferrin in Escherichia coli containing a recombinant bacte
A'Reference number: I52203; MUID:84307580; PMID:6236811
A'Accession: I52203
A'Status: preliminary; translated from GB/EMBL/DBJ
A'Molecule type: mRNA
A'Residuals: 7-25, 'X', 27-56, 'A', 58-64, 267-295 <RES>
A'Cross-references: GB:M26113; NID:9207437; PIDN:AAA42266.1; PID:9207438
C'Genetics:
A'Gene: TF
C'Superfamily: transferrin; transferrin repeat homology
C'Keywords: duplication
F.20-348/Domain: transferrin repeat homology <TRH1>
Query Match 75.0%; Score 51; DB 2; Length 695;
Best Local Similarity 69.2%; Pred. No. 0.99;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 YEKYLGESEYKAV 13
Db 663 YEKYLGESEYKAV 675
RESULT 6
I47228
carbonic anhydrase II inhibitor (transferrin homolog) precursor - pig
C'Species: Sus scrofa domestica (domestic pig)
C'Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #ext_change 09-Jul-2004

C/Accession: I47228
 R/Roush, E.D.; Pierke, C.A.
 Biochemistry 31, 12536-12542, 1992
 A>Title: Purification and characterization of a carbonic anhydrase II inhibitor from por
 A/Reference number: I47228; MUID:93099129; PMID:1463741
 A/Accession: I47228
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-704 <ROU>
 A/Cross-references: UNIPROT:Q29545; EMBL:U36916; NID:q1016329; PIDD:AA58956.1; PID:q101
 C/Genetics:
 A/Gene: PICA
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication
 F/20-350/Domain: transferrin repeat homology <TRH1>
 Query Match 75.0%; Score 51; DB 2; Length 704;
 Best Local Similarity 61.5%; Pred. No. 1;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 YEKYLGEERYKAV 13
 ||||| |||||
 Db 672 YOKLIGPEYLOAI 684

RESULT 7
 TFBO
 lactotransferrin precursor - bovine
 M/Alternate names: lactoferrin
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text_change 09-Jul-2004
 C/Accession: I45919; S14674; S14110; S18517; J70595; S13097; S18518; S13881; PLO148; S21
 R/Teang, T.C.; Burns, D.K.; Wang, F.; Pan, Y.
 FASEB J. 6, 233, 1991
 A>Title: Cloning of a 80-kD advanced glycosylation end product (AGE) binding protein fro
 A/Reference number: I45919
 A/Accession: I45919
 A>Status: translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-708 <TSA>
 A/Cross-references: UNIPROT:Q24677; GB:L08604; NID:q163269; PIDD:AAA0609.1; PID:q163270
 R/Pierce, A.
 Submitted to the EMBL Data Library, November 1990
 A/Reference number: S14674
 A/Accession: S14674
 A/Molecule type: mRNA
 A/Residues: 1-144, 'V', 146-163, 'PP', 166-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <PI1>
 A/Cross-references: EMBL:X57084; NID:9505; PIDD:CAA40366.1; PID:9506
 R/Pierce, A.; Colavizza, D.; Benaisa, M.; Maes, P.; Tartar, A.; Montreuil, J.; Spik, G.
 Eur. J. Biochem. 196, 177-184, 1991
 A>Title: Molecular cloning and sequence analysis of bovine lactotransferrin.
 A/Reference number: S14110; MUID:91160550; PMID:2001696
 A/Accession: S14110
 A/Molecule type: mRNA
 A/Residues: 3-144, 'V', 146-339, 'A', 341-438, 'Y', 440-513, 'R', 515-708 <PI2>
 A/Cross-references: EMBL:X57084
 A/Accession: S18517
 A/Molecule type: protein
 A/Residues: 20-35,82-114,148-163, 'PP', 166-178, 'V', 'P', 183-190,205-212,230-239,304-339,55
 R/Goodman, R.E.; Schanbacher, F.L.
 Biochem. Biophys. Res. Commun. 180, 75-84, 1991
 A>Title: Bovine lactoferrin mRNA: sequence, analysis, and expression in the mammary glar
 A/Reference number: J70595; MUID:92028986; PMID:1718281
 A/Accession: J70595
 A/Molecule type: mRNA
 A/Residues: 1-65, 'PG', 68-296, 'S', 298-339, 'A', 341-708 <GOO>
 A/Cross-references: GB:M63502
 A/Note: the authors translated the codon CCG for residue 66 as Arg and TCT for residue 2
 R/Mead, P.E.; Tweedle, J.W.
 Nucleic Acids Res. 18, 7167, 1990
 A>Title: cDNA and protein sequence of bovine lactoferrin.
 A/Reference number: S13097; MUID:91088328; PMID:2263492
 A/Accession: S13097

A/Molecule type: mRNA
 A/Residues: 28-33, 'DS', 36-38, 'P', 40-708 <MEA>
 A/Cross-references: EMBL:X54801
 A/Accession: S18518
 A/Molecule type: protein
 A/Residues: 20-47,59-66,132-139,256-277,278, 305-332,343-351,361-363,586,587-589,598-619
 R/Mead, P.E.
 submitted to the EMBL Data Library, October 1990
 A/Reference number: S13881
 A/Accession: S13881
 A/Molecule type: mRNA
 A/Residues: 28-38, 'P', 40-86, 'C', 88-708 <ME3>
 A/Cross-references: EMBL:X54801
 R/Rejman, J.J.; Hegarty, H.M.; Hurley, W.L.
 Comp. Biochem. Physiol. B 93, 929-934, 1989
 A>Title: Purification and characterization of bovine lactoferrin from secretions of the
 A/Reference number: PLO148; MUID:90031466; PMID:2805645
 A/Accession: PLO148
 A/Molecule type: protein
 A/Residues: 20-27, 'X', 29-37, 'X', 39-54, 'X', 56-59 <REJ>
 R/Bellamy, W.; Takase, M.; Yamauchi, K.; Wakabayashi, H.; Kawase, K.; Tomita, M.
 Biochim. Biophys. Acta 1121, 130-136, 1992
 A>Title: Identification of the bactericidal domain of lactoferrin.
 A/Reference number: S21756; MUID:92287941; PMID:1599934
 A/Accession: S21756
 A/Molecule type: protein
 A/Residues: 36-60 <BEL>
 R/Shimazaki, K.; Tanaka, T.; Kon, H.; Oota, K.; Kawaguchi, A.; Maki, Y.; Sato, T.
 J. Dairy Sci. 76, 946-955, 1993
 A>Title: Separation and characterization of the C-terminal half molecule of bovine lacto
 A/Reference number: A56659; MUID:93253156; PMID:8486845
 A/Accession: A56659
 A/Molecule type: protein
 A/Residues: 20-25,302-308,359-366, 'X', 368-376, 'X', 378 <SHT>
 C/Superfamily: transferrin; transferrin repeat homology
 C/Keywords: duplication; glycoprotein; iron; iron binding; metalloprotein; milk
 F/1-19/Domain: signal sequence #status predicted <SIG>
 F/20-708/Product: lactotransferrin #status experimental <MAT>
 F/20-355/Domain: transferrin repeat homology <TRH1>
 F/36-60/Region: antimicrobial
 F/359-656/Domain: transferrin repeat homology <TRH2>
 F/28-64,134-211,176-192,179-200,189-202,250-264,367-399,377-390,424-703,444-666,476-551,
 F/38-55/Diulfide bonds: #status predicted
 F/79,111,211,272/Binding site: iron (Asp, Tyr, His) #status experimental
 F/140/Binding site: carbonate (Arg) #status experimental
 F/252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F/414,442,545,614/Binding site: iron (Asp, Tyr, Tyr, His) #status experimental
 F/482/Binding site: carbonate (Arg) #status experimental

Query Match 75.0%; Score 51; DB 1; Length 708;
 Best Local Similarity 69.2%; Pred. No. 1;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEKYLGEERYKAV 13
 ||||| |||||
 Db 676 YEBYLGEERYVAI 688

RESULT 8
 A60166
 hemiferrin - bovine (fragment)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 21-Nov-1997
 C/Accession: A60166
 R/Gilmore, R.R.; Coulter, G.H.; Sylvester, S.R.; Griswold, M.D.
 Biol. Reprod. 43, 139-150, 1990
 A>Title: Synthesis of transferrin and transferrin mRNA in bovine Sertoli cells in cultur
 A/Reference number: A60166; MUID:90366647; PMID:2393686
 A/Accession: A60166
 A>Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-215 <GIL>
 C/Comment: The authors designate this protein as transferrin. However, the Sertoli cells

closely resembles the C-terminal duplication in transferrin. This protein is nearly identical to the C-terminal duplication in transferrin. This protein is nearly identical to the C-terminal duplication in transferrin.

C:Superfamily: hemiferrin; transferrin repeat homology

C:Keywords: glycoprotein; transferrin repeat homology

F:1-215/Domain: transferrin repeat homology #status atypical <TRH2>

Query Match 70.6%; Score 48; DB 2; Length 215; Best Local Similarity 53.8%; Pred. No. 0.97; Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
DB 183 YDSYLGDDVVRAM 195

RESULT 9

A:Residues: 1-216 <STA>

A:Cross-references: UNIPROT:Q64599; GB:M60388

A:Superfamily: hemiferrin; transferrin repeat homology

C:Keywords: glycoprotein; transferrin repeat homology

F:1-204/Domain: transferrin repeat homology #status atypical <TRH2>

Query Match 70.6%; Score 48; DB 1; Length 216; Best Local Similarity 53.8%; Pred. No. 0.97; Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
DB 184 YDSYLGDDVVRAM 196

RESULT 10

A:Residues: 1-216 <STA>

A:Cross-references: UNIPROT:Q64599; GB:M60388

A:Superfamily: hemiferrin; transferrin repeat homology

C:Keywords: glycoprotein; transferrin repeat homology

F:1-204/Domain: transferrin repeat homology #status atypical <TRH2>

Query Match 70.6%; Score 48; DB 1; Length 216; Best Local Similarity 53.8%; Pred. No. 0.97; Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
DB 184 YDSYLGDDVVRAM 196

RESULT 10

A:Residues: 1-216 <STA>

A:Cross-references: UNIPROT:Q64599; GB:M60388

A:Superfamily: hemiferrin; transferrin repeat homology

C:Keywords: glycoprotein; transferrin repeat homology

F:1-204/Domain: transferrin repeat homology #status atypical <TRH2>

Query Match 70.6%; Score 48; DB 1; Length 216; Best Local Similarity 53.8%; Pred. No. 0.97; Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
DB 184 YDSYLGDDVVRAM 196

RESULT 10

A:Residues: 1-216 <STA>

A:Cross-references: UNIPROT:Q64599; GB:M60388

A:Superfamily: hemiferrin; transferrin repeat homology

C:Keywords: glycoprotein; transferrin repeat homology

F:1-204/Domain: transferrin repeat homology #status atypical <TRH2>

Query Match 70.6%; Score 48; DB 1; Length 216; Best Local Similarity 53.8%; Pred. No. 0.97; Matches 7; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
DB 184 YDSYLGDDVVRAM 196

A:Note: sequence extracted from NCBI backbone (NCBIP:1222202)

R:Powell, M.J.; Ogden, J.B.

Nucleic Acids Res. 18, 4013, 1990

A:Title: Nucleotide sequence of human lactoferrin cDNA.

A:Reference number: S10324; PMID:90326549; PMID:2374734

A:Accession: S10324

A:Molecule type: mRNA

A:Residues: 3-711 <PWA>

A:Cross-references: EMBL:X52941; NID:G34411; PIDN:CAA37116.1; PID:G34412

R:Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.

Biochem. J. 276, 349-355, 1991

A:Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.

A:Reference number: S15853; PMID:91264786; PMID:2049066

A:Accession: S15853

A:Status: nucleic acid sequence not shown; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 20-31 <ST1>

A:Accession: S20841

A:Molecule type: protein

A:Residues: 20-28, 'X', 30-31 <ST2>

R:Rado, T.A.; Mei, X.; Benz Jr., E.J.

Blood 70, 989-993, 1987

A:Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA

A:Reference number: S07160; PMID:88001031; PMID:3477300

A:Accession: S07160

A:Molecule type: mRNA

A:Residues: 436-487, 'A', 489-711 <RAD>

A:Cross-references: EMBL:M18642; NID:G186815; PIDN:AAA86665.1; PID:G386855

R:Panela, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.

Cancer Res. 51, 3037-3043, 1991

A:Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocytes

A:Reference number: A61169; PMID:91235214; PMID:1674448

A:Accession: A61169

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 3-701, 'SMKPVN' <PAN>

A:Experimental source: normal breast tissue

R:Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.

Bur. J. Biochem. 145, 659-666, 1984

A:Title: Human lactoferrin: amino acid sequence and structural comparisons with other

A:Reference number: A31000; PMID:85076667; PMID:6510420

A:Accession: A31000

A:Molecule type: protein

A:Residues: 20-140, 142-166, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4

A:Note: This is the final paper in a series

A:Residues: 20-140, 142-166, 171-203, 'L', 205, 'K', 207-208, 'K', 210-385, 'Q', 387-391, 'W', 393-4

R:Houen, G.; Hoegedal, E.V.; Barkholt, V.; Nørskov, L.

Bur. J. Biochem. 241, 303-308, 1996

A:Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinity

A:Reference number: S74119; PMID:97054624; PMID:8898921

A:Accession: S74119

A:Molecule type: protein

A:Residues: 'G', 23-24, 'R', 26-27, 'XX', 30-32 <HOU>

A:Experimental source: neutrophil granulocytes

A:Gene: GDB: LTF

A:Cross-references: GDB:119368; OMIM:150210

A:Map position: 3q21-3q23

C:Superfamily: transferrin; transferrin repeat homology

C:Keywords: duplication; glycoprotein; iron binding; milk

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-711/Product: lactoferrin #status experimental <MAT>

F:21-356/Domain: transferrin repeat homology <TRH1>

F:360-699/Domain: transferrin repeat homology <TRH2>

F:729-65, 39-56, 135-218, 177-193, 190-201, 251-265, 503-657, 595-609/Diulfide bonds: #status e

F:1368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Diulfide bonds: #stat

Query Match 70.6%; Score 48; DB 1; Length 711; Best Local Similarity 61.5%; Pred. No. 3.3; Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 YEKYLGEERYKAV 13
DB 183 YDSYLGDDVVRAM 195

Db 679 YEKYLGPQYVAGI 691

RESULT 11

501384

transferrin - pig

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: S01384; A60520; A61573

C:Accession: S01384; A60520; A61573

R:Baizhin, G.S.; Weinstock, J.

Nucleic Acids Res. 16, 8720, 1988

A:Title: Nucleotide sequence of porcine liver transferrin.

A:Reference number: S01384; PMID:88335629; PMID:3419934

A:Accession: S01384

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-696 <BAL>

A:Cross-references: UNIPROT:P09571; EMBL:X12386; NID:g2126; PID:CAA30943.1; PID:g833800

A:Note: 308-Arg was also found

R:Baizhin, G.S.; Baizhin, T.; Chandler, R.; Grego, B.; Pedersen, J.; Simpson, R.J.; Toh, H.

Comp. Biochem. Physiol. B 95, 261-268, 1990

A:Title: Isolation of transferrin from porcine gastric mucosa: comparison with porcine B

A:Reference number: A60520; PMID:90227903; PMID:2328566

A:Accession: A60520

A:Molecule type: protein

A:Residues: 1-8; 'X', 10-11, 'X', 13-15 <BA2>

A:Experimental source: gastric mucosa

A:Note: the authors suggest transferrin from gastric mucosa may act in dietary iron upta

R:Chung, M.C.M.; Chan, S.L.; Shmidt, S.

Int. J. Biochem. 23, 609-616, 1991

A:Title: Purification of transferrins and lactoferrin using DEAE Affi-Gel Blue.

A:Reference number: A61573; PMID:91293379; PMID:2065820

A:Accession: A61573

A:Molecule type: protein

A:Residues: 1-8, 'X', 10-18, 'X', 'E' <CHD>

C:Superfamily: transferrin; transferrin repeat homology

C:Keywords: duplication; glycoprotein; iron transport; plasma

F:1-696/Product: transferrin #status predicted <MAT>

F:1-335/Domain: transferrin repeat homology <TRH1>

Query Match 69.1%; Score 47; DB 1; Length 696;

Best Local Similarity 61.5%; Pred. No. 4.8;

Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13

Db 655 YESTLGADYITAV 667

RESULT 12

533761

transferrin precursor - horse

N:Alternate names: growth-promoting factor

C:Species: Equus caballus (domestic horse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C:Accession: S33761; S02145

R:Carpenner, M.A.; Broad, T.E.

Biochim. Biophys. Acta 1173, 230-232, 1993

A:Title: The cDNA sequence of horse transferrin.

A:Reference number: S33761; PMID:93277958; PMID:8504171

A:Accession: S33761

A:Molecule type: mRNA

A:Residues: 1-706 <CAR>

A:Cross-references: UNIPROT:P27425; EMBL:M69020; NID:g164242; PID:AAA30958.1; PID:g1642

A:Experimental source: liver; developmental stage adult

R:Yoshinari, K.; Yuasa, K.; Iga, F.; Mamura, A.

Biochim. Biophys. Acta 1010, 28-34, 1989

A:Title: A growth-promoting factor for human myeloid leukemia cells from horse serum ide

A:Reference number: S02145; PMID:89076897; PMID:2909248

A:Accession: S02145

A:Molecule type: protein

A:Residues: 20-35, 'X', 37, 'X', 39-40, 'X', 43-44 <YOS>

C:Complex: monomer

C:Superfamily: transferrin; transferrin repeat homology

C:Keywords: duplication; glycoprotein; iron transport; metal binding; plasma

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-706/Product: transferrin #status experimental <MAT>

F:358-694/Domain: transferrin repeat homology <TRH2>

F:26-64, 36-55, 134-215, 174-190, 177-198, 187-200, 248-262, 360-623, 366-398, 376-389, 423-701, 44

Query Match 66.2%; Score 45; DB 2; Length 706;

Best Local Similarity 61.5%; Pred. No. 11;

Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 YEKYLGEYVAV 13

Db 674 YKYLGEYVAV 686

RESULT 13

A28438

lactoferrin precursor - mouse

N:Alternate names: lactotransferrin

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: A28438; A41205

R:Penhag, B.T.; Teng, C.T.

J. Biol. Chem. 262, 10134-10139, 1987

A:Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre

A:Reference number: A92596; PMID:87280033; PMID:3611056

A:Accession: A28438

A:Molecule type: mRNA

A:Residues: 3-707 <PEN>

A:Cross-references: EMBL:J03298

R:Lin, Y.; Teng, C.T.

J. Biol. Chem. 266, 21880-21885, 1991

A:Title: Characterization of estrogen-responsive mouse lactoferrin promoter.

A:Reference number: A41205; PMID:92042099; PMID:1939212

A:Accession: A41205

A:Molecule type: DNA

A:Residues: 1-15 <LIN>

A:Cross-references: GB:M74778

C:Superfamily: transferrin; transferrin repeat homology

C:Keywords: duplication; glycoprotein

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-707/Product: lactotransferrin #status predicted <MAT>

F:358-695/Domain: transferrin repeat homology <TRH2>

F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.2%; Score 45; DB 1; Length 707;

Best Local Similarity 81.8%; Pred. No. 11;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 EKYLGEEYVKA 12

Db 676 EKYLGEEYVKA 686

RESULT 14

D64326

UDPglucose 4-epimerase (EC 5.1.3.2) - Methanococcus jannaschii

C:Species: Methanococcus jannaschii

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004

C:Accession: D64326

R:Bull, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake, R.

Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;

rsen, J.D.; Sadow, P.M.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Huret, M.A.

Science 273, 1058-1073, 1996

A:Authors: Kaine, B.P.; Bordovsky, M.; Klenk, H.P.; Frazer, C.M.; Smith, H.O.; Weese, C

A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii

A:Reference number: A64300; PMID:96337999; PMID:8688087

A:Accession: D64326

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-305 <BLD>

A:Cross-references: UNIPROT:Q57664; GB:U67477; GB:L77117; NID:g1590949; PID:AA898196.1;

C:Genetics:
A:Map position: FOR202715-203632
C:Superfamily: Escherichia coli UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
C:Keywords: Isomerase
F:2-305/Domain: UDPglucose 4-epimerase homology <UDP>

Query Match 64.7%; Score 44; DB 2; Length 305;
Best Local Similarity 77.8%; Pred. No. 6.8;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KYLGEEYVK 11
||:||||:
Db 144 KYVGEEYK 152

RESULT 15

E75153
glyceraldehyde 3-phosphate dehydrogenase (gap) PAB0257 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: E75153
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: E75153
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-334 <KAW>
A:Cross-references: UNIPROT:Q9V1P1; GB:AJ248284; GB:AL096836; NID:G5457730; PIDN:CAB4930
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: gap; PAB0257
C:Superfamily: glyceraldehyde-3-phosphate dehydrogenase

Query Match 63.2%; Score 43; DB 2; Length 334;
Best Local Similarity 61.5%; Pred. No. 11;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 YEKYLGEYVKAV 13
|||:||:
Db 127 YEKALGKSYVRVY 139

Search completed: November 1, 2005, 12:55:51
Job time : 14.1912 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 12:34:09, Search time 63.6618 Seconds
(without alignments)
104.569 Million cell updates/sec

Title: US-10-612-162a-4
Perfect score: 68
Sequence: 1 YEKYIGEEYKAV 13

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: 1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	698	1 TRFE_HUMAN	P02787 homo sapien
2	58	85.3	695	1 TRFE_RABBIT	P19134 oryctolagus
3	56	82.4	304	2 Q6IST2	Q6ytc2 sus scrofa
4	56	82.4	694	2 Q7TSX8	Q7tsx8 marrota mon
5	56	82.4	704	1 TRFL_PIG	P14632 sus scrofa
6	56	82.4	704	2 Q8MNN8	Q8mnn8 sus scrofa
7	56	82.4	704	2 Q6Y7J3	Q6y7j3 sus scrofa
8	56	82.4	704	2 Q7YS20	Q7ys20 sus scrofa
9	55	80.9	708	1 TRFL_CAPHI	Q29477 capra hircu
10	51	75.0	355	2 Q8M1I0	Q8m1i0 bos taurus
11	51	75.0	681	2 Q6LBN7	Q6lbn7 bos taurus
12	51	75.0	698	1 TRFE_RAT	P12346 rattus norv
13	51	75.0	698	2 Q7TNX0	Q7tnx0 rattus norv
14	51	75.0	704	1 ICA_PIG	Q29545 sus scrofa
15	51	75.0	708	1 TRFL_BOVIN	P24627 bos taurus
16	51	75.0	708	1 TRFL_BUBBU	Q77698 bubalus bub
17	51	75.0	708	2 Q6LEC7	Q6lec7 bos taurus
18	51	75.0	711	2 Q9XT72	Q9xt72 trichosurus
19	51	75.0	979	2 Q7TMC7	Q7tmc7 rattus norv
20	51	75.0	980	2 Q7R24	Q7r24 rattus norv
21	49	72.1	695	1 TRFL_HORSE	Q77611 equus cabal
22	48	70.6	216	2 Q64599	Q64599 rattus norv
23	48	70.6	704	1 TRFE_BOVIN	Q29443 bos taurus
24	48	70.6	708	1 TRFL_CAMDR	Q92400 camelus dro
25	47	70.6	711	1 TRFL_HUMAN	P02788 homo sapien
26	47	69.1	696	1 TRFE_PIG	P09571 sus scrofa
27	45	66.2	63	2 Q9TOR4	Q9tor4 equus cabal
28	45	66.2	697	1 TRFE_MOUSE	Q92111 mus musculi
29	45	66.2	706	1 TRFE_HORSE	P27425 equus cabal
30	45	66.2	707	1 TRFL_MOUSE	P08071 mus musculi
31	45	66.2	707	2 Q8CBA0	Q8cba0 mus musculi

32	44	64.7	300	2 Q8ZT13	Q8zt13 pyrobaculum
33	44	64.7	305	1 GALE_METJA	Q57664 methanococc
34	44	64.7	738	1 TRFM_MOUSE	Q91071 mus musculi
35	43	63.2	238	2 Q9DPK5	Q9dtk5 gillichthy
36	43	63.2	301	2 Q97AH2	Q97ah2 thermoplas
37	43	63.2	334	1 G1P_PIRAB	Q9v1p1 pyrococcus
38	43	63.2	501	2 Q6C8P2	Q6c8p2 kluyveromyc
39	43	63.2	613	1 DNK_BACHD	Q9K472 bacillus ha
40	43	63.2	671	2 Q6CUQ3	Q6cuq3 kluyveromyc
41	43	63.2	671	2 Q707Z3	Q707z3 kluyveromyc
42	43	63.2	691	2 Q6UPC0	Q6upc0 acanthopagr
43	43	63.2	692	1 PHSG_AQUAE	Q65932 aquifex aeo
44	42	61.8	115	2 Q9P7Y2	Q9p7y2 schizosacch
45	42	61.8	188	1 Y966_HAEIN	P44065 haemophilus

ALIGNMENTS

RESULT 1
TRFE_HUMAN STANDARD; PRT; 698 AA.
AC P02787; Q43890; Q9NOB8; Q9UHV0;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serotransferrin precursor (transferrin) (Siderophilin) (Beta-1-metal
binding globulin) (PRO1400).
GN Name=TF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS TF*B2; TF*CHI AND TF*DI.
RX MEDLINE=84194084; PubMed=6585826;
RA Yang F., Lum J.B., McGill J.R., Moore C.M., Naylor S.L.,
van Bragt P.H., Baldwin W.D., Bowman B.H.;
RT "Human transferrin: cDNA characterization and chromosomal
localization.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:2752-2756(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=88056305; PubMed=3678832; DOI=10.1016/0378-1119(87)90163-6;
RA Scheffter E., Lucero M.A., Jeltsch U.-M., Py M.-C., Levin M.O.,
Chandon P., Cohen G.N., Zakin M.W.;
RT "Complete structure of the human transferrin gene. Comparison with
RT analogous chicken gene and human pseudogene.";
RL Gene 56:109-116(1987).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=92231399; PubMed=1809186;
RA Herberberger C.L., Larson J.L., Arnold B., Rostock P.R. Jr.,
Williams P., Dehoff B., Dunn P., O'Neal K.L., Rieman M.W., Tice P.A.;
RT "A cloned gene for human transferrin.";
RL Ann. N. Y. Acad. Sci. 646:140-154(1991).
RN [4]
RP SEQUENCE FROM N.A., AND VARIANT ATRANSFERRINEMIA PRO-477.
RX MEDLINE=20563920; PubMed=1110675;
RA Beutler E., Gelbart T., Lee P.L., Trevino R., Fernandez M.A.,
Palzbaks V.F.;
RT "Molecular characterization of a case of atransferrinemia.";
RL Blood 96:4071-4074(2000).
RN [5]
RP SEQUENCE FROM N.A.
RA Rieder M.J., Carlington D.P., da Ponte S.H., Haslings N.C.,
Ahearn M.O., Kulaneck S.A., Rajkumar N., Toth E.J., Yi Q.,
Nickerson D.A.;
RT "SeattleSNPs: NHGRI HL66682 program for genomic applications. WA-
PHCC, Seattle, WA (URL: <http://pga.gs.washington.edu>)."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
RN [6]

RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=2238657; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Kleusner R.D., Collins F.S., Wagner L., Scheen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stolperon M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butcherfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schercher A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [17]
RP SEQUENCE OF 99-698 FROM N.A.
RC TISSUE=Fetal liver;
RA Zhang C., Yu Y., Zhang S., Wei H., Zhou G., Bi J., Zhang Y., Liu M.,
RA He F.;
RT "Functional prediction of the coding sequences of 33 new genes deduced
RT by analysis of cDNA clones from human fetal liver.";
RL Submitted (JAN-1999) to the EMBL/Genbank/DBJ databases.
RN [18]
RP SEQUENCE OF 422-698 FROM N.A.
RX MEDLINE=8415310; PubMed=6322780;
RA Uzan G., Fraim M., Park I., Beemond C., Maessen G., Trepac J.S.,
RA Zakin M.M., Kahn A.;
RT "Molecular cloning and sequence analysis of cDNA for human
RT transferrin.";
RL Biochem. Biophys. Res. Commun. 119:273-281(1984).
RN [9]
RP SEQUENCE OF 20-698.
RX MEDLINE=83160878; PubMed=6833213;
RA McGillivray R.T.A., Mendez E., Shewale J.G., Sinha S.K.,
RA Lineback-Zins J., Brew K.;
RT "The primary structure of human serum transferrin. The structures of
RT seven cyanogen bromide fragments and the assembly of the complete
RT structure.";
RL J. Biol. Chem. 258:3543-3553(1983).
RN [10]
RP SEQUENCE OF 73-698 FROM N.A.
RX MEDLINE=85216459; PubMed=3858812;
RA Park I., Schaeffer E., Sidoli A., Baralle F.E., Cohen G.N.,
RA Zakin M.M.;
RT "Organization of the human transferrin gene: direct evidence that it
RT originated by gene duplication.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:3149-3153(1985).
RN [11]
RP SEQUENCE OF 1-14 FROM N.A.
RX MEDLINE=87066744; PubMed=3786138;
RA Lucero M.A., Schaeffer E., Cohen G.N., Zakin M.M.;
RT "The 5' region of the human transferrin gene: structure and potential
RT regulatory sites.";
RL Nucleic Acids Res. 14:8692-8692(1986).
RN [12]
RP SEQUENCE OF 1-72 AND 291-300 FROM N.A.
RX MEDLINE=87192006; PubMed=3106157; DOI=10.1016/0378-1119(86)90277-5;
RA Adrian G.S., Korinek B.W., Bowman B.H., Yang F.;
RT "The human transferrin gene: 5' region contains conserved sequences
RT which match the control elements regulated by heavy metals,
RT glucocorticoids and acute phase reaction.";
RL Gene 49:167-175(1986).
RN [13]
RP SEQUENCE OF 45-72 FROM N.A.

RX MEDLINE=20392111; PubMed=10931525;
RX DOI=10.1002/1097-4547(20000815)61:4<388::AID-JNRS-3.0.CO;2-Q;
RA de Arriba Zepa G.A., Saleh M.-C., Fernandez P.M., Guillou F.,
RA Espinosa de los Monteros A., de Vellis J., Zakin M.M., Baron B.;
RT "Alternative splicing prevents transferrin secretion during
RT differentiation of a human oligodendrocyte cell line.";
RL J. Neurosci. Res. 61:388-395(2000).
RN [14]
RP SEQUENCE OF 564-624 FROM N.A., AND VARIANT TF*C2.
RC TISSUE=Brain;
RX MEDLINE=97418135; PubMed=9272172;
RA Namekata K., Oyama F., Imagawa M., Ihara Y.;
RT "Human transferrin (Tf): a single mutation at codon 570 determines Tf
RT C1 or Tf C2 variant.";
RL Hum. Genet. 100:457-458(1997).
RN [15]
RP SEQUENCE OF 564-624 FROM N.A.
RA Teuchida S., Ikemoto S., Kaji E.;
RL Submitted (APR-1998) to the EMBL/Genbank/DBJ databases.
RN [16]
RP SEQUENCE OF 636-696 FROM N.A.
RX MEDLINE=89386721; PubMed=2780570;
RA Duguid J.R., Belmont C.W., Lin N.G., Tourtelotte W.W.;
RT "Changes in brain gene expression shared by scrapie and Alzheimer
RT disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:7260-7264(1989).
RN [17]
RP SEQUENCE OF 263-266, 454-458, 531-538 AND 589-595.
RC TISSUE=Heart;
RX MEDLINE=96007936; PubMed=7498159;
RA Kovalyov L.I., Shishkin S.S., Efimovskiy A.S., Kovalyova M.A.,
RA Kovalyova E.S., Egorov T.A., Musalyanov A.K.;
RT "The major protein expression profile and two-dimensional protein
RT database of human heart.";
RL Electrophoresis 16:1160-1169(1995).
RN [18]
RP DISULFIDE BONDS.
RX MEDLINE=8222166; PubMed=6953407;
RA McGillivray R.T.A., Mendez E., Sinha S.K., Sutton M.R.,
RA Lineback-Zins J., Brew K.;
RT "The complete amino acid sequence of human serum transferrin.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2504-2508(1982).
RN [19]
RP MUTAGENESIS.
RX MEDLINE=92031536; PubMed=1932003;
RA Woodworth R.C., Mason A.B., Funk W.D., McGillivray R.T.A.;
RT "Expression and initial characterization of five site-directed mutants
RT of the N-terminal half-molecule of human transferrin.";
RL Biochemistry 30:10824-10829(1991).
RN [20]
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS) OF 22-350.
RX MEDLINE=98272665; PubMed=9609685; DOI=10.1021/b198035j;
RA Macgillivray R.T.A., Moore S.A., Chen J., Anderson B.F., Baker H.,
RA Luo Y., Bewley M.C., Smith C.A., Murphy M.B.P., Wang Y., Mason A.B.,
RA Woodworth R.C., Breyer G.D., Baker E.N.;
RT "Two high-resolution crystal structures of the recombinant N-lobe of
RT human transferrin reveal a structural change implicated in iron
RT release.";
RL Biochemistry 37:7919-7928(1998).
RN [21]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 22-350.
RX MEDLINE=98433369; PubMed=9760232; DOI=10.1021/b19812064;
RA Jeffrey P.D., Bewley M.C., Macgillivray R.T.A., Mason A.B.,
RA Woodworth R.C., Baker E.N.;
RT "Ligand-induced conformational change in transferrin: crystal
RT structure of the open form of the N-terminal half-molecule of human
RT transferrin.";
RL Biochemistry 37:13978-13986(1998).
RN [22]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 23-352.
RX MEDLINE=99155227; PubMed=10029548; DOI=10.1021/b1982454j;
RA Bewley M.C., Tam B.M., Grewal J., He S., Shewale J.G., Murphy M.E.P.,
RA Mason A.B., Woodworth R.C., Baker E.N., Macgillivray R.T.A.;

RT "X-ray crystallography and mass spectroscopy reveal that the N-lobe of
RT human transferrin expressed in *Pichia pastoris* is folded correctly but
Query Match 100.0%; Score 68; DB 1; Length 698;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEKYLGEERYKAV 13
| | | | | | | | | | | | | | | | | |
Db 666 YEKYLGEERYKAV 678
RESULT 2
TRFE_RABIT STANDARD; PRT; 695 AA.
AC P19134; 046514;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Serotransferrin precursor (transferrin) (Siderophilin) (Beta-1-metal
binding globulin).
CN Name="TF";
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxId=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91274362; PubMed=2054387; DOI=10.1016/0167-4781(91)90021-D;
RA Banfield D.K., Chow B.K.-C., Funk W.D., Robertson K.A., Umels T.M.,
RA Woodworth R.C., McGlillivray R.T.A.;
RT "The nucleotide sequence of rabbit liver transferrin cDNA";
RL Biochim. Biophys. Acta 1089:262-265(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=New Zealand white;
RA Chareeb B.A.A., Thepot D., Pulesant C., Cajero-Juarez M.,
RA Houdebine L.M.;
RT "Cloning and structural organisation of the rabbit transferrin encoding
RT gene";
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 20-51.
RX MEDLINE=88209278; PubMed=335531;
RA Godovac-Zimmermann J.;
RT "Isolation, characterization and N-terminal amino-acid sequence of
RT rabbit transferrin";
RL Biol. Chem. Hoppe-Seyler 369:93-96(1988).
RN [4]
RP SEQUENCE OF 483-545.
RX MEDLINE=89005676; PubMed=3169252; DOI=10.1016/0014-5793(88)80221-7;
RA Evans R.W., Aitken A., Patel K.J.;
RT "Evidence for a single glycan moiety in rabbit serum transferrin and
RT location of the glycan within the polypeptide chain.";
RL FEBS Lett. 238:39-42(1988).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
RC TISSUE=Plasma;
RX MEDLINE=89026775; PubMed=3179277;
RA Bailey S., Evans R.W., Garratt R.C., Gorinsky B., Hasnain S.,
RA Horburgh C., Jhoti H., Lindley P.F., Mydin A., Sarrat R., Watson J.L.;
RT "Molecular structure of serum transferrin at 3.3-A resolution.";
RL Biochemistry 27:5804-5812(1988).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RA Sarrat R., Garratt R.C., Gorinsky B., Jhoti H., Lindley P.F.;
RT "High-resolution X-ray studies on rabbit serum transferrin";
RT preliminary structure analysis of the N-terminal half-molecule at 2.3-
RT A resolution.";
RL Acta Crystallogr. B 46:763-771(1990).
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC can bind two atoms of ferric iron in association with the binding

CC of an anion, usually bicarbonate. It is responsible for the
CC transport of iron from sites of absorption and heme degradation to
CC those of storage and utilization. Serum transferrin may also have
CC a further role in stimulating cell proliferation.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by, and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; X58533; CAA41424.1; -;
DR EMBL; AF031625; AAB94136.1; -;
DR EMBL; AF031611; AAB94136.1; JOINED.
DR EMBL; AF031612; AAB94136.1; JOINED.
DR EMBL; AF031613; AAB94136.1; JOINED.
DR EMBL; AF031614; AAB94136.1; JOINED.
DR EMBL; AF031615; AAB94136.1; JOINED.
DR EMBL; AF031616; AAB94136.1; JOINED.
DR EMBL; AF031617; AAB94136.1; JOINED.
DR EMBL; AF031618; AAB94136.1; JOINED.
DR EMBL; AF031619; AAB94136.1; JOINED.
DR EMBL; AF031620; AAB94136.1; JOINED.
DR EMBL; AF031621; AAB94136.1; JOINED.
DR EMBL; AF031622; AAB94136.1; JOINED.
DR EMBL; AF031623; AAB94136.1; JOINED.
DR EMBL; AF031624; AAB94136.1; JOINED.
DR PDB; 1JNF; X-ray; A=20-695.
DR PDB; 1TFD; X-ray; @=20-323.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW 3D-structure; Direct protein sequencing; Glycoprotein; Iron transport;
KW Metal-binding; Repeat; Signal; Transport.
KW Metel-Binding; Repeat; Signal; Transport.
FT CHAIN 1
FT 19
FT 20 695 Serotransferrin.
FT REPEAT 1.
FT 356 695 2.
FT 356 695
FT 356 695
FT DISULFID 38 67
FT DISULFID 38 58
FT DISULFID 137 213
FT DISULFID 156 350
FT DISULFID 177 193
FT DISULFID 180 196
FT DISULFID 190 198
FT DISULFID 246 260
FT DISULFID 358 612
FT DISULFID 364 396
FT DISULFID 374 387
FT DISULFID 421 690
FT DISULFID 436 653
FT DISULFID 468 539
FT DISULFID 492 601
FT DISULFID 502 516
FT DISULFID 513 522
FT DISULFID 579 593
FT DISULFID 631 636
FT CARBOHYD 509 509
FT METAL 82 82
FT METAL 114 114
FT METAL 207 207
FT METAL 268 268
N-Linked (GlcNAc. . .).
Iron 1.
Iron 1.
Iron 1.

```

FT METAL 411 411 Iron 2.
FT METAL 444 444 Iron 2.
FT METAL 533 533 Iron 2.
FT METAL 601 601 Iron 2.
FT BINDING 139 139 Carbonate 1.
FT BINDING 143 143 Carbonate 1.
FT BINDING 145 145 Carbonate 1 (via amide nitrogen).
FT BINDING 146 146 Carbonate 1 (via amide nitrogen).
FT BINDING 470 470 Carbonate 2.
FT BINDING 474 474 Carbonate 2.
FT BINDING 476 476 Carbonate 2 (via amide nitrogen).
FT BINDING 477 477 Carbonate 2 (via amide nitrogen).
FT VARIANT 517 517 V -> I.
FT CONFLICT 7 7 Missing (in Ref. 1).
FT CONFLICT 47 47 K -> S (in Ref. 3).
FT STRAND 50 50 P -> Y (in Ref. 3).
FT HELIX 24 30
FT TURN 31 48
FT TURN 51 52
FT STRAND 55 61
FT HELIX 64 72
FT TURN 73 74
FT STRAND 78 81
FT HELIX 83 90
FT TURN 92 94
FT STRAND 96 104
FT STRAND 111 111
FT STRAND 113 121
FT TURN 122 123
FT HELIX 128 130
FT TURN 132 133
FT STRAND 136 138
FT TURN 141 142
FT TURN 144 147
FT HELIX 148 154
FT HELIX 155 157
FT HELIX 165 172
FT STRAND 176 177
FT TURN 179 180
FT TURN 183 185
FT HELIX 187 190
FT TURN 191 192
FT TURN 194 195
FT TURN 200 201
FT TURN 203 204
FT HELIX 206 215
FT TURN 216 217
FT STRAND 221 225
FT TURN 226 227
FT HELIX 228 232
FT HELIX 236 239
FT TURN 240 241
FT STRAND 242 245
FT TURN 247 248
FT STRAND 251 253
FT HELIX 254 256
FT TURN 257 258
FT STRAND 263 266
FT STRAND 269 273
FT HELIX 279 293
FT TURN 303 304
FT TURN 307 308
FT TURN 316 317
FT STRAND 320 323
FT TURN 326 327
FT HELIX 330 334
FT HELIX 336 346
FT TURN 347 348

Query Match 85.3%; Score 58; DB 1; Length 695;
Best Local Similarity 76.9%; Pred. No. 0.99;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 YEKYLGEYKAV 13
Db 663 YEKYLGEYKAV 675

RESULT 3
ID Q6YST2 PRELIMINARY; PRT; 304 AA.
AC Q6YST2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Lactoferrin (Fragment).
GN Name-LTF;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -! SIMILARITY: Belongs to the transferrin family.
CC EMBL, AP006435; BADD0658.1; -.
DR HSSP; Q8TCD2; 1B0L.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_PER. 1.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 1.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KM Iron transport; Metal-binding; transport.
FT NON_TER 1
SQ SEQUENCE 304 AA; 3315 MW; 16C0B1675D8722A8 CRC64;

Query Match 82.4%; Score 56; DB 2; Length 304;
Best Local Similarity 76.9%; Pred. No. 0.98;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYLGEYKAV 13
Db 272 YEKYLGEYKAV 284

RESULT 4
ID Q7TSX8 PRELIMINARY; PRT; 694 AA.
AC Q7TSX8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Transferrin.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Rinaldo J.A.S., Gerin J.L.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).

```

```

CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL, AY288100; AAP37129.1; -.
DR HSSP, P19134; 1JNF.
DR GO, GO:0005576; C:extracellular; IEA.
DR GO, GO:0008199; F:ferric iron binding; IEA.
DR GO, GO:0006879; P:iron ion homeostasis; IEA.
DR GO, GO:0006826; P:iron ion transport; IEA.
DR GO, GO:0006810; P:transport; IEA.
DR InterPro, IPR001156; Peptidase_S60.
DR Pfam, PF00405; Transferrin; 2.
DR SMART, SM00094; TR_FER; 2.
DR PROSITE, PS00205; TRANSFERRIN_1; 2.
DR PROSITE, PS00206; TRANSFERRIN_2; 2.
DR PROSITE, PS00207; TRANSFERRIN_3; 2.
DR Iron transport; Metal-binding; Transport.
KW SEQUENCE 694 AA; 76466 MW; 40053F7DC1CFCA87 CRC64;

Query Match      82.4%; Score 56; DB 2; Length 694;
Beet Local Similarity 84.6%; Pred. No. 2.1;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 YEKYLGEYKAV 13
Db      662 YEKYLGEYKAV 674

RESULT 5
TRFL_PIG      STANDARD; PRT; 704 AA.
AC P14632; Q29557;
DT 01-APR-1990 (Rel. 14, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Lactotransferrin precursor (Lactoferrin).
GN Name-LTF;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sue.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92379101; PubMed=1511016; DOI=10.1016/0167-4781(92)90061-4;
RA Lyndon J.P., O'Malley B.R., Saucedo O., Lee T., Headon D.R.,
RA Connolly O.W.;
RT "Nucleotide and primary amino acid sequence of porcine lactoferrin.";
RL Blochm. Biophys. Acta 1132:97-99(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92367939; PubMed=1503259;
RA Alexander L.U., Levine W.B., Teng C.T., Beattie C.W.;
RT "Cloning and sequencing of the porcine lactoferrin cDNA.";
RL Anim. Genet. 23:251-256(1992).
RN [3]
RP SEQUENCE OF 20-49.
RX MEDLINE=90105538; PubMed=2605266;
RA Hutchens T.W., Magnuson J.S., Yip T.-T.;
RT "Rapid purification of porcine colostral whey lactoferrin by affinity
chromatography on single-stranded DNA-agarose. Characterization, amino
acid composition and N-terminal amino acid sequence.";
RL Blochm. Biophys. Acta 999:323-329(1989).
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
can bind two atoms of ferric iron in association with the binding
of an anion, usually bicarbonate.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DOMAIN: Composed of two homologous domains.
CC -1- SIMILARITY: Belongs to the transferrin family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC use by non-profit institutions as long as its content is in no way

```

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, M92089; AAA31102.1; -.
DR EMBL, M81327; AAA31059.1; -.
DR PIR, A45543; A45543.
DR HSSP, Q9TUM0; 1DTZ.
DR InterPro, IPR001156; Peptidase_S60.
DR Pfam, PF00405; Transferrin; 2.
DR PRINTS, PR00422; TRANSFERRIN.
DR SMART, SM00094; TR_FER; 2.
DR PROSITE, PS00205; TRANSFERRIN_1; 2.
DR PROSITE, PS00206; TRANSFERRIN_2; 2.
DR PROSITE, PS00207; TRANSFERRIN_3; 1.
KW Direct protein sequencing; Glycoprotein; Iron transport;
KW Metal-binding; Repeat; Signal; Transport.
FT SIGNAL 1
FT CHAIN 20 704
FT REPEAT 20 359
FT DISULFID 360 704
FT DISULFID 28 62
FT DISULFID 38 53
FT DISULFID 130 213
FT DISULFID 172 188
FT DISULFID 185 196
FT DISULFID 246 260
FT DISULFID 363 395
FT DISULFID 373 386
FT DISULFID 420 699
FT DISULFID 472 547
FT DISULFID 496 680
FT DISULFID 506 520
FT DISULFID 517 530
FT DISULFID 588 602
FT DISULFID 640 645
FT METAL 77
FT METAL 107
FT METAL 207
FT METAL 268
FT METAL 410
FT METAL 448
FT METAL 541
FT METAL 541
FT METAL 610
FT BINDING 132 132
FT BINDING 136 136
FT BINDING 138 138
FT BINDING 139 139
FT BINDING 474 474
FT BINDING 478 478
FT BINDING 480 480
FT BINDING 481 481
FT CARBOHYD 385 385
FT CARBOHYD 491 491
FT CONFLICT 12 12
FT CONFLICT 46 48
FT CONFLICT 51 51
FT CONFLICT 85 85
FT CONFLICT 121 121
FT CONFLICT 132 132
FT CONFLICT 284 284
FT CONFLICT 573 573
FT CONFLICT 590 590
FT CONFLICT 625 625
FT CONFLICT 662 662
FT CONFLICT 686 686
FT SEQUENCE 704 AA; 77625 MW; 932618FD68A0358 CRC64;

Query Match      82.4%; Score 56; DB 1; Length 704;

```

Best Local Similarity 76.9%; Pred. No. 2.1;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKYLGEYVAV 13
Db 672 YKYLGEYVAV 684

RESULT 6

Q8MWN8 PRELIMINARY; PRT; 704 AA.
AC Q8MWN8;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Lactoferrin (Fragment).
GN Name=LTF;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Mammary gland;
RA Wang S.-R., Lin T.-Y., Weng C.-N.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which bind ferric iron in association with the binding of an anion, usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL; L77887; AAL40161.1; -.
DR HSSP; P24627; INKX.

DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_PER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KW Iron transport; Metal-binding; Transport.
FT NON TER 1
SQ SEQUENCE 704 AA; 77681 MW; 64EF69F7503CC32 CRC64;

Query Match 82.4%; Score 56; DB 2; Length 704;
Best Local Similarity 76.9%; Pred. No. 2.1;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKYLGEYVAV 13
Db 672 YKYLGEYVAV 684

RESULT 7

Q6Y739 PRELIMINARY; PRT; 704 AA.
AC Q6Y739;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Lactotransferrin.
GN Name=LTF;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.

RC Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RA
RL
RS
RT
RV
RW
RX
RY
RZ
SA
SB
SC
SD
SE
SF
SG
SH
SI
SJ
SK
SL
SM
SN
SO
SQ
SR
ST
SU
SV
SW
SX
SY
SZ
TA
TB
TC
TD
TE
TF
TG
TH
TI
TJ
TK
TL
TM
TN
TO
TP
TP
TR
TS
TT
TV
TW
TX
TY
TZ
UA
UB
UC
UD
UE
UF
UG
UH
UI
UJ
UK
UL
UM
UN
UO
UP
UQ
UR
US
UT
UU
UV
UW
UX
UY
UZ
VA
VB
VC
VD
VE
VF
VG
VH
VI
VJ
VK
VL
VM
VN
VO
VP
VQ
VR
VS
VT
VV
VW
VX
VY
VZ
WA
WB
WC
WD
WE
WF
WG
WH
WI
WJ
WK
WL
WM
WN
WO
WP
WQ
WR
WS
WT
WW
WX
WY
WZ
XA
XB
XC
XD
XE
XF
XG
XH
XI
XJ
XK
XL
XM
XN
XO
XP
XQ
XR
XS
XT
XU
XV
XW
XX
XY
XZ
YA
YB
YC
YD
YE
YF
YG
YH
YI
YJ
YK
YL
YM
YN
YO
YP
YQ
YR
YS
YT
YU
YV
YW
YX
YY
YZ
ZA
ZB
ZC
ZD
ZE
ZF
ZG
ZH
ZI
ZJ
ZK
ZL
ZM
ZN
ZO
ZP
ZQ
ZR
ZS
ZT
ZU
ZV
ZW
ZX
ZY
ZZ

RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Transferrins are iron binding transport proteins which bind ferric iron in association with the binding of an anion, usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL; AP006185; BAD08651.1; -.
DR HSSP; Q29477; LGW1.

DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_PER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KW Iron transport; Metal-binding; Transport.
SQ SEQUENCE 704 AA; 77611 MW; 10DFBA3C136D5DA CRC64;

Query Match 82.4%; Score 56; DB 2; Length 704;
Best Local Similarity 76.9%; Pred. No. 2.1;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YKYLGEYVAV 13
Db 672 YKYLGEYVAV 684

RESULT 8

Q7YS20 PRELIMINARY; PRT; 704 AA.
AC Q7YS20;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Lactoferrin.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Mammary gland;
RA Pecorini C., Fogher C., Baldi A.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which bind ferric iron in association with the binding of an anion, usually bicarbonate (By similarity).
CC -1- DOMAIN: Composed of two homologous domains (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
DR EMBL; AY306198; AAP70487.1; -.
DR HSSP; P24627; INKX.

DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin; 2.
DR SMART; SM00094; TR_PER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 1.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
KW Iron transport; Metal-binding; Transport.
SQ SEQUENCE 704 AA; 77522 MW; AAC8E176E56BF6A CRC64;

Query Match 82.4%; Score 56; DB 2; Length 704;
Best Local Similarity 76.9%; Pred. No. 2.1;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYIGEEYKAV 13
 DB 672 YEKYIGEEYKAV 684

RESULT 9
 TRFL_CAPRI
 ID TRFL_CAPRI STANDARD, PRT, 708 AA.
 AC Q29477, Q29479, 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Lactoferrin precursor (Lactoferrin).
 GN Name-LTF;
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Capra.
 OC NCBI_TaxId=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA Lee T., Yu S., Kim S., Lee K., Yu D.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;
 RA MEDLINE=94380047; PubMed=8093048;
 RA Le Provost F., Nocard M., Guerin G., Martin P.;
 RT "Characterization of the goat lactoferrin cDNA. Assignment of the
 RT relevant locus to bovine U2 synteny group".
 RL Biochem. Biophys. Res. Commun. 203:1334-1332(1994).
 CC -1- FUNCTION: Transferrins are iron binding transport proteins which
 CC can bind two atoms of ferric iron in association with the binding
 CC of an anion, usually bicarbonate.
 CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL, US3857; AAA97958.1; -
 DR EMBL, X78902; CA55517.1; -
 DR PDB, 1W1; X-ray; A=20-708.
 DR InterPro; IPR001156; Peptidase_S60.
 DR Pfam; PF00405; Transferrin; 2.
 DR SMART; SM00094; TR_PRR; 2.
 DR PROSITE; PS00205; TRANSFERRIN_1; 2.
 DR PROSITE; PS00206; TRANSFERRIN_2; 2.
 DR PROSITE; PS00207; TRANSFERRIN_3; 2.
 DR 3D-structure; Glycoprotein; Iron transport; Metal-binding; Repeat;
 KM Signal; Transport.
 FT SIGNAL 1 19 By similarity.
 FT CHAIN 20 708 Lactoferrin.
 FT REPEAT 20 363 1.
 FT REPEAT 364 708 2.
 FT DISULFID 28 64 By similarity.
 FT DISULFID 38 55 By similarity.
 FT DISULFID 134 217 By similarity.
 FT DISULFID 176 192 By similarity.
 FT DISULFID 189 200 By similarity.
 FT DISULFID 250 264 By similarity.
 FT DISULFID 367 399 By similarity.
 FT DISULFID 377 390 By similarity.

FT DISULFID 424 703 By similarity.
 FT DISULFID 444 666 By similarity.
 FT DISULFID 476 551 By similarity.
 FT DISULFID 500 694 By similarity.
 FT DISULFID 510 524 By similarity.
 FT DISULFID 521 534 By similarity.
 FT DISULFID 592 606 By similarity.
 FT DISULFID 644 649 By similarity.
 FT METAL 79 79 Iron 1 (By similarity).
 FT METAL 111 111 Iron 1 (By similarity).
 FT METAL 211 211 Iron 1 (By similarity).
 FT METAL 272 272 Iron 1 (By similarity).
 FT METAL 414 414 Iron 2 (By similarity).
 FT METAL 452 452 Iron 2 (By similarity).
 FT METAL 545 545 Iron 2 (By similarity).
 FT METAL 614 614 Iron 2 (By similarity).
 FT BINDING 140 140 Carbonate 1 (By similarity).
 FT BINDING 142 142 Carbonate 1 (via amide nitrogen) (By similarity).
 FT BINDING 143 143 Carbonate 1 (via amide nitrogen) (By similarity).
 FT BINDING 478 478 Carbonate 2 (By similarity).
 FT BINDING 482 482 Carbonate 2 (By similarity).
 FT BINDING 484 484 Carbonate 2 (via amide nitrogen) (By similarity).
 FT BINDING 485 485 Carbonate 2 (via amide nitrogen) (By similarity).
 FT CARBOHYD 252 252 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 300 300 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 387 387 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 495 495 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 554 554 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 56 56 I -> V (in Ref. 2).
 FT CONFLICT 88 88 L -> R (in Ref. 2).
 FT CONFLICT 124 124 Q -> K (in Ref. 2).
 FT CONFLICT 154 154 F -> P (in Ref. 2).
 FT CONFLICT 304 304 S -> R (in Ref. 2).
 FT CONFLICT 414 414 D -> G (in Ref. 2).
 SQ SEQUENCE 708 AA; 77358 MW; F2EDAJC8359960D CRC64;

Query Match
 Best Local Similarity 80.9%; Score 55; DB 1; Length 708;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKYIGEEYKAV 13
 DB 676 YEKYIGEEYKAV 688

RESULT 10
 Q8MT10 PRELIMINARY, PRT, 355 AA.
 AC Q8MT10;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Lactoferrin (Fragment).
 OS Bos taurus (Bovine).
 OC Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OK NCBI_TaxId=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=91160550; PubMed=2001696;
 RA Pierce A., Colavizza D., Benalissa M., Maes P., Tartar A.,
 RA Montreuil J., Spik G.;
 RT "Molecular cloning and sequence analysis of bovine lactoferrin."
 RL Eur. J. Biochem. 196:177-184(1991).
 CC -1- FUNCTION: Transferrins are iron binding transport proteins which
 CC bind ferric iron in association with the binding of an anion,
 CC usually bicarbonate (By similarity).
 CC -1- SIMILARITY: Belongs to the transferrin family.

```

DR EMBL; X17066; CAA34912.1; -.
DR HSSP; P24627; IBLF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin_1.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 1.
DR PROSITE; PS00205; TRANSFERRIN_1; 1.
DR PROSITE; PS00206; TRANSFERRIN_2; 1.
DR PROSITE; PS00207; TRANSFERRIN_3; 1.
DR Iron transport; Metal-binding; Transport.
KW NON TER
FT
SQ SEQUENCE 355 AA; 38861 MW; 92CF0C274EBC6893 CRC64;
Query Match 75.0%; Score 51; DB 2; Length 355;
Best Local Similarity 69.2%; Pred. No. 7.1;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 1 YEKYLGEYVYKAV 13
Db 323 YEYLGTEYVTAI 335

RESULT 11
ID Q6LBN7 PRELIMINARY; PRT; 681 AA.
AC Q6LBN7;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Lactoferrin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary;
RX MEDLINE=91086328; PubMed=2263492;
RA Mead P.E.; Tweedie J.W.;
RT "cDNA and protein sequence of bovine lactoferrin.";
RL Nucleic Acids Res. 18:7167-7167(1990).
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary;
RA Tweedie J.;
RL Submitted (JUN-1991) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: Transferrins are iron binding transport proteins which
CC bind ferric iron in association with the binding of an anion,
CC usually bicarbonate (By similarity).
CC -1- SIMILARITY: Belongs to the transferrin family.
CC EMBL; X54801; CAA38572.1; -.
DR HSSP; Q29477; IWL1.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0008199; F:ferric iron binding; IEA.
DR GO; GO:0006879; P:iron ion homeostasis; IEA.
DR GO; GO:0006826; P:iron ion transport; IEA.
DR InterPro; IPR001156; Peptidase_S60.
DR Pfam; PF00405; Transferrin_2.
DR PRINTS; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR_FER; 2.
DR PROSITE; PS00205; TRANSFERRIN_1; 2.
DR PROSITE; PS00206; TRANSFERRIN_2; 2.
DR PROSITE; PS00207; TRANSFERRIN_3; 2.
KW Iron transport; Metal-binding; Transport.
FT
CHAIN <1 681 Bovine lactoferrin.

```

```

SQ SEQUENCE 681 AA; 75181 MW; 4927DB88144D99BA CRC64;
Query Match 75.0%; Score 51; DB 2; Length 681;
Best Local Similarity 69.2%; Pred. No. 13;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Cy 1 YEKYLGEYVYKAV 13
Db 649 YEYLGTEYVTAI 661

RESULT 12
ID TRFE_RAT STANDARD; PRT; 698 AA.
AC P12346; O63602; O64628; O64630;
DT 01-OCT-1989 (Rel. 12, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Sero-transferrin precursor (Transferrin) (Siderophilin) (Beta-1-metal
DE binding globulin).
GN Name=Trf;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RX [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=Mistar; TISSUE=Mammary gland;
RX MEDLINE=95234054; PubMed=7717992;
RA Escrivá H., Pierce A., Coddeville B., Gonzalez F., Benaisa M.,
RA Leger D., Wieruszewski J.M., Spik G., Pambianco M.;
RT "Rat mammary-gland transferrin: nucleotide sequence, phylogenetic
RT analysis and glycan structure.";
RL Biochem. J. 307:47-55(1995).
RN
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=Mistar; TISSUE=Liver;
RX MEDLINE=96208933; PubMed=8829802; DOI=10.1016/0305-0491(95)02068-3;
RA Hosino A., Hisayasu S., Shimada T.;
RT "Complete sequence analysis of rat transferrin and expression of
RT transferrin but not lactoferrin in the digestive glands.";
RL Comp. Biochem. Physiol. 113B:491-497(1996).
RN
RP SEQUENCE OF 7-295 FROM N.A. (ISOFORM 2).
RX MEDLINE=84307580; PubMed=6236811;
RA Aldred A.R., Howlett G.J., Schreiber G.;
RT "Synthesis of rat transferrin in Escherichia coli containing a
RT recombinant bacteriophage.";
RL Biochem. Biophys. Res. Commun. 122:960-965(1984).
RN
RP SEQUENCE OF 521-698 FROM N.A.
RX MEDLINE=87053639; PubMed=3023031;
RA Huggenvik J.T., Idzerda R.L., Haywood L., Lee D.C., McKnight G.S.,
RA Grissold M.D.;
RT "Transferrin messenger ribonucleic acid: molecular cloning and
RT hormonal regulation in rat Sertoli cells.";
RL Endocrinology 120:332-340(1987).
RN
RP SEQUENCE OF 20-47.
RX MEDLINE=80049855; PubMed=500689;
RA Schreiber G., Dryburgh H., Millerlith A., Matsuda Y., Inglis A.,
RA Phillips J., Edwards K., Mages J.;
RT "The synthesis and secretion of rat transferrin.";
RL J. Biol. Chem. 254:12013-12019(1979).
RN
RP SEQUENCE OF 20-30 AND 642-653.
RX PubMed=3046665;
RA Purves L.R., Purves M., Linton N., Brandt W., Johnson G., Jacobs P.;
RT "Properties of the transferrin associated with rat intestinal
RT mucosa.";
RL Biochim. Biophys. Acta 966:318-327(1988).
FT
RP SEQUENCE OF 89-102; 232-243 AND 404-411.

```

RX	PubMed-1791188;			
RA	Cavanaugh P.G., Nicolson G.L.			
RT	"lung-derived growth factor that stimulates the growth of lung-			
RL	J. Cell. Biochem. 47:261-271(1991).			
CC	-1- FUNCTION: Transferrins are iron binding transport proteins which			
CC	can bind two atoms of ferric iron in association with the binding			
CC	of an anion, usually bicarbonate. It is responsible for the			
CC	transport of iron from sites of absorption and heme degradation to			
CC	those of storage and utilization. Serum transferrin may also have			
CC	a further role in stimulating cell proliferation.			
CC	-1- SUBUNIT: Monomer.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- ALTERNATIVE PRODUCTS:			
CC	Event-Alternative splicing; Named isoforms=2;			
CC	Name=1;			
CC	IsoId=P12346-1; Sequence=Displayed;			
CC	Name=2;			
CC	IsoId=P12346-2; Sequence=VSP_011840;			
CC	-1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.			
CC	-1- DOMAIN: Composed of two homologous domains.			
CC	-1- SIMILARITY: Belongs to the transferrin family.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC	or send an email to licenses@isb-sib.ch).			
CC	-----			
DR	EMBL; X71158; CAA54403.1; .			
DR	EMBL; D38380; BAA07458.1; .			
DR	EMBL; M26113; AAA42266.1; .			
DR	EMBL; M27966; AAA42267.1; .			
DR	PIR; S49163; S49163.			
DR	HSSP; P19134; ITFD.			
DR	GlycoSuiteDB; P12346; .			
DR	InterPro; IPR001156; Peptidase_S60.			
DR	Pfam; PF00405; Transferrin; 2.			
DR	PRINTS; PRO0422; TRANSFERRIN.			
DR	SMART; SMO0094; TR_PIR; 2.			
DR	PROSITE; PS00205; TRANSFERRIN_1; 1.			
DR	PROSITE; PS00206; TRANSFERRIN_2; 1.			
DR	PROSITE; PS00207; TRANSFERRIN_3; 2.			
KW	Alternative splicing; Direct protein sequencing; Glycoprotein;			
KW	iron transport; Metal-binding; Repeat; Signal; Transport.			
FT	SIGNAL	1	19	
FT	CHAIN	20	698	Serotransferrin.
FT	REPEAT	20	355	1.
FT	REPEAT	356	698	2.
FT	DISULFID	28	67	By similarity.
FT	DISULFID	38	58	By similarity.
FT	DISULFID	137	213	By similarity.
FT	DISULFID	156	350	By similarity.
FT	DISULFID	177	193	By similarity.
FT	DISULFID	180	196	By similarity.
FT	DISULFID	190	198	By similarity.
FT	DISULFID	246	260	By similarity.
FT	DISULFID	363	395	By similarity.
FT	DISULFID	373	386	By similarity.
FT	DISULFID	420	693	By similarity.
FT	DISULFID	435	656	By similarity.
FT	DISULFID	471	542	By similarity.
FT	DISULFID	495	684	By similarity.
FT	DISULFID	505	519	By similarity.
FT	DISULFID	516	525	By similarity.
FT	DISULFID	582	596	By similarity.
FT	DISULFID	634	639	By similarity.
FT	METAL	82	82	Iron 1 (By similarity).
FT	METAL	114	114	Iron 1 (By similarity).
FT	METAL	207	207	Iron 1 (By similarity).
FT	METAL	268	268	Iron 1 (By similarity).

FT	METAL	410	410	Iron 2 (By similarity).
FT <td>METAL</td> <td>447</td> <td>447</td> <td>Iron 2 (By similarity).</td>	METAL	447	447	Iron 2 (By similarity).
FT <td>METAL</td> <td>536</td> <td>536</td> <td>Iron 2 (By similarity).</td>	METAL	536	536	Iron 2 (By similarity).
FT <td>METAL</td> <td>604</td> <td>604</td> <td>Iron 2 (By similarity).</td>	METAL	604	604	Iron 2 (By similarity).
FT <td>BINDING</td> <td>139</td> <td>139</td> <td>Carbonate 1 (By similarity).</td>	BINDING	139	139	Carbonate 1 (By similarity).
FT <td>BINDING</td> <td>143</td> <td>143</td> <td>Carbonate 1 (By similarity).</td>	BINDING	143	143	Carbonate 1 (By similarity).
FT <td>BINDING</td> <td>145</td> <td>145</td> <td>Carbonate 1 (via amide nitrogen) (By similarity).</td>	BINDING	145	145	Carbonate 1 (via amide nitrogen) (By similarity).
FT <td>BINDING</td> <td>146</td> <td>146</td> <td>Carbonate 1 (via amide nitrogen) (By similarity).</td>	BINDING	146	146	Carbonate 1 (via amide nitrogen) (By similarity).
FT <td>BINDING</td> <td>473</td> <td>473</td> <td>Carbonate 2 (By similarity).</td>	BINDING	473	473	Carbonate 2 (By similarity).
FT <td>BINDING</td> <td>477</td> <td>477</td> <td>Carbonate 2 (By similarity).</td>	BINDING	477	477	Carbonate 2 (By similarity).
FT <td>BINDING</td> <td>479</td> <td>479</td> <td>Carbonate 2 (via amide nitrogen) (By similarity).</td>	BINDING	479	479	Carbonate 2 (via amide nitrogen) (By similarity).
FT <td>BINDING</td> <td>480</td> <td>480</td> <td>Carbonate 2 (via amide nitrogen) (By similarity).</td>	BINDING	480	480	Carbonate 2 (via amide nitrogen) (By similarity).
FT <td>CARBOHYD</td> <td>512</td> <td>512</td> <td>N-linked (GlcNAc...) (Potential).</td>	CARBOHYD	512	512	N-linked (GlcNAc...) (Potential).
FT <td>VARSPLIC</td> <td>65</td> <td>266</td> <td>Missing (in isoform 2).</td>	VARSPLIC	65	266	Missing (in isoform 2).
FT <td>CONFLICT</td> <td>57</td> <td>57</td> <td>Missing (in isoform 2).</td>	CONFLICT	57	57	Missing (in isoform 2).
FT <td>CONFLICT</td> <td>110</td> <td>110</td> <td>A -> P (in Ref. 1).</td>	CONFLICT	110	110	A -> P (in Ref. 1).
FT <td>CONFLICT</td> <td>318</td> <td>354</td> <td>P -> R (in Ref. 1).</td>	CONFLICT	318	354	P -> R (in Ref. 1).
FT <td>CONFLICT</td> <td></td> <td></td> <td>AFGCGVPMRDRLVGHGVYTAIRNQRGVCPKAS -> RFGILRAPKQGLQAVPRPQLCHKSHKSNAGSCPDA (in Ref. 1).</td>	CONFLICT			AFGCGVPMRDRLVGHGVYTAIRNQRGVCPKAS -> RFGILRAPKQGLQAVPRPQLCHKSHKSNAGSCPDA (in Ref. 1).
FT <td>CONFLICT</td> <td>380</td> <td>380</td> <td>S -> G (in Ref. 1).</td>	CONFLICT	380	380	S -> G (in Ref. 1).
FT <td>CONFLICT</td> <td>691</td> <td>691</td> <td>E -> D (in Ref. 4).</td>	CONFLICT	691	691	E -> D (in Ref. 4).
FT <td>CONFLICT</td> <td>696</td> <td>697</td> <td>HK -> TA (in Ref. 4).</td>	CONFLICT	696	697	HK -> TA (in Ref. 4).
SEQ <td>SEQUENCE</td> <td>698 AA;</td> <td>76363 MW;</td> <td>DDFC1918E2A1B0E CRC64;</td>	SEQUENCE	698 AA;	76363 MW;	DDFC1918E2A1B0E CRC64;
Query Match			75.0%;	Score 51; DB 1; Length 698;
Best Local Similarity		69.2%;		Pred. No. 13;
Matches	9;	Conservative	3;	Mismatches 1; Indels 0; Gaps 0;
Oy	1	YEKYLGEYKAV	13	
Db	666	YEYLGAEYLGAV	678	
RESULT 13				
Q7TNXO				
ID	Q7TNXO	PRELIMINARY;	PRT;	698 AA.
AC	Q7TNXO			
DT	01-OCT-2003	(TrEMBLrel. 25, Created)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last sequence update)		
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)		
DE	Liver regeneration-related protein LRRG03.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sclerogasthi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Xu C.S., Li W.Q., Li Y.C., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,			
RA	Yang K.J., Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F.,			
RA	Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;			
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.			
CC	FUNCTION: Transferrins are iron binding transport proteins which			
CC	bind ferric iron in association with the binding of an anion,			
CC	usually bicarbonate (By similarity).			
CC	-1- DOMAIN: Composed of two homologous domains (By similarity).			
CC	-1- SIMILARITY: Belongs to the transferrin family.			
CC	EMBL: AY327504; AAP9736.1; -.			
DR	EMBL	AY327504	AAAP9736.1	-.
DR	HSP	P03787	1BP5	
DR	GO	GO:0005576	C:extracellular;	IEA.
DR	GO	GO:0008199	F:ferric iron binding;	IEA.
DR	GO	GO:0006879	P:iron ion homeostasis;	IEA.
DR	GO	GO:0006826	P:iron ion transport;	IEA.
DR	GO	GO:0006810	P:transport;	IEA.
DR	InterPro	IPR001156	Peptidase_S60.	
DR	Pfam	PF00405	Transferrin_2.	
DR	SMART	SM00084	TR_PER_2	
DR	PROSITE	PS00205	TRANSFERRIN_1	1.
DR	PROSITE	PS00206	TRANSFERRIN_2	2.

DR PROSITE: PS00207; TRANSFERRIN_3; 2.
 KW Iron transport; Metal-binding; Transport.
 SQ SEQUENCE 698 AA; 76395 MW; B91ABB41C447194 CRC64;
 Query Match 75.0%; Score 51; DB 2; Length 698;
 Best Local Similarity 69.2%; Pred. No. 13;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 YEKYLGEYKAV 13
 ||| ||| ||| |||
 DB 666 YEKYLGEYKAV 678

RESULT 14
 ICA_PIG STANDARD; PRT; 704 AA.
 AC Q29545;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Inhibitor of carbonic anhydrase precursor.
 GN Name=ICA;
 OS Sue scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=97254619; PubMed=9100029; DOI=10.1021/bi9627424;
 RA Wuebbens M.W., Roush E.D., Decastro C.M., Fierke C.A.;
 RT "Cloning, sequencing, and recombinant expression of the porcine
 RT inhibitor of carbonic anhydrase: a novel member of the transferrin
 RT family";
 RL Biochemistry 36:4327-4336(1997).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=93099129; PubMed=1463741;
 RA Roush E.D., Fierke C.A.;
 RT "Purification and characterization of a carbonic anhydrase II
 RT inhibitor from porcine plasma";
 RL Biochemistry 31:12536-12542(1992).
 CC -1- FUNCTION: Specifically binds and inhibits carbonic anhydrase II
 CC with nanomolar affinity.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- DOMAIN: Composed of two homologous domains.
 CC -1- PTM: N-glycosylated.
 CC -1- SIMILARITY: Belongs to the transferrin family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U36916; AAB58956.1; -.
 DR PIR: I47228; I47228.
 DR HSBP: P09571; I4728.
 DR InterPro: IPR001156; Peptidase_S60.
 DR Pfam: PF00405; Transferrin; 2.
 DR PRINTS: PR00422; TRANSFERRIN.
 DR SMART: SM00094; TR_FER; 2.
 DR PROSITE: PS00205; TRANSFERRIN_1; 2.
 DR PROSITE: PS00206; TRANSFERRIN_2; 1.
 DR PROSITE: PS00207; TRANSFERRIN_3; 2.
 KW Direct protein sequencing; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 704 Inhibitor of carbonic anhydrase.
 FT REPEAT 20 351 1.
 FT REPEAT 352 704 2.

FT DISULFID 28 67 By similarity.
 FT DISULFID 38 58 By similarity.
 FT DISULFID 137 213 By similarity.
 FT DISULFID 172 188 By similarity.
 FT DISULFID 175 196 By similarity.
 FT DISULFID 185 198 By similarity.
 FT DISULFID 246 260 By similarity.
 FT DISULFID 360 392 By similarity.
 FT DISULFID 370 383 By similarity.
 FT DISULFID 417 699 By similarity.
 FT DISULFID 440 662 By similarity.
 FT DISULFID 472 549 By similarity.
 FT DISULFID 496 690 By similarity.
 FT DISULFID 506 520 By similarity.
 FT DISULFID 517 532 By similarity.
 FT DISULFID 589 603 By similarity.
 FT CARBOHYD 491 491 By similarity.
 SQ SEQUENCE 704 AA; 77634 MW; 16BBO651931E336 CRC64;
 Query Match 75.0%; Score 51; DB 1; Length 704;
 Best Local Similarity 61.5%; Pred. No. 13;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 YEKYLGEYKAV 13
 ||| ||| ||| |||
 DB 672 YEKYLGEYKAV 684

RESULT 15
 TRFL_BOVIN STANDARD; PRT; 708 AA.
 AC P24627; Q29629; Q9MEX3;
 ID 01-MAR-1992 (Rel. 21, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Lactotransferrin precursor (Lactoferrin) [Contains: Lactoferricin B
 DE (Licin B)].
 GN Name=LTF;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Submaxillary gland;
 RX MEDLINE=91160550; PubMed=2001696;
 RA Pierce A., Colavizza D., Benalissa M., Maes P., Tartar A.,
 RA Montreuil J., Spik G.;
 RT "Molecular cloning and sequence analysis of bovine lactotransferrin";
 RL Eur. J. Biochem. 196:177-184(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92028986; PubMed=1718281;
 RA Goodman R.E., Schaubacher F.L.;
 RT "Bovine lactoferrin mRNA: sequence, analysis, and expression in the
 RT mammary gland";
 RL Biochem. Biophys. Res. Commun. 180:75-84(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Tsang T.C., Burns D.K., Wang F., Pan Y.C.E., Schmidt A.M., Stern D.;
 RT "Cloning of a 80-kD advanced glycosylation end product (AGE) binding
 RT protein from bovine lung";
 RL FASEB J. 6:233-233(1991).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood; and Mammary gland;
 RX MEDLINE=94266164; PubMed=8206385; DOI=10.1016/0378-1119(94)90108-2;
 RA Seyfert H.-M., Tuckoritz A., Interthal H., Koczan D., Hobom G.;
 RT "Structure of the bovine lactoferrin-encoding gene and its promoter";
 RL Gene 143:265-269(1994).
 RN [5]

FT	STRAND	25	29
FT	HELIX	32	45
FT	HELIX	46	48
FT	STRAND	53	57
FT	HELIX	61	69
FT	TURN	70	71
FT	STRAND	75	78
FT	HELIX	80	87
FT	TURN	89	91
FT	STRAND	93	102
FT	STRAND	107	108

Query Match 75.0%; Score 51; DB 1; Length 708;
 Best Local Similarity 69.2%; Pred. No. 13;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 YEKTLGEEYKAV 13
 ||:|||||
 Db 676 YEEYLGTEYVTAI 688

Search completed: November 1, 2005, 12:54:34
 Job time : 64.6618 secs

CC lacks glycosylation at Asn413 and/or Asn 611, is present only in
CC alcoholice. The antibodies allow direct detection of CDT in solution,
CC eliminating the need for immobilizing it on a solid phase (as required
CC when using known antibodies). ADG46075-ADG46094 represent CDT peptide
CC fragments used in the method of the invention.

CC Sequence 13 AA;

Query Match 100.0%; Score 68; DB 8; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEERYVKA 13
DB 1 YEKYLGEERYVKA 13

RESULT 2
AAV24760
ID AAV24760 standard; peptide; 12 AA.

AC AAV24760;

DT 24-AUG-1999 (first entry)

DE Lactoferrin duodecapeptide #10.

KM Lactoferrin; LF; human; monoclonal antibody; hybridoma cell line; IGM;

KM Immunoglobulin M; HIV-1; AIDS.

OS Synthetic.

PN MO9926656-A1.

PD 03-JUN-1999.

PF 24-NOV-1998; 98WO-US025258.

PR 24-NOV-1997; 97US-0066464P.

PA (HUMA-) INST HUMAN GENETICS & BIOCHEMISTRY.

PI Rodman TC;

DR WPI; 1999-394785/33.

PT New hybridoma cell lines producing monoclonal human natural IGM

PT antibodies.

PS Example 2; Page 15; 52pp; English.

CC The present invention describes hybridoma cell lines having the following
CC accession numbers: (a) ATCC CRU-12431 (I); (b) ATCC CRU 12477 (II); and
CC (c) ATCC CRU 12472 (III), producing monoclonal forms of human natural IGM
CC antibodies. These are useful for treating HIV-1 infected individuals.
CC Methods from the present invention can be used treating, or increasing
CC CD4+T cells, in a patient suffering from an infection caused by HIV-1, by
CC administering the human IGM monoclonal antibodies produced by (II) and
CC (III) cells individually or together. The antibodies can be used as
CC positive controls in assays for prognosing the onset of AIDS. The present
CC sequence represents a lactoferrin peptide from an example of the present
CC invention

CC Sequence 12 AA;

Query Match 67.6%; Score 46; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.2;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLGEERYV 10
DB 2 YEKYLGEERYV 11

RESULT 3
ADRI5983
ID ADRI5983 standard; peptide; 8 AA.

AC ADRI5983;

DT 04-NOV-2004 (first entry)

DE Transferrin peptide fragment #141.

KM glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.

OS Synthetic.

PN WO2004070389-A1.

PD 19-AUG-2004.

PF 06-FEB-2004; 2004WO-GB000480.

PR 06-FEB-2003; 2003GB-00002740.

PA (AXIS-) AXIS-SHIELD ASA.

PI Rye PD;

DR WPI; 2004-625547/60.

PT Assay for differentiating protein isoforms to determine their
PT concentrations in sample e.g. blood, involves contacting the sample with
PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
PT detecting.

PS Disclosure; Page 18; 30pp; English.

CC The present invention describes an assay for a protein having at least
CC two isoforms with different glycosylation patterns. The assay involves
CC contacting a sample containing the protein with a proteolytic enzyme,
CC followed by detecting the content or relative content of at least one
CC peptide fragment produced by proteolysis. Also described is a kit for the
CC assay method comprising the proteolytic enzyme and a substrate bound
CC specific binding partner (S1) for at least 2 of the isoforms of the
CC proteins. The method can be used for assaying isoforms of proteins
CC according to their glycosylation pattern to determine their concentration
CC or relative concentration in the sample or material (e.g. blood). The
CC method avoids use of antibodies for distinguishing between glycosylated
CC isoforms of the proteins. The present sequence represents a transferrin
CC peptide fragment which is used in the exemplification of the present
CC invention.

CC Sequence 8 AA;

Query Match 63.2%; Score 43; DB 8; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YLGEERYV 11
DB 1 YLGEERYV 8

RESULT 4

ADRI5928
ID ADRI5928 standard; peptide; 8 AA.

AC ADRI5928;

DT 04-NOV-2004 (first entry)

DE Transferrin peptide fragment #86.

KM glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.

XX OS Synthetic.
XX PN WO2004070389-A1.
XX PD 19-AUG-2004.
XX PF 06-FEB-2004; 2004WO-GB000480.
XX PR 06-FEB-2003; 2003GB-00002740.
XX PA (AXIS-) AXIS-SHIELD ASA.
XX PI Rye PD;
XX DR WPI; 2004-625547/60.
XX PT Assay for differentiating protein isoforms to determine their
PT concentrations in sample e.g. blood, involves contacting the sample with
PT proteolytic enzyme to produce peptide fragment by proteolysis followed by
PT detecting.
XX PS Disclosure; Page 16; 30pp; English.
XX CC The present invention describes an assay for a protein having at least
CC two isoforms with different glycosylation patterns. The assay involves
CC contacting a sample containing the protein with a proteolytic enzyme,
CC followed by detecting the content or relative content of at least one
CC peptide fragment produced by proteolysis. Also described is a kit for the
CC assay method comprising the proteolytic enzyme and a substrate bound
CC specific binding partner (S1) for at least 2 of the isoforms of the
CC proteins. The method can be used for assaying isoforms of proteins
CC according to their glycosylation pattern to determine their concentration
CC or relative concentration in the sample or material (e.g. blood). The
CC method avoids use of antibodies for distinguishing between glycosylated
CC isoforms of the proteins. The present sequence represents a transferrin
CC peptide fragment which is used in the exemplification of the present
CC invention.
XX SQ Sequence 8 AA;
XX
XX Query Match 63.2%; Score 43; DB 8; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 YLGEYVK 11
XX |||||
XX 1 YLGEYVK 8
XX DB
XX
XX RESULT 5
XX ADS13391
XX ID ADS13391 standard; peptide; 8 AA.
XX AC ADS13391;
XX XX
XX DT 16-DEC-2004 (first entry)
XX DE Human rheumatoid arthritis marker peptide - SEQ ID 182.
XX KM rheumatoid arthritis; marker; antiinflammatory; antiarthritic.
XX OS Homo sapiens.
XX PN WO2004082617-A2.
XX PD 30-SEP-2004.
XX PF 15-MAR-2004; 2004WO-US007880.
XX PR 14-MAR-2003; 2003US-0455037P.
XX PA (SURR-) SURROMED INC.

XX PI Kantor AB, Becker CH, Schulman H;
XX DR WPI; 2004-690929/67.
XX PT New isolated marker for rheumatoid arthritis, useful in preparing a
PT composition for diagnosing or treating rheumatoid arthritis.
XX PS Claim 1; SEQ ID NO 182; 184pp; English.
XX CC The invention relates to a novel isolated marker for rheumatoid arthritis
CC selected from one of many (around 400) markers defined in the
CC specification. Rheumatoid arthritis is a chronic inflammatory disorder of
CC the small joints which is estimated to affect 2.1 million people in the
CC United States alone. Current approaches to treat the disease include the
CC use of non-steroidal antiinflammatory drugs (NSAIDs), which may reduce
CC pain, swelling and inflammation, and disease-modifying anti-rheumatic
CC drugs (DMARDs), which act to slow the progression of the disease and
CC avoid further joint injury. These drugs are associated with a number of
CC serious side effects and the search for improved therapeutics is a
CC subject of active research. The marker of the invention demonstrates
CC antiarthritic activity and may be useful in preparing a composition for
CC diagnosing or treating rheumatoid arthritis. The current sequence is that
CC of a human rheumatoid arthritis marker peptide of the invention.
XX SQ Sequence 8 AA;
XX
XX Query Match 63.2%; Score 43; DB 8; Length 8;
XX Best Local Similarity 100.0%; Pred. No. 1.8e+06;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 4 YLGEYVK 11
XX |||||
XX 1 YLGEYVK 8
XX DB
XX
XX RESULT 6
XX ABP99131
XX ID ABP99131 standard; peptide; 12 AA.
XX AC ABP99131;
XX XX
XX DT 18-MAR-2003 (first entry)
XX DE Erbb2 cell overexpression EOP1-120 peptide SEQ ID NO:241.
XX KM Erbb2; cancer; oncogene; Erbb2 overexpression-associated protein isoform;
XX KM EOP1; EOP1; Erbb2 overexpression feature; cytosol; vaccine;
XX KM gene therapy.
XX OS Homo sapiens.
XX PN WO200290991-A2.
XX PD 14-NOV-2002.
XX PF 02-MAY-2002; 2002WO-GB002047.
XX PR 03-MAY-2001; 2001GB-00010886.
XX PR 23-NOV-2001; 2001GB-00028183.
XX PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX PI Herath HMAc, Page MJ;
XX DR WPI; 2003-103531/09.
XX PT Diagnosing and treating Erbb2-related cancer, comprises generating Erbb2
PT Overexpression Features (EOPs) from test samples from a subject by
PT electrophoresis, and comparing the EOPs in the sample with a
PT predetermined reference range.
XX PS Claim 3; Page 22; 106pp; English.

XX The present invention describes a method for screening or diagnosing
CC ErbB2-related cancer. The method comprises generating ErbB2
CC overexpression features (EOPs) from test samples of body fluid from the
CC subject by electrophoresis, and comparing the EOPs in the test sample
CC with that from normal subjects or with an expression reference feature
CC (ERP) in the test sample. Also described: (1) an antibody capable of
CC immunospecific binding to an ErbB2 overexpression protein isoform (EOP1);
CC (2) pharmaceutical compositions comprising an EOP1, a nucleic acid
CC encoding an EOP1, an amount of the above antibody or its fragment, and a
CC carrier; (3) a kit comprising one or more antibodies and/or EOPs cited
CC above, other reagents and instructions for use; (4) methods of treating
CC or preventing ErbB2-related cancer; (5) methods of screening for or
CC identifying agents that interact with or modulate the expression or
CC activity of one or more EOPs, EOP1 fragment, EOP1-related polypeptides,
CC or EOP1-fusion proteins; (6) a method for modulating the activity of one
CC or more of the ErbB2 EOPs, comprising administering to a subject an
CC agent identified by the method of (5); and (7) a method for identifying
CC targets for therapeutic modulation of ErbB2-related cancer. EOPs have
CC cytostatic activity and can be used in vaccines and gene therapy. The
CC method is useful in screening, diagnosing, preventing or treating ErbB2-
CC related cancer, determining the stage or severity of ErbB2-related
CC cancer, identifying a subject at risk of developing ErbB2-related cancer,
CC monitoring the effect of therapy administered to a subject with ErbB2-
CC related cancer, and for drug screening or drug development. The kit is
CC useful in carrying out the above methods. ABB98940 to ABB99206 represent
CC specifically claimed EOPs from the present invention

XX Sequence 12 AA;

Query Match 63.2%; Score 43; DB 6; Length 12;
Best Local Similarity 54.5%; Pred. No. 3.7;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 YEKYGEERYK 11
|:|:|:|:|:
Db 2 YDSYLGDDYVR 12

RESULT 7

AAV41865 standard; peptide; 12 AA.

AAV41865;

09-DEC-1999 (first entry)

Rheumatoid arthritis diagnostic protein isoform peptide #16.

Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;

rheumatoid arthritis diagnostic feature; ERP1; synovial fluid;

rheumatoid arthritis diagnostic protein isoform; screening;

expression reference protein isoform; prognosis.

Homo sapiens.

MO9947925-A2.

23-SEP-1999.

15-MAR-1999; 99WO-GB000763.

13-MAR-1998; 98GB-00005477.

(OXFO-) OXFORD GLYCOSCIENCES UK LTD.

Parekh RB, Patel TP, Townsend RR;

WPI, 1999-571871/48.

Diagnosis of human rheumatoid arthritis by two-dimensional
electrophoresis.

PS Disclosure; Page 18; 157pp; English.

XX A method has been developed for the diagnosis of human rheumatoid
CC arthritis (RA) using two-dimensional electrophoresis to generate a two-
CC dimensional array of features. The method can be used for screening,
CC diagnosis and prognosis of RA in a subject or for monitoring the effect
CC of an anti-RA drug or therapy administered to a subject. The method
CC comprises: (a) analysing a sample of serum or plasma and optionally
CC synovial fluid by two-dimensional electrophoresis, to generate a two-
CC dimensional array of features; (b) identifying at least one chosen
CC feature whose relative abundance correlates with the presence or absence
CC of RA; and (c) comparing the abundance of each chosen feature in the
CC sample with the abundance of that chosen feature in serum or plasma from
CC one or more persons without RA, where the relative abundance of the
CC chosen feature or features in the sample indicates the presence or
CC absence of RA in the subject. The method can also be used in clinical
CC studies for testing drugs for therapy of RA, for purification of RA-
CC diagnostic protein isoforms (RPIs), and for production of antibodies to
CC RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify
CC compounds that promote or inhibit their activity, which are then used as
CC RA drugs. Nucleic acid encoding RADFs can be used in gene therapy
CC protocols. AAV41864 to AAV42100 represent RPI peptides, AAV42101 to
CC AAV42103 represent expression reference protein isoform peptides and
CC AA225066 to AA225068 represent degenerate probes for RPIs, which are all
CC used in the exemplification of the present invention

XX Sequence 12 AA;

Query Match 54.4%; Score 37; DB 2; Length 12;
Best Local Similarity 70.0%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 YLGEYVKAV 13
|:|:|:|:|:
Db 2 YLGEYVTAI 11

RESULT 8

AAV41864 standard; peptide; 12 AA.

AAV41864;

09-DEC-1999 (first entry)

Rheumatoid arthritis diagnostic protein isoform peptide #15.

Human; rheumatoid arthritis; RA; diagnosis; RPI; RADF; detection;

rheumatoid arthritis diagnostic feature; ERP1; synovial fluid;

rheumatoid arthritis diagnostic protein isoform; screening;

expression reference protein isoform; prognosis.

Homo sapiens.

MO9947925-A2.

23-SEP-1999.

15-MAR-1999; 99WO-GB000763.

13-MAR-1998; 98GB-00005477.

(OXFO-) OXFORD GLYCOSCIENCES UK LTD.

Parekh RB, Patel TP, Townsend RR;

WPI, 1999-571871/48.

Diagnosis of human rheumatoid arthritis by two-dimensional
electrophoresis.

Disclosure; Page 18; 157pp; English.

CC A method has been developed for the diagnosis of human rheumatoid
CC arthritis (RA) using two-dimensional electrophoresis to generate a two-
CC dimensional array of features. The method can be used for screening,
CC diagnosis and prognosis of RA in a subject or for monitoring the effect
CC of an anti-RA drug or therapy administered to a subject. The method
CC comprises: (a) analyzing a sample of serum or plasma and optionally
CC synovial fluid by two-dimensional electrophoresis, to generate a two-
CC dimensional array of features; (b) identifying at least one chosen
CC feature whose relative abundance correlates with the presence or absence
CC of RA; and (c) comparing the abundance of each chosen feature in the
CC sample with the abundance of that chosen feature in serum or plasma from
CC one or more persons without RA, where the relative abundance of the
CC chosen feature or features in the sample indicates the presence or
CC absence of RA in the subject. The method can also be used in clinical
CC studies for testing drugs for therapy of RA, for purification of RA-
CC diagnostic protein isoforms (RPIs), and for production of antibodies to
CC RPIs. The RA-diagnostic feature (RADF) proteins can be used to identify
CC compounds that promote or inhibit their activity, which are then used as
CC RA drugs. Nucleic acid encoding RADFs can be used in gene therapy
CC protocols. AA141844 to AA142100 represent RPI peptides, AA142101 to
CC AA142103 represent expression reference protein isoform peptides and
CC AA225066 to AA225068 represent degenerate probes for RPIs, which are all
CC used in the exemplification of the present invention

XX Sequence 12 AA;

Query Match 54.4%; Score 37; DB 2; Length 12;
Best Local Similarity 70.0%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YIGEEYVKAV 13
Db 2 YIGEEYVTAI 11

XX RESULT 9

XX ADR15914

XX ID ADR15914 standard; peptide; 12 AA.

XX AC ADR15914;

XX DT 04-NOV-2004 (first entry)

XX DE Transferrin peptide fragment #72.

XX KM glycosylation; proteolytic enzyme; proteolysis; detection; transferrin.

XX OS Synthetic.

XX PN WO2004070389-A1.

XX PD 19-AUG-2004.

XX PF 06-FEB-2004; 2004WO-GB000480.

XX PR 06-FEB-2003; 2003GB-00002740.

XX PA (AXIS-) AXIS-SHIELD ASA.

XX PI Rye PD;

XX DR WPI; 2004-625547/60.

XX Assay for differentiating protein isoforms to determine their
XX concentrations in sample e.g. blood, involves contacting the sample with
XX proteolytic enzyme to produce peptide fragment by proteolysis followed by
XX detecting.

XX PS Disclosure; Page 15; 30pp; English.

XX The present invention describes an assay for a protein having at least
XX two isoforms with different glycosylation patterns. The assay involves
XX contacting a sample containing the protein with a proteolytic enzyme,

CC followed by detecting the content or relative content of at least one
CC peptide fragment produced by proteolysis. Also described is a kit for the
CC assay method comprising the proteolytic enzyme and a substrate bound
CC specific binding partner (S1) for at least 2 of the isoforms of the
CC proteins. The method can be used for assaying isoforms of proteins
CC according to their glycosylation pattern to determine their concentration
CC or relative concentration in the sample or material (e.g. blood). The
CC method avoids use of antibodies for distinguishing between glycosylated
CC isoforms of the proteins. The present sequence represents a transferrin
CC peptide fragment which is used in the exemplification of the present
CC invention.

XX Sequence 12 AA;

Query Match 54.4%; Score 37; DB 8; Length 12;
Best Local Similarity 70.0%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YIGEEYVKAV 13
Db 2 YIGEEYVTAI 11

XX RESULT 10

XX ADS13240

XX ID ADS13240 standard; peptide; 12 AA.

XX AC ADS13240;

XX DT 16-DEC-2004 (first entry)

XX DE Human rheumatoid arthritis marker peptide - SEQ ID 31.

XX KM rheumatoid arthritis; marker; antiinflammatory; antiarthritic.

XX OS Homo sapiens.

XX PN WO2004082617-A2.

XX PD 30-SEP-2004.

XX PF 15-MAR-2004; 2004WO-US007880.

XX PR 14-MAR-2003; 2003US-0455037P.

XX PA (SURR-) SURROMED INC.

XX PI Kantor AB, Becker CH, Schulman H;

XX DR WPI; 2004-690929/67.

XX New isolated marker for rheumatoid arthritis, useful in preparing a
XX composition for diagnosing or treating rheumatoid arthritis.
XX Claim 1; SEQ ID NO 31; 184pp; English.

XX The invention relates to a novel isolated marker for rheumatoid arthritis
XX selected from one of many (around 400) markers defined in the
XX specification. Rheumatoid arthritis is a chronic inflammatory disorder of
XX the small joints which is estimated to affect 2.1 million people in the
XX United States alone. Current approaches to treat the disease include the
XX use of non-steroidal antiinflammatory drugs (NSAIDs), which may reduce
XX pain, swelling and inflammation, and disease-modifying anti-rheumatic
XX drugs (DMARDs), which act to slow the progression of the disease and
XX avoid further joint injury. These drugs are associated with a number of
XX serious side effects and the search for improved therapeutics is a
XX subject of active research. The marker of the invention demonstrates
XX antiarthritic activity and may be useful in preparing a composition for
XX diagnosing or treating rheumatoid arthritis. The current sequence is that
XX of a human rheumatoid arthritis marker peptide of the invention.

XX Sequence 12 AA;

Query Match 54.4%; Score 37; DB 8; Length 12;
 Best Local Similarity 70.0%; Pred. No. 35;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 YLGEYKAV 13
 |||||
 2 YLGYSYVTAI 11

RESULT 11

ABG69560 standard; peptide; 12 AA.

AC ABG69560;

DT 21-OCT-2002 (first entry)

DE Human CRPI tryptic digest peptide #41.

KW Human; cardiac response; CR; cardiac response-associated protein isoform;

KW CRPI; aneurysm; angina; arrhythmia; cardiomyopathy; cardiac arrest;

KW myocardial infarction; coronary; atherosclerosis; oedema; endocarditis;

KW haemorrhage; stenosis; shock; tryptic digest peptide.

OS Homo sapiens.

PN WO200254079-A2.

PD 11-JUL-2002.

PF 24-DEC-2001; 2001WO-GB005763.

PR 29-DEC-2000; 2000US-0260389P.

PT 24-OCT-2001; 2001US-0254978P.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Herman EH, Holt GD, Sistare FD, Zhang J;

PT WPI; 2002-583635/62.

PS Disclosure; Page 30; 138pp; English.

CC The present invention relates to a new method for screening, diagnosis or
 CC prognosis of cardiac response (CR) in a subject. The method of the
 CC invention involves analysing a test sample of body fluid or tissue from
 CC subject by 2D electrophoresis to generate a 2D array of features, whose
 CC relative abundance correlates with the presence, absence, stage or
 CC severity of CR and comparing abundance of each feature with the abundance
 CC of that chosen feature in body fluid from persons free from CR. The
 CC method is useful for screening, diagnosis or prognosis of CR in a
 CC subject, for determining the stage or severity of CR in a subject, for
 CC identifying a subject at risk of developing CR, or for monitoring the
 CC effect of therapy administered to a subject with CR. The method is also
 CC useful for screening agents that interact with one or more of the CRPs
 CC (cardiac response-associated protein isoforms). The invention is useful
 CC for diagnosis or to determine the efficacy of a given treatment regimen.
 CC The cardiac response includes aneurysm, angina, arrhythmia,
 CC cardiomyopathy, cardiac arrest (myocardial infarction), coronary
 CC atherosclerosis, oedema, endocarditis, haemorrhage, stenosis, and shock.
 CC The present amino acid sequence represents one of a collection (ABG69520-
 CC ABG69591) of human CRPI tryptic digest peptides, as described in the
 CC specification

Sequence 12 AA;

Query Match 50.0%; Score 34; DB 5; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.1e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 4 YLGEYKAV 13
 |||||
 2 YLGHSYVTAI 11

RESULT 12

ABG69449 standard; peptide; 12 AA.

AC ABG69449;

DT 21-OCT-2002 (first entry)

DE Vascular response-associated protein isoform tryptic digest peptide #80.

KW Vascular response; VR; vascular response-associated feature; VRP;

KW vascular response-associated protein isoform; VRPI; blood; serum; plasma;

KW aneurysm; stenosis; atherosclerosis; congestion; oedema; haemorrhage;

KW shock; stroke; varicose vein; vasculitis; angitis;

KW VRPI tryptic digest peptide; antiatherosclerotic; haemostatic;

OS Unidentified.

PN WO200254080-A2.

PD 11-JUL-2002.

PF 24-DEC-2001; 2001WO-GB005774.

PR 29-DEC-2000; 2000US-0260387P.

PT 24-OCT-2001; 2001US-00260387.

PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Herman EH, Holt GD, Sistare FD, Zhang J;

PT WPI; 2002-583636/62.

PS Disclosure; Page 37; 156pp; English.

CC The present invention relates to methods and compositions for the
 CC screening, diagnosis or prognosis of vascular response (VR) in a subject.
 CC The method comprises analysing a test sample of body fluid from the
 CC subject by two-dimensional electrophoresis to generate a 2D array of
 CC vascular response-associated features (VRFs), whose relative abundance
 CC correlates with presence, absence, stage or severity of VR and comparing
 CC the abundance of each feature with the abundance of that chosen feature
 CC in body fluid from persons free from VR. The invention also describes
 CC vascular response-associated protein isoforms (VRPIs) detectable in
 CC blood, serum or plasma. The methods and compositions of the invention are
 CC useful for the screening, diagnosis or prognosis of VR in a subject, for
 CC determining the stage or severity of VR in a subject, for identifying a
 CC subject at risk of developing VR, or for monitoring the effect of therapy
 CC administered to a subject having VR. Antibodies capable of binding to
 CC VRPIs are useful for treating or preventing VR. An agent that modulates
 CC the activity of VRPI is useful in the manufacture of a medicament for the
 CC treatment or prevention of VR in a subject. The vascular response
 CC includes aneurysm, stenosis, atherosclerosis, congestion, oedema,
 CC haemorrhage, shock, stroke, varicose veins, and vasculitis (angitis).

Sequence 12 AA;

Query Match 50.0%; Score 34; DB 5; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.1e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YLGEYVAV 13
||| |||
DB 2 YLGHSYVTAI 11

RESULT 13

AAAB14919
ID AAB14919 standard; peptide; 10 AA.

AC AAB14919;

DT 11-JAN-2001 (first entry)

DE Random 27-mer library peptide R6-52.

KM RNA-protein fusion; protein library; protein isolation; gene cloning;

KW myc epitope tag.

OS Synthetic.

PN WO200047775-A1.

XX 17-AUG-2000.

PF 01-FEB-2000; 2000WO-US002589.

PR 09-FEB-1999; 99US-00247190.

PA (GENO) GEN HOSPITAL CORP.

PI Szebeck JW, Roberts RW, Liu R;

DR WPI; 2000-533022/48.

PT Producing protein or DNA libraries which are useful for improving
existing proteins, by in vitro translating protein coding sequences to
produce RNA-protein fusions and incubating these protein fusions under
high salt conditions.

PS Disclosure; Fig 22; 121pp; English.

XX The present sequence was isolated from an RNA-protein fusion library
CC following selection for peptides that bound to a c-myc monoclonal
CC antibody. RNA-protein fusions comprise a protein covalently linked to the
CC 3' end of its own mRNA. The fusions are made by synthesis and in vitro or
CC in situ translation of an mRNA molecule with a peptide acceptor attached
CC to its 3' end. The RNA-protein fusions are incubated under high salt
CC conditions to produce a protein library. This method is useful for
CC improving or altering existing proteins, as well as for isolating new
CC proteins and nucleic acid or small molecule targets. It may also be used
CC to improve human or humanised single-chain antibodies for the treatment
CC of a number of diseases. The method is useful for the isolation of
CC proteins with specific binding properties, for screening cDNA libraries
CC and cloning new genes on the basis of protein-protein interactions.
CC Unlike prior art, the new method does not rely on maintaining the
CC integrity of an mRNA:ribosome:nascent chain ternary complex, which is
CC very fragile and is therefore of limited use. The method does not rely on
CC topological links between the protein and the nucleic acid so that the
CC information of the protein is retained and can be recovered in readable,
CC nucleic acid form

XX Sequence 10 AA;

Query Match 44.1%; Score 30; DB 3; Length 10;

Best Local Similarity 66.7%; Pred. No. 3.8e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKYLGEEYV 10
|:|:|:|:|
DB 1 EBYLVSEYV 9

RESULT 14

AAAY04623

ID AAY04623 standard; peptide; 10 AA.

AC AAY04623;

DT 22-JUN-1999 (first entry)

DE Factor VII catalytic domain-interacting peptide #23.

KM Receptor; catalytic domain; Factor VII; epidermal growth factor-2; EGF-2;

KW tissue factor; blood clotting disorder; thrombosis; restenosis;

KW myocardial infarction; angina; restenosis; cerebrovascular disease;

KW peripheral arterial occlusive disease; hypercoagulability;

OS Synthetic.

PN WO9913063-A1.

XX 18-MAR-1999.

PF 08-SEP-1998; 98WO-GB002701.

PR 09-SEP-1997; 97GB-00019162.

PA (NYCO-) NYCOMED IMAGING AS.

PI (MATT/) MATTHEWS D P.

DR WPI; 1999-229234/19.

PT New anticoagulant compounds for coagulating blood clotting disorders.
XX Claim 10; Page 37; 46pp; English.
PS Peptides AAY04601-Y04623 represent claimed compounds which are capable of
XX interacting with an internal receptor in the catalytic domain of Factor
XX VII (FVII) defined by the residues Leu263, Pro264, Glu265, Phe268,
XX Ser269, Tyr357 and Arg353 or a ligand defined by residues Cys98-Cys102 of
XX the epidermal growth factor-2 (EGF-2) domain of FVIIa/tissue factor (TF)
XX complex, with the exclusion of the peptide from amino acids 82-128 of
XX FVII. The compounds can be used to prevent the formation of a functional
XX FVIIa/TF complex, so can be used to combat or prevent blood clotting
XX disorders, e.g. thrombosis (particularly vascular thrombosis or deep vein
XX thrombosis), acute myocardial infarction, restenosis, angina, restenosis,
XX cerebrovascular disease, peripheral arterial occlusive disease,
XX hypercoagulability or pulmonary embolism. They can also be used to
XX prevent the occurrence of blood clotting disorders caused by e.g.
XX grafting surgery, vessel wall potency restoration or sepsis

XX Sequence 10 AA;

Query Match 42.6%; Score 29; DB 2; Length 10;

Best Local Similarity 62.5%; Pred. No. 5.6e+02;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKYLGEEYV 9
|:|:|:|:|
DB 2 EYRGGEQY 9

RESULT 15

```

AAV04647
ID AAV04647 standard; peptide; 10 AA.
XX
XX AAV04647;
AC
XX
XX 22-JUN-1999 (first entry)
DT
XX
XX Factor IXa/Xa catalytic domain-interacting peptide #23.
DE
XX
XX Receptor; catalytic domain; Factor IXa; Factor Xa; tissue factor; angina;
KM blood clotting disorder; thrombosis; restenosis; myocardial infarction;
KM rectosure; cerebrovascular disease; hypercoagulability; anticoagulant;
KM peripheral arterial occlusive disease; pulmonary embolism; cyclic.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "peptide is cyclic due to a lactam bond between
FT the side chains of residues 1 and 10"
FT 10
FT /note= "peptide is cyclic due to a lactam bond between
FT the side chains of residues 1 and 10"
FT
FT
XX WO9913062-A1.
XX
XX 18-MAR-1999.
XX
XX 08-SEP-1998; 98WO-GB002700.
XX
XX 09-SEP-1997; 97GB-00019157.
XX
XX (NYCO-) NYCOMED IMAGING AS.
XX (MATT/) MATTHEWS D P.
XX
XX Sakariassen KS, Fischer PM;
XX
XX WPI; 1999-215061/18.
XX
XX New anticoagulant compounds for treating blood clotting disorder capable
XX of interacting with internal receptor.
XX
XX Claim 10; Page 38; 50pp; English.
XX
XX Peptides AAV04625-Y04647 represent claimed compounds which are capable of
XX interacting with an internal receptor in the catalytic domain of Factor
XX IXa (FIXa) or Factor X (FX) defined by the residues Ile290, Ala291,
XX Asp292, Tyr293, Thr294, Glu374 and Phe378 of FIXa, and Leu300, Pro301,
XX Glu302, Tyr303, Ala306, Lys385 and Phe389 of FXa, or the ligand defined
XX by residues Cys95-Cys99 of FIXa or Cys96-Cys100 of FXa. The compounds can
XX be used to prevent the formation of a functional FVIIa/FIXa or
XX FVIIa/FXa complex, so can be used to combat or prevent blood clotting
XX disorders, e.g. thrombosis (particularly vascular thrombosis or deep vein
XX thrombosis), acute myocardial infarction, restenosis, angina, rectosure,
XX cerebrovascular disease, peripheral arterial occlusive disease,
XX hypercoagulability or pulmonary embolism. They can also be used to
XX prevent the occurrence of blood clotting disorders caused by e.g.
XX grafting surgery, vessel wall potency restoration or sepsis
XX
XX
XX Sequence 10 AA;
SQ
Query Match 42.6%; Score 29; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 5.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 2 EKYLGEEY 9
|:| | | |
Db 2 EYGGGEY 9

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 14:26:15 ; Search time 42 Seconds
(without alignments)
23.106 Million cell updates/sec

Title: US-10-612-162A-4

Perfect score: 68

Sequence: 1 YEKYLGEYKAV 13

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 143084

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/1aa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/1aa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfiles1.pep:*

SUMMARIES

Result No	Score	Query Match	Length	ID	Description
1	46	67.6	12	US-09-462-118-22	Sequence 22, Appl
2	29	42.6	12	US-07-954-213-24	Sequence 24, Appl
3	28	41.2	11	US-10-053-485-21	Sequence 21, Appl
4	28	41.2	12	US-09-462-118-21	Sequence 21, Appl
5	27	39.7	10	US-09-187-859-1150	Sequence 1150, Ap
6	27	39.7	10	US-09-839-542B-1150	Sequence 1150, Ap
7	27	39.7	11	US-08-082-844-8	Sequence 8, Appl
8	27	39.7	11	PCT-US94-07040-8	Sequence 8, Appl
9	27	39.7	12	US-08-728-742A-41	Sequence 41, Appl
10	27	39.7	12	US-08-728-742A-68	Sequence 68, Appl
11	26	38.2	9	US-09-171-654-65	Sequence 65, Appl
12	26	38.2	9	US-09-171-654-66	Sequence 66, Appl
13	26	38.2	10	US-09-755-630B-185	Sequence 185, Appl
14	26	38.2	12	US-07-954-213-11	Sequence 11, Appl
15	26	38.2	12	US-07-954-213-17	Sequence 17, Appl
16	26	38.2	12	US-07-954-213-18	Sequence 18, Appl
17	26	38.2	12	US-07-954-213-19	Sequence 19, Appl
18	26	38.2	12	US-07-954-213-20	Sequence 20, Appl
19	26	38.2	12	US-07-954-213-21	Sequence 21, Appl
20	26	38.2	12	US-07-954-213-22	Sequence 22, Appl
21	26	38.2	12	US-07-954-213-23	Sequence 23, Appl
22	26	38.2	12	US-08-196-989B-6	Sequence 6, Appl
23	26	38.2	12	US-08-760-935-6	Sequence 6, Appl
24	26	38.2	12	US-09-225-024-6	Sequence 6, Appl
25	25	36.8	8	US-09-187-859-1102	Sequence 1102, Ap
26	25	36.8	8	US-09-187-859-1230	Sequence 1230, Ap
27	25	36.8	8	US-09-839-542B-1102	Sequence 1102, Ap

28	25	36.8	8	US-09-839-542B-1230	Sequence 1230, Ap
29	25	36.8	10	US-09-187-859-1104	Sequence 1104, Ap
30	25	36.8	10	US-09-187-859-1192	Sequence 1192, Ap
31	25	36.8	10	US-09-187-859-1232	Sequence 1232, Ap
32	25	36.8	10	US-09-187-859-2361	Sequence 2361, Ap
33	25	36.8	10	US-09-839-542B-1104	Sequence 1104, Ap
34	25	36.8	10	US-09-839-542B-1192	Sequence 1192, Ap
35	25	36.8	10	US-09-839-542B-1232	Sequence 1232, Ap
36	25	36.8	10	US-09-839-542B-2361	Sequence 2361, Ap
37	25	36.8	12	US-09-091-071-8	Sequence 8, Appl
38	24	35.3	9	US-08-266-514-30	Sequence 30, Appl
39	24	35.3	9	US-08-654-604-30	Sequence 30, Appl
40	24	35.3	9	US-08-341-018-40	Sequence 40, Appl
41	24	35.3	9	US-08-470-335-216	Sequence 216, Appl
42	24	35.3	9	US-08-470-335-216	Sequence 216, Appl
43	24	35.3	9	US-08-467-602-410	Sequence 410, Appl
44	24	35.3	9	US-08-411-295F-35	Sequence 35, Appl
45	24	35.3	9	US-08-411-295F-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-09-462-118-22
; Sequence 22, Application US/09462118
; Patent No. 6610833
; GENERAL INFORMATION:
; APPLICANT: Rodman, Toby C.
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies
; FILE REFERENCE: 4436/1C074-US1
; CURRENT APPLICATION NUMBER: US/09/462,118
; CURRENT FILING DATE: 1999-12-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
US-09-462-118-22

Query Match 67.6%; Score 46; DB 4; Length 12;
Best Local Similarity 80.0%; Pred. No. 0.089;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYLGEYKAV 10
DB 2 YEKYLGPQYV 11

RESULT 2
US-07-954-213-24
; Sequence 24, Application US/07954213
; Patent No. 5387504
; GENERAL INFORMATION:
; APPLICANT: Mumford, Richard A.
; APPLICANT: Lark, Michael W.
; APPLICANT: Bayne, Ellen B.K.
; APPLICANT: Hoerner, Lori A.
; TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AND ASSAY SYSTEM
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESS: Merck & Co., Inc.
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/954,213
FILING DATE: 19920930
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W. III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 18842
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
TELEFAX: (908) 594-3905
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-954-213-24

Query Match 42.6%; Score 29; DB 1; Length 12;
Best Local Similarity 55.6%; Pred. No. 84;
Matches 5; Conservative 2; Mismatches 2; Gaps 0;

OY 4 YLGEYVKA 12
| | | | |
Db 1 YTGEDVFDA 9

RESULT 3
US-10-053-485-21
Sequence 21, Application US/10053485
Patent No. 6576896
GENERAL INFORMATION:
APPLICANT: Figeys, Daniel
APPLICANT: Aebbersold, Ruedi
TITLE OF INVENTION: ELECTROSMOTIC FLUIDIC DEVICE AND RELATED METHODS
FILE REFERENCE: UMOTL18617
CURRENT APPLICATION NUMBER: US/10/053,485
CURRENT FILING DATE: 2002-05-28
PRIOR APPLICATION NUMBER: US 09/209,880
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: US 60/069,398
PRIOR FILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn version 3.0
SEQ ID NO 21
LENGTH: 11
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-10-053-485-21

Query Match 41.2%; Score 28; DB 4; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 KYLGEYVKA 11
| | | | |
Db 3 KDLGEHFRK 11

RESULT 4
US-09-462-118-21
Sequence 21, Application US/09462118
Patent No. 6610833
GENERAL INFORMATION:
APPLICANT: Rodman, Toby C.
TITLE OF INVENTION: Monoclonal Human Natural Antibodies
FILE REFERENCE: 4436/1C074-US1
CURRENT APPLICATION NUMBER: US/09/462,118
CURRENT FILING DATE: 1999-12-18
NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21
LENGTH: 12
TYPE: PRT
ORGANISM: Human
US-09-462-118-21

Query Match 41.2%; Score 28; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEKYL 5
| | | | |
Db 8 YEKYL 12

RESULT 5
US-09-187-859-1150
Sequence 1150, Application US/09187859A
Patent No. 6358920
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Gouir, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100066.407C1
CURRENT APPLICATION NUMBER: US/09/187,859A
CURRENT FILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1150
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-09-187-859-1150

Query Match 39.7%; Score 27; DB 3; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 EKYLGEYVKA 11
| | | | |
Db 1 EFKLEBYTK 10

RESULT 6
US-09-839-542B-1150
Sequence 1150, Application US/09839542B
Patent No. 6569996
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Symonds, James Matthew
APPLICANT: Gouir, Barbara J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
FILE REFERENCE: 100066.407D1
CURRENT APPLICATION NUMBER: US/09/839,542B
CURRENT FILING DATE: 2001-04-20
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1150
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Representative cyclic modulating agent based on
OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence
US-09-839-542B-1150

Query Match 39.7%; Score 27; DB 4; Length 10;

Best Local Similarity 60.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EKYLGEEYK 11
| : | | | |
Db 1 EPLLLEBYTK 10

RESULT 7

US-08-082-844-8
Sequence 8, Application US/08082844
Patent No. 5443978

GENERAL INFORMATION:

APPLICANT: Ellenberger, Suzanne R.
APPLICANT: Peiser, Galen D.
APPLICANT: Bell, Russell N.
APPLICANT: Husey Jr., Charles E.
APPLICANT: Shattuck-Bidens, Donna M.
APPLICANT: Swedlund, Bradley D.
TITLE OF INVENTION: Chrysanthenyl Diphosphate Synthase,
TITLE OF INVENTION: Corresponding Genes and Use in Pyrethrin Synthesis
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: United States of America
ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,844
FILING DATE: 19930625

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 22-90A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..11
OTHER INFORMATION: /label=Xaa
OTHER INFORMATION: /note="Xaa equals residues which could not be
OTHER INFORMATION: identified with certainty."
US-08-082-844-8

Query Match 39.7%; Score 27; DB 1; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEKYLGEEY 9
| | | | |
Db 3 YEDYESNEY 11

RESULT 8
PCT-US94-07040-8
Sequence 8, Application PC/TUS9407040

GENERAL INFORMATION:

APPLICANT: Ellenberger, Suzanne R.
APPLICANT: Peiser, Galen D.
APPLICANT: Bell, Russell N.
APPLICANT: Husey Jr., Charles E.
APPLICANT: Shattuck-Bidens, Donna M.
APPLICANT: Swedlund, Bradley D.
TITLE OF INVENTION: Chrysanthenyl Diphosphate Synthase,
TITLE OF INVENTION: Corresponding Genes and Use in Pyrethrin Synthesis
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: United States of America
ZIP: 80303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07040
FILING DATE: 21-JUNE-1994

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/082,844
FILING DATE: 25-JUNE-1993
ATTORNEY/AGENT INFORMATION:

NAME: Caruthers, Jennie M.
REGISTRATION NUMBER: 34,464
REFERENCE/DOCKET NUMBER: 22-90A PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..11
OTHER INFORMATION: /label=Xaa
OTHER INFORMATION: /note="Xaa equals residues which could not be
OTHER INFORMATION: identified with certainty."
PCT-US94-07040-8

Query Match 39.7%; Score 27; DB 5; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 YEKYLGEEY 9
| | | | |
Db 3 YEDYESNEY 11

RESULT 9

US-08-728-742A-41
Sequence 41, Application US/08728742A
Patent No. 6579695

GENERAL INFORMATION:

APPLICANT: Ralph H. Lambaot, Amy M. Gehring, Ralph Reid and Christopher T. Wals
TITLE OF INVENTION: PHOSPHOPANTETHEINYL TRANSFERASES AND USES THEREOF
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESSES:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston

STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,742A
FILING DATE: October 11, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/005,152
FILING DATE: October 13, 1995
APPLICATION NUMBER: 60/021,650
FILING DATE: July 12, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Amy B. Mandragouras
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: HMI-015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-728-742A-41

Query Match 39.7%; Score 27; DB 4; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 EBYKAV 13
| : | : | :
Db 5 ESYIKAI 11

RESULT 10
US-08-728-742A-68
; Sequence 68, Application US/08728742A
; Patent No. 6579695
; GENERAL INFORMATION:
; APPLICANT: Ralph H. Lambaot, Amy M. Gehring, Ralph Reid and Christopher T. Wales
; TITLE OF INVENTION: PHOSPHOPANTHETHEINYL TRANSFERASES AND USES THEREOF
; NUMBER OF SEQUENCES: 78
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,742A
; FILING DATE: October 11, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,152
; FILING DATE: October 13, 1995
; APPLICATION NUMBER: 60/021,650
; FILING DATE: July 12, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy B. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: HMI-015

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: Internal
US-08-728-742A-68

Query Match 39.7%; Score 27; DB 4; Length 12;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 EBYKAV 13
| : | : | :
Db 5 ESYIKAI 11

RESULT 11
US-09-171-654-65
; Sequence 65, Application US/09171654A
; Patent No. 6239107
; GENERAL INFORMATION:
; APPLICANT: FRIDKIN, Matityahu
; TITLE OF INVENTION: CONJUGATES OF LIPOPHILIC MOETIES AND FRAGMENTS OF
; FILE REFERENCE: GOZES-4
; CURRENT APPLICATION NUMBER: US/09/171,654A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: PCT/IL97/00129
; EARLIER FILING DATE: 1997-04-18
; EARLIER APPLICATION NUMBER: IL 118003
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 65
; LENGTH: 9
; TYPE: PPT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Artificial
; OTHER INFORMATION: The N-terminus is modified with a stearyl moiety;
; OTHER INFORMATION: the C-terminal residue is amidated;
; OTHER INFORMATION: residue 5 is aminocaproic acid.
US-09-171-654-65

Query Match 38.2%; Score 26; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 4.1e+05;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 EBYLGEYV 10
: | | : | :
Db 1 KXYLKKYL 9

RESULT 12
US-09-171-654-66
; Sequence 66, Application US/09171654A
; Patent No. 6239107
; GENERAL INFORMATION:
; APPLICANT: GOZES, Illana
; APPLICANT: FRIDKIN, Matityahu
; TITLE OF INVENTION: CONJUGATES OF LIPOPHILIC MOETIES AND FRAGMENTS OF
; FILE REFERENCE: GOZES-4
; CURRENT APPLICATION NUMBER: US/09/171,654A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: PCT/IL97/00129

EARLIER FILING DATE: 1997-04-18
EARLIER APPLICATION NUMBER: IL 118003
EARLIER FILING DATE: 1996-04-23
NUMBER OF SEQ ID NOS: 80
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 66
LENGTH: 9
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Artificial
FEATURE:
OTHER INFORMATION: The N-terminus is modified with a stearyl moiety;
OTHER INFORMATION: the C-terminal residue is amidated;
OTHER INFORMATION: residue 5 is amino lauric acid.
US-09-171-654-66

Query Match 38.2%; Score 26; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 4.1e+05;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKYLGEEYV 10
DB 1 KKYLKXKYL 9

RESULT 13
US-09-755-630B-185
Sequence 185, Application US/09755630B
Patent No. 6639054
GENERAL INFORMATION:
APPLICANT: ALIBHAI, MURTAZA F.
APPLICANT: ASTWOOD, JAMES D.
APPLICANT: SAMPSON, HUGH A.
APPLICANT: MCHESTER, CHARLES A.
TITLE OF INVENTION: PREPARATION OF DEALKERGENIZED PROTEINS AND PERMUTINS
FILE REFERENCE: 11899.0217.NPUS00 (MOBT217)
CURRENT APPLICATION NUMBER: US/09/755,630B
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,669
PRIOR FILING DATE: 2000-01-06
NUMBER OF SEQ ID NOS: 295
SOFTWARE: Patentin version 3.0
SEQ ID NO 185
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic polypeptide
US-09-755-630B-185

Query Match 38.2%; Score 26; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKYLGEEYV 11
DB 1 EKYTABQCAK 10

RESULT 14
US-07-954-213-11
Sequence 11, Application US/07954213
Patent No. 5387504
GENERAL INFORMATION:
APPLICANT: Mumford, Richard A.
APPLICANT: Lark, Michael W.
APPLICANT: Bayne, Ellen B.K.
APPLICANT: Hoerner, Lori A.
TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AND ASSAY SYSTEM
TITLE OF INVENTION: FOR DETECTING STROMELYSIN CLEAVAGE PRODUCTS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:

ADDRESSER: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/954,213
FILING DATE: 19920930
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W. III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 18842
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-954-213-11

Query Match 38.2%; Score 26; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YLGEDEV 10
DB 1 YTGEDFV 7

RESULT 15
US-07-954-213-17
Sequence 17, Application US/07954213
Patent No. 5387504
GENERAL INFORMATION:
APPLICANT: Mumford, Richard A.
APPLICANT: Lark, Michael W.
APPLICANT: Bayne, Ellen B.K.
APPLICANT: Hoerner, Lori A.
TITLE OF INVENTION: MONOSPECIFIC ANTIBODIES AND ASSAY SYSTEM
TITLE OF INVENTION: FOR DETECTING STROMELYSIN CLEAVAGE PRODUCTS
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSER: Merck & Co., Inc.
STREET: 126 E. Lincoln Avenue
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/954,213
FILING DATE: 19920930
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W. III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 18842
TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-954-213-17

Query Match 38.2%; Score 26; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 YLGEERYV 10
| | | | |
Db 1 YTGEDFV 7

Search completed: November 1, 2005, 14:41:34
Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 14:32:10 ; Search time 162 Seconds

(without alignments)
33.547 Million cell updates/sec

Title: US-10-612-162a-4

Perfect score: 68

Sequence: 1 YEKYLGEYVKAV 13

Scoring table: BLOSUM62

Searched: 1865214 seqs, 418043040 residues

Total number of hits satisfying chosen parameters: 285352

Minimum DB seq length: 0

Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09C_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*
22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	13	US-10-612-162-4	Sequence 4, Appli
2	46	67.6	12	US-10-247-946-22	Sequence 22, Appli
3	46	67.6	12	US-10-251-526-22	Sequence 22, Appli
4	43	63.2	8	US-10-801-990-182	Sequence 182, App
5	43	63.2	12	US-10-700-330-241	Sequence 241, App
6	37	54.4	12	US-10-801-990-31	Sequence 31, Appli
7	34	50.0	12	US-10-033-741-41	Sequence 41, Appli
8	34	50.0	12	US-10-033-662-41	Sequence 41, Appli
9	30	44.1	13	US-10-823-253-3	Sequence 3, Appli
10	30	44.1	13	US-10-823-810-3	Sequence 3, Appli
11	28	41.2	9	US-10-482-284A-11	Sequence 11, Appli

12	28	41.2	9	US-10-482-284A-25	Sequence 25, Appli
13	28	41.2	9	US-10-482-284A-28	Sequence 28, Appli
14	28	41.2	9	US-10-505-929-8	Sequence 8, Appli
15	28	41.2	10	US-10-464-576-1	Sequence 1, Appli
16	28	41.2	11	US-10-053-485-21	Sequence 21, Appli
17	28	41.2	12	US-09-991-800-2	Sequence 2, Appli
18	28	41.2	12	US-10-247-946-21	Sequence 21, Appli
19	28	41.2	12	US-10-251-526-21	Sequence 21, Appli
20	27	39.7	10	US-10-006-869-1150	Sequence 1150, Ap
21	27	39.7	10	US-10-395-032-1150	Sequence 1150, Ap
22	27	39.7	10	US-11-004-107-1150	Sequence 1150, Ap
23	26	38.2	9	US-10-948-707-221	Sequence 221, App
24	26	38.2	10	US-09-572-404B-976	Sequence 976, App
25	26	38.2	10	US-09-755-630A-185	Sequence 185, App
26	26	38.2	10	US-10-209-372-36	Sequence 36, Appli
27	26	38.2	10	US-10-658-180-185	Sequence 185, Appli
28	26	38.2	11	US-10-239-313A-76	Sequence 76, Appli
29	26	38.2	13	US-10-280-139-11	Sequence 11, Appli
30	25	36.8	8	US-10-006-869-1102	Sequence 1102, Ap
31	25	36.8	8	US-10-006-869-1230	Sequence 1230, Ap
32	25	36.8	8	US-10-395-032-1102	Sequence 1102, Ap
33	25	36.8	8	US-10-395-032-1230	Sequence 1230, Ap
34	25	36.8	8	US-11-004-107-1102	Sequence 1102, Ap
35	25	36.8	8	US-11-004-107-1230	Sequence 1230, Ap
36	25	36.8	9	US-10-119-536A-109	Sequence 109, App
37	25	36.8	9	US-10-128-520-29	Sequence 29, Appli
38	25	36.8	9	US-10-275-652-50	Sequence 50, Appli
39	25	36.8	9	US-10-948-707-682	Sequence 682, App
40	25	36.8	10	US-09-840-277-128	Sequence 128, App
41	25	36.8	10	US-10-006-869-1104	Sequence 1104, Ap
42	25	36.8	10	US-10-006-869-1192	Sequence 1192, Ap
43	25	36.8	10	US-10-006-869-1232	Sequence 1232, Ap
44	25	36.8	10	US-10-006-869-2361	Sequence 2361, Ap
45	25	36.8	10	US-10-395-032-1104	Sequence 1104, Ap

ALIGNMENTS

RESULT 1
US-10-612-162-4
; Sequence 4, Application US/10612162
; Publication No. US20040014145A1
; GENERAL INFORMATION:
; APPLICANT: Dade Behring Marburg GmbH
; TITLE OF INVENTION: Carbohydrate deficient transferrin (CDT) -specific
; FILE REFERENCE: 2002/B001
; CURRENT APPLICATION NUMBER: US/10/612,162
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 10230550.1
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: 03011334.4
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-612-162-4

Query Match 100.0%; Score 68; DB 15; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.00016;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 YEKYLGEYVKAV 13
| | | | | | | | | | | | |
Db 1 YEKYLGEYVKAV 13

RESULT 2
US-10-247-946-22

```
; Sequence 22, Application US/10247946
; Publication No. US20030144485A1
; GENERAL INFORMATION:
; APPLICANT: Rodman, Toby C.
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies
; FILE REFERENCE: 4436/1C074-US1
; CURRENT APPLICATION NUMBER: US/10/247,946
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/462,118
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
US-10-247-946-22
```

```
Query Match      67.6%; Score 46; DB 14; Length 12;
Best Local Similarity 80.0%; Pred. No. 0.72;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 YEKYLGEERYV 10
        |||||:
Db      2 YEKYLGPOYV 11
```

RESULT 3

```
US-10-251-526-22
; Sequence 22, Application US/10251526
; Publication No. US20030144486A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Rodman, Toby C.
; TITLE OF INVENTION: Monoclonal Human Natural Antibodies
; FILE REFERENCE: 4436/1C074-US1
; CURRENT APPLICATION NUMBER: US/10/251,526
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US/09/462,118
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Human
US-10-251-526-22
```

```
Query Match      67.6%; Score 46; DB 14; Length 12;
Best Local Similarity 80.0%; Pred. No. 0.72;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 YEKYLGEERYV 10
        |||||:
Db      2 YEKYLGPOYV 11
```

RESULT 4

```
US-10-801-990-182
; Sequence 182, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Kantor, Aaron B.
; APPLICANT: Schulman, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121
; CURRENT APPLICATION NUMBER: US/10/801,990
; PRIOR FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.2
US-10-801-990-182
```

```
Query Match      54.4%; Score 37; DB 17; Length 12;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-182
```

```
Query Match      63.2%; Score 43; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      4 YLGEERYK 11
        |||||
Db      1 YLGEERYK 8
```

RESULT 5

```
US-10-700-330-241
; Sequence 241, Application US/10700330
; Publication No. US20040203022A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Herath, Mudiyanselage Alhula Chandrasiri Herath
; APPLICANT: Page, Martin John
; TITLE OF INVENTION: Proteins and Genes for Diagnosis And Treatment of ErbB2-Related C
; FILE REFERENCE: 2543-1-031
; CURRENT APPLICATION NUMBER: US/10/700,330
; PRIOR FILING DATE: 2003-11-03
; PRIOR APPLICATION NUMBER: GB 0110886.9
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: GB 0128183.1
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 241
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-700-330-241
```

```
Query Match      63.2%; Score 43; DB 16; Length 12;
Best Local Similarity 54.5%; Pred. No. 2.3;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 YEKYLGEERYK 11
        |||||:
Db      2 YDSYLGDDYVR 12
```

RESULT 6

```
US-10-801-990-31
; Sequence 31, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Kantor, Aaron B.
; APPLICANT: Schulman, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121
; CURRENT APPLICATION NUMBER: US/10/801,990
; PRIOR FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 31
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-31
```

```
Query Match      54.4%; Score 37; DB 17; Length 12;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      4 YLGEERYKAV 13
```

Db 2 YLGEYVTAI 11

RESULT 7
US-10-033-741-41
Sequence 41, Application US/10033741
Publication No. US2003009640A1
GENERAL INFORMATION:
APPLICANT: Herman, et al.
TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of Vasc
FILE REFERENCE: 9195-079
CURRENT APPLICATION NUMBER: US/10/033,741
CURRENT FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.0
SEQ ID NO 41
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-10-033-741-41

Query Match 50.0%; Score 34; DB 14; Length 12;
Best Local Similarity 60.0%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YLGEYVTAKV 13
||| |||
Db 2 YLGHSTVTAI 11

RESULT 8
US-10-033-662-41
Sequence 41, Application US/10033662
Publication No. US20030092197A1
GENERAL INFORMATION:
APPLICANT: Herman, et al.
TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of Card
FILE REFERENCE: 9195-081
CURRENT APPLICATION NUMBER: US/10/033,662
CURRENT FILING DATE: 2001-12-27
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn version 3.0
SEQ ID NO 41
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-10-033-662-41

Query Match 50.0%; Score 34; DB 14; Length 12;
Best Local Similarity 60.0%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YLGEYVTAKV 13
||| |||
Db 2 YLGHSTVTAI 11

RESULT 9
US-10-823-253-3
Sequence 3, Application US/10823253
Publication No. US20050002934A1
GENERAL INFORMATION:
APPLICANT: Reed, Jennifer
TITLE OF INVENTION: RECOMBINANT IL-9 ANTIBODIES AND USES THEREOF
FILE REFERENCE: 10271-112-999
CURRENT APPLICATION NUMBER: US/10/823,253
CURRENT FILING DATE: 2004-04-12
PRIOR APPLICATION NUMBER: 60/462,259
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 60/477,797

PRIOR FILING DATE: 2003-06-10
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-823-253-3

Query Match 44.1%; Score 30; DB 17; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YLGEYTVK 11
||| |||
Db 3 YYGSDYVK 10

RESULT 10
US-10-823-810-3
Sequence 3, Application US/10823810
Publication No. US20050147607A1
GENERAL INFORMATION:
APPLICANT: Reed, Jennifer
TITLE OF INVENTION: METHODS OF PREVENTING OR TREATING RESPIRATORY CONDITIONS
FILE REFERENCE: 10271-113-999
CURRENT APPLICATION NUMBER: US/10/823,810
CURRENT FILING DATE: 2004-04-12
PRIOR APPLICATION NUMBER: 60/462,307
PRIOR FILING DATE: 2003-04-11
PRIOR APPLICATION NUMBER: 60/477,801
PRIOR FILING DATE: 2003-06-10
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-823-810-3

Query Match 44.1%; Score 30; DB 18; Length 13;
Best Local Similarity 62.5%; Pred. No. 3.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 YLGEYTVK 11
||| |||
Db 3 YYGSDYVK 10

RESULT 11
US-10-482-284A-11
Sequence 11, Application US/10482284A
Publication No. US20050019344A1
GENERAL INFORMATION:
APPLICANT: KHANNA, Rajiv
APPLICANT: ELKINGTON, Rebecca A.
APPLICANT: WALKER, Susan J.
TITLE OF INVENTION: Novel human cytomegalovirus (HCMV) cytotoxic T cell epitopes, ct
TITLE OF INVENTION: polypeptides, compositions comprising same and diagnostic and ct
FILE REFERENCE: 47-203
CURRENT APPLICATION NUMBER: US/10/482,284A
CURRENT FILING DATE: 2003-12-29
PRIOR APPLICATION NUMBER: AU PR5931
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 318
SOFTWARE: PatentIn version 3.2
SEQ ID NO 11
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human cytomegalovirus pp65 C

OTHER INFORMATION: epitope peptide
US-10-482-284A-11

Query Match 41.2%; Score 28; DB 17; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 5 LGEEYVK 11
:|:|:|
Db 2 IGDQYVK 8

RESULT 12

US-10-482-284A-25
Sequence 25, Application US/10482284A
Publication No. US20050019344A1
GENERAL INFORMATION:
APPLICANT: KHANNA, Rajiv
APPLICANT: ELKINGTON, Rebecca A.
APPLICANT: WALKER, Susan J.
TITLE OF INVENTION: Novel human cytomagalovirus (HCMV) cytotoxic T cell epitopes,
TITLE OF INVENTION: polypeptides, compositions comprising same and diagnostic and th
FILE REFERENCE: 47-203
CURRENT APPLICATION NUMBER: US/10/482,284A
PRIOR FILING DATE: 2003-12-29
PRIOR APPLICATION NUMBER: AU PR5931
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 318
SOFTWARE: Patentin version 3.2
SEQ ID NO 25
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human cytomagalovirus pp65 C
US-10-482-284A-25

Query Match 41.2%; Score 28; DB 17; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 5 LGEEYVK 11
:|:|:|
Db 1 IGDQYVK 7

RESULT 13

US-10-482-284A-28
Sequence 28, Application US/10482284A
Publication No. US20050019344A1
GENERAL INFORMATION:
APPLICANT: KHANNA, Rajiv
APPLICANT: ELKINGTON, Rebecca A.
APPLICANT: WALKER, Susan J.
TITLE OF INVENTION: Novel human cytomagalovirus (HCMV) cytotoxic T cell epitopes,
TITLE OF INVENTION: polypeptides, compositions comprising same and diagnostic and th
FILE REFERENCE: 47-203
CURRENT APPLICATION NUMBER: US/10/482,284A
PRIOR FILING DATE: 2003-12-29
PRIOR APPLICATION NUMBER: AU PR5931
PRIOR FILING DATE: 2001-06-26
NUMBER OF SEQ ID NOS: 318
SOFTWARE: Patentin version 3.2
SEQ ID NO 28
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human cytomagalovirus pp65 C
US-10-482-284A-28

US-10-482-284A-28

Query Match 41.2%; Score 28; DB 17; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 5 LGEEYVK 11
:|:|:|
Db 3 IGDQYVK 9

RESULT 14

US-10-505-929-8
Sequence 8, Application US/10505929
Publication No. US20050221381A1
GENERAL INFORMATION:
APPLICANT: KLADE, CHRISTOF
APPLICANT: SCHALICH, JULIANE
APPLICANT: VYTYTSKA, ORESTA
APPLICANT: AICHINGER, GERALD
APPLICANT: OTAVA, ALEXANDER
APPLICANT: MATTER, FRANK
TITLE OF INVENTION: METHOD FOR ISOLATING LIGANDS
FILE REFERENCE: SONN: 055US
CURRENT APPLICATION NUMBER: US/10/505,929
PRIOR FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: PCT/EP03/02005
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: A 316/2002
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: A 1376/2002
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 584
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 9
TYPE: PRT
ORGANISM: Cytomegalovirus
US-10-505-929-8

Query Match 41.2%; Score 28; DB 18; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 5 LGEEYVK 11
:|:|:|
Db 2 IGDQYVK 8

RESULT 15

US-10-464-576-1
Sequence 1, Application US/10464576
Publication No. US20040188603A1
GENERAL INFORMATION:
APPLICANT: Bateman, Robert H
APPLICANT: Bateman, Robert H
APPLICANT: Langridge, James I
APPLICANT: McKenna, Therese
APPLICANT: Richardson, Keith
TITLE OF INVENTION: Method of Mass Spectrometry and a Mass Spectrometer
FILE REFERENCE: deH055
CURRENT APPLICATION NUMBER: US/10/464,576
PRIOR FILING DATE: 2003-06-19
PRIOR APPLICATION NUMBER: uk 0217146.0
PRIOR FILING DATE: 2002-07-24
PRIOR APPLICATION NUMBER: uk 0218719.3
PRIOR FILING DATE: 2002-08-12
PRIOR APPLICATION NUMBER: uk 0221914.5
PRIOR FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: uk 0305796.5
PRIOR FILING DATE: 2003-03-13
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.2
US-10-464-576-1

```

; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: unknown
; FEATURE:
; OTHER INFORMATION: Chemically synthesized
US-10-464-576-1

```

```

Query Match      41.2%; Score 28; DB 16; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      3 KYLGEEYVK 11
        | ||||:|
Db      2 KDLGSEHFK 10

```

```

Search completed: November 1, 2005, 14:46:02
Job time : 163 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 14:21:39 ; Search time 38 Seconds
(without alignments)
32.916 Million cell updates/sec

Title: US-10-612-162a-4

Perfect score: 68

Sequence: 1 YEKYLGEYKAV 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1828

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR 79 : *

1: PIR1 : *

2: PIR2 : *

3: PIR3 : *

4: PIR4 : *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	26	38.2	12	2 PH0746	T-cell receptor be
2	26	38.2	12	2 PH0771	T-cell receptor be
3	26	38.2	13	2 PH1479	T-cell receptor be
4	23	33.8	9	2 PH0108	late G1-69 protein
5	23	33.8	12	2 S25056	Ig heavy chain - m
6	20	29.4	10	2 PT0215	T-cell receptor be
7	20	29.4	11	2 PT0214	T-cell receptor be
8	20	29.4	13	2 S47359	T-cell antigen rec
9	20	29.4	13	2 S47361	T-cell antigen rec
10	20	29.4	13	2 S47365	T-cell antigen rec
11	20	29.4	13	2 S47368	T-cell antigen rec
12	20	29.4	13	2 S47372	T-cell antigen rec
13	20	29.4	13	2 S47383	T-cell antigen rec
14	20	29.4	13	2 S47384	T-cell antigen rec
15	20	29.4	13	2 S47374	T-cell antigen rec
16	19	27.9	11	2 A58838	hemolysin - Porphy
17	19	27.9	13	2 E60396	antigen 7H8/2 - ma
18	18	26.5	9	2 S70334	endospore protein,
19	18	26.5	9	2 PT0324	Ig heavy chain CRD
20	18	26.5	10	2 S62880	polygalacturonase
21	18	26.5	10	2 A24867	scyllothein I - s
22	18	26.5	11	2 S68392	H+-transporting tw
23	18	26.5	11	2 I60434	68kDa neurofilamen
24	18	26.5	12	2 C49315	urease (EC 3.5.1.5
25	18	26.5	13	2 A32734	enkephalin precurs
26	18	26.5	13	2 G44644	neurotoxin-associa
27	17	25.0	6	2 S11556	hydrogensulfite re
28	17	25.0	8	2 PN0043	phosphatidylethano
29	17	25.0	9	2 PT0315	Ig heavy chain CRD

30	17	25.0	10	2 A13687	caerulein-like pep
31	17	25.0	11	2 B60769	Ig H2 chain - Pac1
32	17	25.0	12	2 S18722	mark protein - bee
33	17	25.0	12	2 PH1466	T-cell receptor be
34	17	25.0	13	2 PT0263	Ig heavy chain CRD
35	17	25.0	13	2 PT0290	Ig heavy chain CRD
36	17	25.0	13	2 S47373	T-cell antigen rec
37	16	23.5	7	2 A38081	amine oxidase (cop
38	16	23.5	9	2 A41978	callifMRamide 5 -
39	16	23.5	9	2 F41978	callifMRamide 6 -
40	16	23.5	9	2 G41978	callifMRamide 7 -
41	16	23.5	9	2 A37027	macrophage chemot
42	16	23.5	11	2 PH1375	T antigen variant
43	16	23.5	12	2 PH1308	Ig heavy chain DJ
44	16	23.5	12	2 S23168	Z protein - guinea
45	16	23.5	12	2 T46794	hypothetical prote

ALIGNMENTS

RESULT 1

PH0746 T-cell receptor beta chain (B28) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999

C:Accession: PH0746

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-

allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0746

A:Molecule type: mRNA

A:Residues: 1-12 <CDS>

A:Cross-references: EMBL:X60837; NID:950098; PIDN:CAA43230.1; PID:950099

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match 38.2% Score 26; DB 2; Length 12;

Best Local Similarity 66.7% Pred. No. 2.9e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYL G 6

DB 7 YEQYFG 12

RESULT 2

PH0771 T-cell receptor beta chain (PB5.1.1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999

C:Accession: PH0771

R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-

allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0771

A:Molecule type: mRNA

A:Residues: 1-12 <CDS>

A:Cross-references: EMBL:X60865; NID:953624; PIDN:CAA43255.1; PID:953625

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match 38.2% Score 26; DB 2; Length 12;

Best Local Similarity 66.7% Pred. No. 2.9e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKYL G 6

DB 7 YEQYFG 12

RESULT 3
PH1479
T-cell receptor beta chain (clone A3/72.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
C:Accession: PH1479
R:Caanovaa, J.L.; Marilion, F.; Gounnier, H.; Barra, C.; Pannetier, C.; Regnault, A.; Kc
J. Exp. Med. 177, 811-820, 1993
A:Title: T cell receptor selection by and recognition of two class I major histocompatih
A:Reference number: PH1430; MUID:93171821; PMID:8436911
A:Accession: PH1479
A:Molecule type: mRNA
A:Residues: 1-13 <CAS>
A:Experimental source: cytolytic T-lymphocyte
C:Keywords: receptor; T-cell

Query Match 38.2%; Score 26; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 YEKYIG 6
||:|
Db 8 YEQYFG 13

RESULT 4
PH0108
late G1-69 protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH0108
R:Nikaido, T.; Bradley, D.W.; Pardee, A.B.
Exp. Cell Res. 192, 102-109, 1991
A:Title: Molecular cloning of transcripts that accumulate during the late G1 phase in cu
A:Reference number: PH0108; MUID:91078351; PMID:1984406
A:Accession: PH0108
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-9 <NTK>

Query Match 33.8%; Score 23; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GEY 9
|||
Db 6 GEY 9

RESULT 5
S25056
1g heavy chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 25-Feb-1994 #sequence_revision 01-Dec-1995 #text_change 20-Jun-2000
C:Accession: S25056
R:Jacob, J.; Kelsce, G.
submitted to the EMBL Data Library, July 1992
A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitropheny
A:Reference number: S25024
A:Accession: S25056
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-12 <TAC>
A:Cross-references: EMBL:X67386; NID:G50927; PIDN:CAA47798.1; PID:G1333920
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology
C:Keywords: heterotrimer; Immunoglobulin

Query Match 33.8%; Score 23; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 9.6e+02;
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 YEKYGEY 9
||:|
Db 3 YPYTGGSY 11

RESULT 6
PT0215
T-cell receptor beta chain V-J region (4-1-K.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C:Accession: PT0215
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restric
A:Reference number: PT0209; MUID:91217621; PMID:1902501
A:Accession: PT0215
A:Molecule type: mRNA
A:Residues: 1-10 <NAK>
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEKY 4
||:|
Db 6 YEQY 9

RESULT 7
PT0214
T-cell receptor beta chain V-J region (4-1-L.6) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C:Accession: PT0214
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restric
A:Reference number: PT0209; MUID:91217621; PMID:1902501
A:Accession: PT0214
A:Molecule type: mRNA
A:Residues: 1-11 <NAK>
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 YEKY 4
||:|
Db 7 YEQY 10

RESULT 8
S47359
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47359
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A:Reference number: S47355
A:Accession: S47359
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35683; NID:G527455; PIDN:CAA84752.1; PID:G527456
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEKY 4
||:|
Db 9 YEQY 12

RESULT 9

847361
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47361
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Status: preliminary
A:Accession: S47361
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:235685; NID:g527459; PIDN:CAA84754.1; PID:g527460
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEKY 4
||:|
Db 9 YEQY 12

RESULT 10

847365
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47365; S47375; S47379; S47396; S47397; S47398; S47355
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Status: preliminary
A:Accession: S47365
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:235690; NID:g527471; PIDN:CAA84759.1; PID:g527472; EMBL:235679;
A:Accession: S47375
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE2>
A:Cross-references: EMBL:235700; NID:g527493; PIDN:CAA84769.1; PID:g527494
A:Accession: S47379
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE3>
A:Cross-references: EMBL:235708; NID:g527509; PIDN:CAA84777.1; PID:g527510
A:Accession: S47396
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE4>
A:Cross-references: EMBL:235674; NID:g527527; PIDN:CAA84743.1; PID:g527528
A:Accession: S47397
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE5>
A:Cross-references: EMBL:235675; NID:g527529; PIDN:CAA84744.1; PID:g527530
A:Accession: S47398
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LE6>
A:Cross-references: EMBL:235676; NID:g527531; PIDN:CAA84745.1; PID:g527532
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEKY 4
||:|
Db 9 YEQY 12

RESULT 11

847368
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47368
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Status: preliminary
A:Accession: S47368
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:235693; NID:g527477; PIDN:CAA84762.1; PID:g527478
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEKY 4
||:|
Db 9 YEQY 12

RESULT 12

847372
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47372
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Status: preliminary
A:Accession: S47372
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:235697; NID:g527485; PIDN:CAA84766.1; PID:g527486
A:Accession: S47372
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:235697; NID:g527485; PIDN:CAA84766.1; PID:g527486
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 YEKY 4
||:|
Db 9 YEQY 12

RESULT 13

847383
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47383
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T
A:Reference number: S47355
A:Status: preliminary
A:Accession: S47383

Job time : 38 secs

A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35709; NID:G527513; PIDN:CAA84778.1; PID:G527514
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEXY 4
||:|
Db 9 YEQY 12

RESULT 14

S47384
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47384
R:Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A:Reference number: S47355
A:Accession: S47384
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35704; NID:G527501; PIDN:CAA84773.1; PID:G527502
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEXY 4
||:|
Db 9 YEQY 12

RESULT 15

S47374
T-cell antigen receptor VJ junction beta chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 25-Oct-1996 #text_change 05-Nov-1999
C:Accession: S47374; S47399; S47364
R:Lehner, P.J.
Submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c
A:Reference number: S47355
A:Accession: S47374
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35699; NID:G527491; PIDN:CAA84768.1; PID:G527492; EMBL:Z35689;
A:Accession: S47399
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <LEH>
A:Cross-references: EMBL:Z35677; NID:G527533; PIDN:CAA84746.1; PID:G527534
C:Keywords: T-cell receptor

Query Match 29.4%; Score 20; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 YEXY 4
||:|
Db 9 YEQY 12

Search completed: November 1, 2005, 14:32:40

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2005, 14:20:48 / Search time 172 Seconds
(without alignments)
38.704 Million cell updates/sec

Title: US-10-612-162a-4
Perfect score: 68
Sequence: 1 YEKYLGESEYKAV 13

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 4955

Minimum DB seq length: 0
Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 03:*
1: uniprot_prot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	41.2	10	2 Q7WUG1	Q7WUG1 pseudomons
2	26	38.2	12	1 S015_BACSU	P80863 bacillus su
3	23	33.8	13	2 Q50038	Q50038 mycobacteri
4	22	32.4	8	2 Q6BC29	Q6BC29 homo sapien
5	22	32.4	8	2 Q90ZV5	Q90ZV5 fulica leuc
6	21	30.9	10	2 Q6RTV4	Q6RTV4 carlia leuc
7	21	30.9	11	2 Q6T302	Q6T302 chlamydomon
8	21	30.9	11	2 Q6BLE0	Q6BLE0 pyritiglena 1
9	21	30.9	11	2 Q6BLE9	Q6BLE9 myrmotherul
10	21	30.9	13	1 TEM1_RANTE	P57104 rana tempor
11	20	29.4	12	2 Q9N2B8	Q9N2B8 pongo pygma
12	20	29.4	12	2 Q9N2B9	Q9N2B9 gorilla gor
13	20	29.4	12	2 Q9N2C0	Q9N2C0 pan troglod
14	20	29.4	12	2 Q7T862	Q7T862 latemouth
15	20	29.4	13	2 Q6S4R5	Q6S4R5 leishmania
16	19	27.9	9	1 NC34_STRAT	P83222 streptomyce
17	19	27.9	9	2 Q7RBS8	Q7RBS8 plasmodium
18	19	27.9	11	2 Q6QVDS	Q6QVDS phaseolus v
19	19	27.9	11	2 Q84073	Q84073 influenza a
20	19	27.9	12	1 UKA2_HUMAN	P31144 homo sapien
21	19	27.9	12	2 Q9XNR6	Q9XNR6 pyralisella 1
22	19	27.9	12	2 Q50959	Q50959 neisseria g
23	19	27.9	13	2 Q93824	Q93824 candida tro
24	19	27.9	13	2 Q86129	Q86129 vesicular s
25	18	26.5	7	2 Q8K3H6	Q8K3H6 rattus norv
26	18	26.5	10	1 SPI_HAIRO	Q10997 halocynthia
27	18	26.5	10	1 TKNI_SCTCA	P08608 scyllorhinu
28	18	26.5	10	2 Q7M500	Q7M500 aspergillus
29	18	26.5	10	2 Q51812	Q51812 plasmodi f.
30	18	26.5	11	1 ASL1_BACSE	P83146 bacteroides
31	18	26.5	11	2 Q703F4	Q703F4 mus acumin

32	18	26.5	12	2 Q6DKZ0	Q6DKZ0 homo sapien
33	18	26.5	12	2 Q9T2U3	Q9T2U3 bos taurus
34	18	26.5	12	2 Q945C3	Q945C3 cryptosporidi
35	18	26.5	12	2 Q83U71	Q83U71 salmonella
36	18	26.5	12	2 Q9R3B3	Q9R3B3 helicobacte
37	18	26.5	12	2 Q61331	Q61331 mus musculu
38	18	26.5	12	2 Q61D52	Q61D52 mus sp. cyc
39	18	26.5	13	2 Q7M2Z6	Q7M2Z6 ovis aries
40	18	26.5	13	2 Q9TU76	Q9TU76 ovis aries
41	18	26.5	13	2 Q86260	Q86260 klebsiella
42	18	26.5	13	2 Q9RSN5	Q9RSN5 clostridium
43	17	25.0	9	2 Q61DB5	Q61DB5 homo sapien
44	17	25.0	9	2 Q8MPT4	Q8MPT4 diadema ant
45	17	25.0	9	2 Q70T12	Q70T12 staphylococ

ALIGNMENTS

RESULT 1	ID	Q7WUG1	PRELIMINARY;	PRT;	10 AA.
AC	Q7WUG1				
DT	01-OCT-2003 (TREMBlrel. 25, Created)				
DT	01-OCT-2003 (TREMBlrel. 25, Last sequence update)				
DE	Probable ATP-binding component of ABC transporter (fragment).				
OS	Pseudomonas fluorescens.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;				
OC	Pseudomonadaceae; Pseudomonas.				
OX	NCBI_Taxid=294;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CHAO;				
RA	Pechy-Tarr M., Bottiglieri M., Bang Lejbolle K., Gigot-Bonnefoy C.,				
RA	Keel C.;				
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AY341911; AA017034.1; -				
DR	GO; GO:0005524; F:ATP binding; IEA.				
KW	ATP-binding.				
FT	NON TER				
SQ	SEQUENCE 10 AA; 1262 MW; 08EF18CB1E8773B CRC64;				
Query Match		41.2%	Score 28; DB 2; Length 10;		
Best Local Similarity		62.5%;	Pred. No. 1.3e+03;		
Matches	5; Conservative	1; Mismatches	2; Indels	0; Gaps	0;
QY	2 EKYLGSEY 9				
DB	1 EYVLGHEP 8				
RESULT 2					
ID	S015_BACSU	STANDARD;	PRT;	12 AA.	
AC	P80863;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DE	Superoxide-inducible protein 5 (S015) (Fragment).				
OS	Bacillus subtilis.				
OC	Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus.				
OX	NCBI_Taxid=1423;				
RN	[1]				
RP	SEQUENCE.				
RC	STRAIN=168 / ISS8;				
RX	MEDLINE=97443988; PubMed=9298659;				
RA	Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U., Hecker M.;				
RT	"First steps from a two-dimensional protein index towards a response-				
RT	regulation map for Bacillus subtilis.";				
RL	Electrophoresis 18:1451-1463 (1997).				
CC	-I- INDUCTION: By superoxide.				
CC	-I- CAUTION: Could not be found in the genome of B. subtilis 168.				

KW Direct protein sequencing.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1170 MW; 25718A96B37B1338 CRC64;

Query Match 38.2%; Score 26; DB 1; Length 12;
Best Local Similarity 55.6%; Pred. No. 3.2e+03;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 5 LGEEYVKAV 13
DB 4 LGKEGLKAI 12

RESULT 3

OS0038 PRELIMINARY; PRT; 13 AA.

AC Q50038; 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBlrel. 01, Last annotation update)
DE U22661.
OS Mycobacterium leprae.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.R.; Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Robison K.; Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U15182; AAA62970.1; -.
SQ SEQUENCE 13 AA; 1589 MW; C7CCD7E47D025B06 CRC64;

Query Match 33.8%; Score 23; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 1e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 EKYLGEE 8
DB 6 QEYLGEV 12

RESULT 4

Q6BCZ9 PRELIMINARY; PRT; 8 AA.

AC Q6BCZ9; 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Protein S (Fragment).
CN Name=PROS1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamabaki N.; "Protein S variant in Exon3,"
RT Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB162156; BAD36740.1; -.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 1108 MW; D33B53277B59DB5A CRC64;

Query Match 32.4%; Score 22; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 YEKYL 5

DB 4 YPKYL 8

RESULT 5

O90ZV5 PRELIMINARY; PRT; 8 AA.

AC Q90ZV5; 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Adenylate kinase (Fragment).
OS Fulica leucopeptera.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruliformes; Rallidae; Fulica.
OX NCBI_TaxID=156758;
RN [1]
RP SEQUENCE FROM N.A.
RA Shapiro L.H.; Dumbacher J.P.; "Adenylate kinase intron 5: a new nuclear locus for avian systematics,"
RT Auk 118:248-255(2001).
DR EMBL; AF307898; AAK43537.1; -.
DR GO; GO:0016301; F:kinase activity; IEA.
KW Kinase.
FT NON_TER 1 1
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 994 MW; 96333B19CB1B1866 CRC64;

Query Match 32.4%; Score 22; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 6 GEEYVK 11
DB 2 GEEFEK 7

RESULT 6

O6R7V4 PRELIMINARY; PRT; 10 AA.

AC Q6R7V4; 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
CN Name=GAPDH;
OS Carlia zuma.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidae;
OC Scincidae; Carlia.
OX NCBI_TaxID=260893;
RN [1]
RP SEQUENCE FROM N.A.
RA Doiman G.; Phillips B.; "Single copy nuclear DNA markers characterized for comparative phylogeography in Australian wet tropics rainforest skinks,"
RT Mol. Ecol. Notes 4:185-187(2004).
DR EMBL; AY508912; AAS09890.1; -.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1171 MW; 9D0AB2322C9C1EA CRC64;

Query Match 30.9%; Score 21; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.7e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 5 LGEEYVKAV 13
DB 1 LNDHFVKLV 9

RESULT 7

06T302
ID 06T302; PRELIMINARY; PRT; 11 AA.
AC 06T302;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE COX2B (Fragment).
GN Name=COX2B;
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
ON NCBI_TaxID=3055;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CC-2290;
RX MEDLINE=22570934; PubMed=12684385; DOI=10.1128/EC.2.2.362-379.2003;
RA Kachir P., Lavie M., Brazelton W.D., Haas N.A., Lefebvre P.A.,
RA Silflow C.D.;
RT "Molecular map of the Chlamydomonas reinhardtii nuclear genome."
RL Eukaryotic Cell 2:362-379(2003).
DR EMBL; AY439091; AAR14690.1; -.
FT NON_TER 1 1
FT SEQUENCE 11 AA; 1414 MW; 74EA69AD3322DB5B CRC64;
SQ

Query Match 30.9%; Score 21; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.9e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 EYVK 11
| | | |
| | | |
Db 4 EYVK 7

RESULT 8
ID 068LE0 PRELIMINARY; PRT; 11 AA.
AC 068LE0;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
GN Name=NADPH;
OS Pyricularia leuconora.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Formicariidae;
OC Pyricularia.
ON NCBI_TaxID=183187;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15283860;
RA Irestedt M., Fjeldsa J., Nylander J.A., Ericson P.G.;
RT "Phylogenetic relationships of typical antibodies (Thamophilidae) and
RT test of incongruence based on Bayes factors."
RL BMC Evol. Biol. 4:23-23(2004).
DR EMBL; AY677056; AAT96981.1; -.
FT NON_TER 1 1
FT SEQUENCE 11 AA; 1242 MW; 9D0AEB2622C9C1EA CRC64;
SQ

Query Match 30.9%; Score 21; DB 2; Length 11;
Best Local Similarity 44.4%; Pred. No. 1.9e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 LGBEYKAV 13
| : | | |
| : | | |
Db 2 LNDHFWKLV 10

RESULT 9
ID 068LE9 PRELIMINARY; PRT; 11 AA.
AC 068LE9;
ID 068LE9;
AC 068LE9;

DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Glyceraldehyde-3-phosphate dehydrogenase (Fragment).
GN Name=NADPH;
OS Myrmotherula fulviventris.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Thamophilidae;
OC Myrmotherula.
ON NCBI_TaxID=288045;
RX [1]
RP SEQUENCE FROM N.A.
RX PubMed=15283860;
RA Irestedt M., Fjeldsa J., Nylander J.A., Ericson P.G.;
RT "Phylogenetic relationships of typical antibodies (Thamophilidae) and
RT test of incongruence based on Bayes factors."
RL BMC Evol. Biol. 4:23-23(2004).
DR EMBL; AY677047; AAT96972.1; -.
FT NON_TER 1 1
FT SEQUENCE 11 AA; 1242 MW; 9D0AEB2622C9C1EA CRC64;
SQ

Query Match 30.9%; Score 21; DB 2; Length 11;
Best Local Similarity 44.4%; Pred. No. 1.9e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 LGBEYKAV 13
| : | | |
| : | | |
Db 2 LNDHFWKLV 10

RESULT 10
ID 068LE0 PRELIMINARY; PRT; 13 AA.
AC P57104;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Temporin L.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
ON NCBI_TaxID=8407;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=97175050; PubMed=9022710;
RA Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA Barra D.;
RT "Temporin, antimicrobial peptides from the European red frog Rana
RT temporaria."
RL Eur. J. Biochem. 242:788-792(1996).
CC -1- FUNCTION: Has antibacterial activity against Gram-negative and
CC Gram-positive bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
KW Brevinin subfamily.
KW Amidation; Amphibian defense peptide; Antibiotic;
KW Direct protein sequencing.
FT MOD_RES 13 13
FT SEQUENCE 13 AA; 1641 MW; 9EBDCB1FAFF7C325 CRC64;
SQ

Query Match 30.9%; Score 21; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.2e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 YEKVLG 6
| : | | |
| : | | |
Db 5 FSKFLG 10

RESULT 11

Q9N2B8
ID Q9N2B8 PRELIMINARY; PRT; 12 AA.
AC Q9N2B8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Indolethylamine N-methyltransferase (Fragment).
GN Name=INMT;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB041365; BAA94454.1; -
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Methyltransferase; Transferase.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1290 MW; CF079554917861A9 CRC64;

Query Match 29.4%; Score 20; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.9e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 GEEY 9
|:|:
Db 8 GDEY 11

RESULT 12
Q9N2B9
ID Q9N2B9 PRELIMINARY; PRT; 12 AA.
AC Q9N2B9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Indolethylamine N-methyltransferase (Fragment).
GN Name=INMT;
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Gorilla.
OX NCBI_TaxID=9593;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB041364; BAA94453.1; -
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Methyltransferase; Transferase.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1289 MW; CF0798E2917861A9 CRC64;

Query Match 29.4%; Score 20; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.9e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 GEEY 9
|:|:
Db 8 GDEY 11

RESULT 13
Q9N2C0
ID Q9N2C0 PRELIMINARY; PRT; 12 AA.
AC Q9N2C0;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Indolethylamine N-methyltransferase (Fragment).

GN Name=INMT;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Kitano T., Kobayakawa H., Saitou N.;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB041363; BAA94452.1; -
DR GO; GO:0008168; F:methyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
KW Methyltransferase; Transferase.
FT NON TER 12 12
SQ SEQUENCE 12 AA; 1289 MW; CF0798E2917861A9 CRC64;

Query Match 29.4%; Score 20; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.9e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 GEEY 9
|:|:
Db 8 GDEY 11

RESULT 14
Q7T862
ID Q7T862 PRELIMINARY; PRT; 12 AA.
AC Q7T862;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE NTPase I (Fragment).
OS Largemouth bass ranavirus.
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Ranavirus.
OX NCBI_TaxID=7956;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LMBasc;
RX MEDLINE=22768205; PubMed=12885900;
RX DOI=10.1128/JVI.77.16.8812-8818.2003;
RA Goldberg T.L., Coleman D.A., Grant E.C., Irendino K.R., Philipp D.P.;
RT "Strain variation in an emerging iridovirus of warm-water fishes.";
J. Virol. 77:8812-8818(2003).
DR EMBL; AY208993; AAP57096.1; -
FT NON TER 1 1
SQ SEQUENCE 12 AA; 1357 MW; 108D85D5F25B73B CRC64;

Query Match 29.4%; Score 20; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 2.9e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 EKYIGEY 9
|:|:
Db 3 EAYLSKLY 10

RESULT 15
Q6S4R5
ID Q6S4R5 PRELIMINARY; PRT; 13 AA.
AC Q6S4R5;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Alpha tubulin (Fragment).
OS Leishmania chagasi.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=44271;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MHOM/BR/00/1669;
RA Purdy J.E., Wilson M.E.;
Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY466450; AAR8132.1; -.
 FT NON TER 1 1
 SQ SEQUENCE 13 AA; 148 MW; 3F361B0689741B18 CRC64;
 Query Match 29.4%; Score 20; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 3.1e+04;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 5 LGGEYVK 11
 : ||| | :
 Db 5 MGEDVE 11

Search completed: November 1, 2005, 14:32:02
 Job time : 183 secs

THIS PAGE BLANK (USPTO)